

SEQUENCE LISTING

<110> Pompejus, Markus
Kroger, Burkhard
Schroder, Hartwig
Zelder, Oskar
Haberhauer, Gregor

<120> CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
METABOLIC PATHWAY PROTEINS

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<212> DNA

<213> Corynebacterium glutamicum

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<223> RXA02229

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                                         Leu Thr Ile Pro Phe
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Ala Lys Gly His Ala Thr Glu Asn Asp Phe Ile Ile Ile Pro Asp Glu
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Asp Ala Arg Leu Asp Leu Thr Pro Glu Met Val Val Thr Leu Cys Asp
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cgc cgc gcc ggg atc ggt gct gat ggt atc ctc cgc gtg gtt aaa gct 259
Arg Arg Ala Gly Ile Gly Ala Asp Gly Ile Leu Arg Val Val Lys Ala
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Ala Asp Val Glu Gly Ser Thr Val Asp Pro Ser Leu Trp Phe Met Asp
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Tyr Arg Asn Ala Asp Gly Ser Leu Ala Glu Met Cys Gly Asn Gly Val
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cgc ctg ttc gcg cac tgg ctg tac tcc cgc ggt ctt gtt gat aat acg 403
Arg Leu Phe Ala His Trp Leu Tyr Ser Arg Gly Leu Val Asp Asn Thr
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Ser Phe Asp Ile Gly Thr Arg Ala Gly Val Arg His Val Asp Ile Leu
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Gln Ala Asp Gln His Ser Ala Gln Val Arg Val Asp Met Gly Ile Pro

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Gly Leu Gly Val Asp Met Gly Asn Pro His Leu Ala Cys Val Val Pro			
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Gly Leu Ser Ala Ser Ala Leu Ala Asp Met Glu Leu Arg Ala Pro Thr			
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Phe Asp Gln Glu Phe Phe Pro His Gly Val Asn Val Glu Ile Val Thr			
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Glu Leu Glu Asp Asp Ala Val Ser Met Arg Val Trp Glu Arg Gly Val			
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Gly Glu Thr Arg Ser Cys Gly Thr Gly Thr Val Ala Ala Ala Cys Ala			
215	220	225	
gct tta gct gat gct gga ttg gga gaa ggc aca gct aaa gtg tgc gtt			835
Ala Leu Ala Asp Ala Gly Leu Gly Glu Gly Thr Ala Lys Val Cys Val			
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cca cgt ggg gaa gta gaa gtc cag atc ttt gac gac ggc tcc aca ctc			883
Pro Arg Gly Glu Val Glu Val Gln Ile Phe Asp Asp Gly Ser Thr Leu			
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acc ggc cca agc gcc atc atc gca ctc ggt gag gtg cag atc			925
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<213> Corynebacterium glutamicum

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 35 40 45

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Leu Trp Phe Met Asp Tyr Arg Asn Ala Asp Gly Ser Leu Ala Glu Met
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Leu	Val	Asp	Asn	Thr	Ser	Phe	Asp	Ile	Gly	Thr	Arg	Ala	Gly	Val	Arg	
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His	Val	Asp	Ile	Leu	Gln	Ala	Asp	Gln	His	Ser	Ala	Gln	Val	Arg	Val	
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Asp	Met	Gly	Ile	Pro	Asp	Val	Thr	Gly	Leu	Ser	Thr	Cys	Asp	Ile	Asn	
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Gly	Gln	Val	Phe	Ala	Gly	Leu	Gly	Val	Asp	Met	Gly	Asn	Pro	His	Leu	
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Ala	Cys	Val	Val	Pro	Gly	Leu	Ser	Ala	Ser	Ala	Leu	Ala	Asp	Met	Glu	
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Leu	Arg	Ala	Pro	Thr	Phe	Asp	Gln	Glu	Phe	Phe	Pro	His	Gly	Val	Asn	
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Val	Glu	Ile	Val	Thr	Glu	Leu	Glu	Asp	Asp	Ala	Val	Ser	Met	Arg	Val	
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Asp	Gly	Ser	Thr	Leu	Thr	Gly	Pro	Ser	Ala	Ile	Ile	Ala	Leu	Gly	Glu	
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<223> RXS02970
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                                                    Leu Ala Leu Lys Gly
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tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
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His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala	
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gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac	307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp	
55 60 65	
atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga	355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg	
70 75 80 85	
tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac	403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn	
90 95 100	
ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg	451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val	
105 110 115	
tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc	499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly	
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gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga	547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly	
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cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga	595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly	
150 155 160 165	
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Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr	
170 175 180	
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Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
185 190 195	
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Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys	
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cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
215 220 225	
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Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
230 235 240 245	
gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc	883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile	
250 255 260	

ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa 931
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 265 270 275

ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc 979
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 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile
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 345 350 355

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 375 380 385

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<213> Corynebacterium glutamicum

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 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
 65 70 75 80
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
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 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
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 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
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 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
 130 135 140
 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
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 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
 165 170 175
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
 180 185 190
 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
 195 200 205
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
 210 215 220
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
 225 230 235 240
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
 245 250 255
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
 260 265 270
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
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 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
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 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
 305 310 315 320
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
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Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
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Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
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Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
 370 375 380

Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala
 385 390 395 400

Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser
 405 410 415

Gly Asn Arg Phe His Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu
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 Leu Ala Leu Lys Gly
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 Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
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cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
 His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
 40 45 50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
 Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
 55 60 65

atg ggt tcc caa ctt gtc tgc gca aac tta ggc cac aac aac cct cga 355
 Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
 70 75 80 85

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Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn	
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Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val	
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tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc	499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly	
120 125 130	
gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga	547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly	
135 140 145	
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga	595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly	
150 155 160 165	
tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc	643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr	
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Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
185 190 195	
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Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys	
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His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
215 220 225	
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Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
230 235 240 245	
gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc	883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile	
250 255 260	
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa	931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys	
265 270 275	
ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc	979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile	
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acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc	1027
Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile	
295 300 305	
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Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser	
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375 380 385

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<213> *Corynebacterium glutamicum*

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Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
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Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
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His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
85 90 95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
100 105 110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
115 120 125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
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Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
145 150 155 160

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His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
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 180 185 190
 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Cys
 195 200 205
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
 210 215 220
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
 225 230 235 240
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
 245 250 255
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
 260 265 270
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
 275 280 285
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
 290 295 300
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
 305 310 315 320
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
 325 330 335
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
 340 345 350
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
 355 360 365
 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
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<222> (101)..(769)

<223> RXC02390

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Phe Gly Thr Leu Ile Leu Leu Asn Leu Val Gly Ser Leu Ser Pro Gly		
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Pro Asp Thr Phe Phe Leu Leu Arg Leu Ala Thr Arg Ser Arg Ala His		
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Ala Ile Ala Gly Val Ala Gly Ile Val Thr Gly Leu Thr Val Trp Val		
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acg ctg acg gtc gtg gga gca gcg gcg ctg ctc acc act tat ccg tcg	307	
Thr Leu Thr Val Val Gly Ala Ala Leu Leu Thr Thr Tyr Pro Ser		
	55 60 65	
att ctc gga atc atc cag ctc gtc ggc ggc acg tac cta agc ttc att	355	
Ile Leu Gly Ile Ile Gln Leu Val Gly Gly Thr Tyr Leu Ser Phe Ile		
	70 75 80 85	
ggg tac aag ttg ctg cgc tcg gcg tcg aga gag ctt atc gac gcc cgc	403	
Gly Tyr Lys Leu Leu Arg Ser Ala Ser Arg Glu Leu Ile Asp Ala Arg		
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Gln Phe Arg Phe Asn Ala Asp Ala Arg Pro Ile Pro Asp Ala Val Glu		
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Ala Leu Gly Thr Arg Thr Gln Val Tyr Arg Gln Gly Leu Ala Thr Asn		
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Ala Ile Leu Val Gln Thr Phe Val Thr Phe Ser Ala Val Cys Leu Ile		
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Val Ser Thr Glu Arg Val Arg Lys Ala Met Leu Arg Ala Gly Pro Trp		
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Phe Asp Leu Leu Ala Gly Val Val Phe Leu Val Val Gly Val Thr Leu		
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792

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 35 40 45
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 65 70 75 80
 Tyr Leu Ser Phe Ile Gly Tyr Lys Leu Leu Arg Ser Ala Ser Arg Glu
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 100 105 110
 Pro Asp Ala Val Glu Ala Leu Gly Thr Arg Thr Gln Val Tyr Arg Gln
 115 120 125
 Gly Leu Ala Thr Asn Leu Ser Asn Pro Lys Val Val Met Tyr Phe Ala
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 Ala Ile Leu Ala Pro Leu Met Pro Ala His Pro Ser Pro Val Leu Ala
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 Ala Val Cys Leu Ile Val Ser Thr Glu Arg Val Arg Lys Ala Met Leu
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Asn Pro Ala Glu Ile Asp Gln Val Leu Gly Gly Asp Gln Thr Gln Ile 10 15 20																
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Glu Ser Gly Glu Ser Thr Gly Ala Gly Asp Phe Asp His Cys Gln Thr 25 30 35																
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Gly Ala Asp Ala Asn Ala Ser Asp Asp Cys Arg Leu Tyr Tyr Thr Ser 40 45 50																
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Phe Ser Val Asn Glu Met Trp Gln Thr Leu Leu Pro Ala Gln Ala Gly 55 60 65																
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Ile Glu Tyr Thr Glu Pro Thr Leu Thr Leu Phe Lys Asn Ser Thr Gln 70 75 80 85																
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Thr Gly Cys Gly Phe Ala Ser Ala Ser Thr Gly Pro Phe Tyr Cys Pro 90 95 100																
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Ser Asp Gln Asp Ala Tyr Phe Asp Leu Thr Phe Phe Asp Gln Met Arg 105 110 115																
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Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln Met Tyr Ile Val Ala 120 125 130																
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His Glu Tyr Gly His His Val Gln Asn Leu Glu Gly Thr Leu Gly Leu 135 140 145																
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Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn Ala Val Lys Ile Glu 150 155 160 165																
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Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala Asn His Ser Ser Glu 170 175 180																
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Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu Ser Glu Leu Asp Ser 185 190 195																
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 cag cgc aaa gac gcg ttc ctc gcc ggc tac aac acc ggc cag atg agc 835
 Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn Thr Gly Gln Met Ser
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 gcc tgc gac ttc ctc ggc cgg ggc gtc tac aac gac gct taaagcattg 884
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 35 40 45
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 Pro Ala Gln Ala Gly Ile Glu Tyr Thr Glu Pro Thr Leu Thr Leu Phe
 65 70 75 80
 Lys Asn Ser Thr Gln Thr Gly Cys Gly Phe Ala Ser Ala Ser Thr Gly
 85 90 95
 Pro Phe Tyr Cys Pro Ser Asp Gln Asp Ala Tyr Phe Asp Leu Thr Phe
 100 105 110
 Phe Asp Gln Met Arg Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln
 115 120 125
 Met Tyr Ile Val Ala His Glu Tyr Gly His His Val Gln Asn Leu Glu
 130 135 140
 Gly Thr Leu Gly Leu Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn
 145 150 155 160
 Ala Val Lys Ile Glu Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala
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 Asn His Ser Ser Glu Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu
 180 185 190
 Ser Glu Leu Asp Ser Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp
 195 200 205
 Asn Ile Gln Gln Arg Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr
 210 215 220

His Gly Ser Ser Gln Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn
225 230 235 240

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<212> DNA

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Val Ser Arg Ile Tyr
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gac tgt gcc gac caa gac tcc cgt gca gca ggc cta aag gcg gct gtc 163
Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly Leu Lys Ala Ala Val
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gat gca gtc aaa gcc ggt cag ctc gtt gtc ctt ccc acg gat acc ctt 211
Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu Pro Thr Asp Thr Leu
25 30 35

tat gga ctc ggc tgc gac gct ttc aac aac gag gca gta gcc aac ctt 259
Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu Ala Val Ala Asn Leu
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ctg gcc acc aaa cac cgt ggc ccc gat atg ccc gtt cca gtg ctc gtc 307
Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro Val Pro Val Leu Val
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ggc agc tgg gac acc att caa gga ctt gtg cac tcc tat tct gcg cag 355
Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His Ser Tyr Ser Ala Gln
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gca aaa gcg ctt gtg gag gcg ttc tgg cct ggt gga ctg tcc atc atc 403
Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly Gly Leu Ser Ile Ile
90 95 100

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Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu Gly Asp Thr Arg Gly
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acc gta atg ctg cgc atg cca ctg cac cca gtt gcc att gaa ttg ctg 499
Thr Val Met Leu Arg Met Pro Leu His Pro Val Ala Ile Glu Leu Leu
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cgc caa acc gga cca atg gct gtc tcc tcc gcc aac atc tcc gga cat 547

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Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala Asn Ile Ser Gly His
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150                      155                      160                      165

gtc gct gtc tac ctc gat ggt ggc gaa tgc gcg ctg gcc acc cct tca    643
Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala Leu Ala Thr Pro Ser
                      170                      175                      180

acc atc gtg gat att tca ggc ccc gca cca aag att ttg cgt gag ggt    691
Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys Ile Leu Arg Glu Gly
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gcc atc agc gca gaa cgc gtt ggc gaa gta ctt gga gtg tcg gca gaa    739
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Ser Leu Arg
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Ala Val Ala Asn Leu Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro
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Val Pro Val Leu Val Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His
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Ser Tyr Ser Ala Gln Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly
          85                      90                      95

Gly Leu Ser Ile Ile Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu
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Gly Asp Thr Arg Gly Thr Val Met Leu Arg Met Pro Leu His Pro Val
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Ala Ile Glu Leu Leu Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala
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Asn Ile Ser Gly His Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln
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Gln Leu Asn Gln Asn Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala

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Leu Ala Thr	Pro Ser Thr Ile Val	Asp Ile Ser Gly	Pro Ala Pro Lys		
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 Met Ser Thr Glu Asp 5
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 Ile Val Val Val Ala Val Asp Gly Ser Asp Ala Ser Lys Gln Ala Val 20
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 Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly Ile Pro Leu Arg Leu 35
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 Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr Ala Glu Gly Met Val 50
 40 45
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 Pro Pro Gln Glu Leu Phe Asp Leu Gln Ala Glu Ala Leu Glu Lys 60 65
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 Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val Ala Pro Glu Ile Lys 70 75 80 85
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 Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile Asp Met Leu Leu Glu 90 95 100
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 Met Ser Pro Asp Ala Thr Met Ile Val Met Gly Ser Arg Gly Leu Gly 105 110 115
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 Gly Leu Ser Gly Met Val Met Gly Ser Val Ser Gly Ala Val Val Ser 120 125 130

cac gca aag tgt cca gtc gtt gtt gtc cgt gaa gac agc gca gtc aac 547
 His Ala Lys Cys Pro Val Val Val Val Arg Glu Asp Ser Ala Val Asn
 135 140 145

 gaa gac agc aag tac ggc cca gtc gtc gtc ggt gtg gat ggc tcc gaa 595
 Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly Val Asp Gly Ser Glu
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 Gly Ala Glu Leu Val Ala Val His Thr Trp Met Asp Met Gln Val Gln
 185 190 195

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 Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln Gln Trp Asp Glu Val
 200 205 210

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 215 220 225

 gaa aag tac cca agt gta acc gtc aag aag atc atc acc cgt gac cgc 835
 Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile Ile Thr Arg Asp Arg
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 cca gtt cgc gca ctt gca gaa gca tct gaa aac gcg cag ctc cta gtc 883
 Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn Ala Gln Leu Leu Val
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 Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly Met Leu Leu Gly Ser
 265 270 275

 acc tcc cgc gca ctg ctg caa tcc gca ccg tgc cca atg atg gtg gtt 979
 Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys Pro Met Met Val Val
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<211> 301

<212> PRT

<213> Corynebacterium glutamicum

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 35 40 45

Ala Glu Gly Met Val Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala

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Asp Met Leu Leu Glu Met Ser Pro Asp Ala Thr Met Ile Val Met Gly 100 105 110		
Ser Arg Gly Leu Gly Gly Leu Ser Gly Met Val Met Gly Ser Val Ser 115 120 125		
Gly Ala Val Val Ser His Ala Lys Cys Pro Val Val Val Val Arg Glu 130 135 140		
Asp Ser Ala Val Asn Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly 145 150 155 160		
Val Asp Gly Ser Glu Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala 165 170 175		
Glu Ala Glu Ala Arg Gly Ala Glu Leu Val Ala Val His Thr Trp Met 180 185 190		
Asp Met Gln Val Gln Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln 195 200 205		
Gln Trp Asp Glu Val Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg 210 215 220		
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Ile Thr Arg Asp Arg Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn 245 250 255		
Ala Gln Leu Leu Val Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly 260 265 270		
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<212> DNA

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Gln Leu Trp Gln Arg Glu Leu Cys Glu Ser Leu Asn Leu Arg Gly Arg		
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Asp Asp Cys Lys Ala Tyr Ile Lys Lys Thr Arg Glu Tyr Pro Gly Phe		
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Asn Arg Met Gln Phe Lys Trp Ser Glu Gly Gly Ala Glu Asp Phe Pro		
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Lys Leu Ser Val Lys Val Arg Asp Glu Ile Val Ala Phe Gly Ala Pro		
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Asp Glu Leu Lys Val Asp Glu Asn Gly Val Val Gly Gly Gly Val His		
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Leu Lys Pro Gln Gln Val Asn Glu Leu Val Glu Ala Arg Gly Asp Glu		
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Val Val Phe Phe Asp Gly Arg Asn Ala Met Glu Ala Gln Ile Gly Lys		
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Phe Lys Asp Ala Val Val Pro Asp Val Glu Thr Thr His Asp Phe Ile		
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170 175 180		
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Val Thr Tyr Cys Thr Gly Gly Ile Arg Cys Glu Ile Leu Ser Ser Leu		
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Val Arg Tyr Gly Glu Gln Phe Gly Asn Lys Gly Leu Trp Glu Gly Ser		
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 Lys Glu Val Gly His Cys Ile His Cys Asp Thr Pro Thr Asn Lys Phe
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 Glu His Cys Leu Asn Glu Asp Asp Cys Arg Glu Leu Val Leu Met Cys
 265 270 275
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 Pro Asp Cys Phe Ala Asn Val Glu Thr Arg His Cys Lys Arg Glu Arg
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 Val Gly Gly Asp Ile Asp Asp Cys Lys Ala Tyr Ile Lys Lys Thr Arg
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 65 70 75 80
 Ala Glu Asp Phe Pro Lys Leu Ser Val Lys Val Arg Asp Glu Ile Val
 85 90 95
 Ala Phe Gly Ala Pro Asp Glu Leu Lys Val Asp Glu Asn Gly Val Val
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 Gly Gly Gly Val His Leu Lys Pro Gln Gln Val Asn Glu Leu Val Glu
 115 120 125
 Ala Arg Gly Asp Glu Val Val Phe Phe Asp Gly Arg Asn Ala Met Glu
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 145 150 155 160
 Thr His Asp Phe Ile Ala Glu Ile Glu Ser Gly Lys Tyr Asp Asp Leu

165										170					175						
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Leu	Val	Leu	Met	Cys	Pro	Asp	Cys	Phe	Ala	Asn	Val	Glu	Thr	Arg	His						
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Cys	Lys	Arg	Glu	Arg	Cys	Ala	Ala	Ile	Ala	Ala	Asp	Phe	Ala	Glu	Gln						
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Gly	Ile	Asp	Pro	Leu	Val	Thr	Ser														
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<212> DNA

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<222> (101)..(1555)

<223> RXN00351

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				Met	Asp	Asp	Ser	Asn	
				1				5	

agc	ttt	gta	gtt	gtt	gct	aac	cgt	ctg	cca	gtg	gat	atg	act	gtc	cac	163
Ser	Phe	Val	Val	Val	Ala	Asn	Arg	Leu	Pro	Val	Asp	Met	Thr	Val	His	
				10					15					20		

cca	gat	ggt	agc	tat	agc	atc	tcc	ccc	agc	ccc	ggt	ggc	ctt	gtc	acg	211
Pro	Asp	Gly	Ser	Tyr	Ser	Ile	Ser	Pro	Ser	Pro	Gly	Gly	Leu	Val	Thr	
			25					30					35			

ggg	ctt	tcc	ccc	gtt	ctg	gaa	caa	cat	cgt	gga	tgt	tgg	gtc	gga	tgg	259
Gly	Leu	Ser	Pro	Val	Leu	Glu	Gln	His	Arg	Gly	Cys	Trp	Val	Gly	Trp	
		40					45					50				

cct	gga	act	gta	gat	gtt	gca	ccc	gaa	cca	ttt	cga	aca	gat	acg	ggt	307
Pro	Gly	Thr	Val	Asp	Val	Ala	Pro	Glu	Pro	Phe	Arg	Thr	Asp	Thr	Gly	

55	60	65	
gtt ttg ctg cac cct gtt gtc ctc act gca agt gac tat gaa ggc ttc			355
Val Leu Leu His Pro Val Val Leu Thr Ala Ser Asp Tyr Glu Gly Phe			
70	75	80	85
tac gag ggc ttt tca aac gca acg ctg tgg cct ctt ttc cac gat ctg			403
Tyr Glu Gly Phe Ser Asn Ala Thr Leu Trp Pro Leu Phe His Asp Leu			
	90	95	100
att gtt act ccg gtg tac aac acc gat tgg tgg cat gcg ttt cgg gag			451
Ile Val Thr Pro Val Tyr Asn Thr Asp Trp Trp His Ala Phe Arg Glu			
	105	110	115
gta aac ctc aag ttc gct gaa gcc gtg agc caa gtg gcg gca cac ggt			499
Val Asn Leu Lys Phe Ala Glu Ala Val Ser Gln Val Ala Ala His Gly			
	120	125	130
gcc act gtg tgg gtg cag gac tat cag ctg ttg ctg gtt cct ggc att			547
Ala Thr Val Trp Val Gln Asp Tyr Gln Leu Leu Leu Val Pro Gly Ile			
	135	140	145
ttg cgc cag atg cgc cct gat ttg aag atc ggt ttc ttc ctc cac att			595
Leu Arg Gln Met Arg Pro Asp Leu Lys Ile Gly Phe Phe Leu His Ile			
	150	155	160
ccc ttc cct tcc cct gat ctg ttc cgt cag ctg ccg tgg cgt gaa gag			643
Pro Phe Pro Ser Pro Asp Leu Phe Arg Gln Leu Pro Trp Arg Glu Glu			
	170	175	180
att gtt cga ggc atg ctg ggc gca gat ttg gtg gga ttc cat ttg gtt			691
Ile Val Arg Gly Met Leu Gly Ala Asp Leu Val Gly Phe His Leu Val			
	185	190	195
caa aac gca gaa aac ttc ctt gcg tta acc cag cag gtt gcc ggc act			739
Gln Asn Ala Glu Asn Phe Leu Ala Leu Thr Gln Gln Val Ala Gly Thr			
	200	205	210
gcc ggg tct cat gtg ggt cag ccg gac acc ttg cag gtc agt ggt gaa			787
Ala Gly Ser His Val Gly Gln Pro Asp Thr Leu Gln Val Ser Gly Glu			
	215	220	225
gca ttg gtg cgt gag att ggc gct cat gtt gaa acc gct gac gga agg			835
Ala Leu Val Arg Glu Ile Gly Ala His Val Glu Thr Ala Asp Gly Arg			
	230	235	240
cga gtt agc gtc ggg gcg ttc ccg atc tcg att gat gtt gaa atg ttt			883
Arg Val Ser Val Gly Ala Phe Pro Ile Ser Ile Asp Val Glu Met Phe			
	250	255	260
ggg gag gcg tcg aaa agc gcc gtt ctt gat ctt tta aaa acg ctc gac			931
Gly Glu Ala Ser Lys Ser Ala Val Leu Asp Leu Leu Lys Thr Leu Asp			
	265	270	275
gag ccg gaa acc gta ttc ctg ggc gtt gac cga ctg gac tac acc aag			979
Glu Pro Glu Thr Val Phe Leu Gly Val Asp Arg Leu Asp Tyr Thr Lys			
	280	285	290
ggc att ttg cag cgc ctg ctt gcg ttt gag gaa ctg ctg gaa tcc ggc			1027
Gly Ile Leu Gln Arg Leu Leu Ala Phe Glu Glu Leu Leu Glu Ser Gly			
	295	300	305

gcg ttg gag gcc gac aaa gct gtg ttg ctg cag gtc gcg acg cct tcg 1075
 Ala Leu Glu Ala Asp Lys Ala Val Leu Leu Gln Val Ala Thr Pro Ser
 310 315 320 325

 cgt gag cgc att gat cac tat cgt gtg tcg cgt tcg cag gtc gag gaa 1123
 Arg Glu Arg Ile Asp His Tyr Arg Val Ser Arg Ser Gln Val Glu Glu
 330 335 340

 gcc gtc ggc cgt atc aat ggt cgt ttc ggt cgc atg ggg cgt ccc gtg 1171
 Ala Val Gly Arg Ile Asn Gly Arg Phe Gly Arg Met Gly Arg Pro Val
 345 350 355

 gtg cat tat cta cac agg tca ttg agc aaa aat gat ctc cag gtg ctg 1219
 Val His Tyr Leu His Arg Ser Leu Ser Lys Asn Asp Leu Gln Val Leu
 360 365 370

 tat acc gca gcc gat gtc atg ctg gtt acg cct ttt aaa gac ggt atg 1267
 Tyr Thr Ala Ala Asp Val Met Leu Val Thr Pro Phe Lys Asp Gly Met
 375 380 385

 aac ttg gtg gct aaa gaa ttc gtg gcc aac cac cgc gac ggc act ggt 1315
 Asn Leu Val Ala Lys Glu Phe Val Ala Asn His Arg Asp Gly Thr Gly
 390 395 400 405

 gct ttg gtg ctg tcc gaa ttt gcc ggc gcg gcc act gag ctg acc ggt 1363
 Ala Leu Val Leu Ser Glu Phe Ala Gly Ala Ala Thr Glu Leu Thr Gly
 410 415 420

 gcg tat tta tgc aac cca ttt gat gtg gaa tcc atc aaa cgg caa atg 1411
 Ala Tyr Leu Cys Asn Pro Phe Asp Val Glu Ser Ile Lys Arg Gln Met
 425 430 435

 gtg gca gct gtc cat gat ttg aag cac aat ccg gaa tct gcg gca acg 1459
 Val Ala Ala Val His Asp Leu Lys His Asn Pro Glu Ser Ala Ala Thr
 440 445 450

 cga atg aaa acg aac agc gag cag gtc tat acc cac gac gtc aac gtg 1507
 Arg Met Lys Thr Asn Ser Glu Gln Val Tyr Thr His Asp Val Asn Val
 455 460 465

 tgg gct aat agt ttc ctg gat tgt ttg gca cag tcg gga gaa aac tca 1555
 Trp Ala Asn Ser Phe Leu Asp Cys Leu Ala Gln Ser Gly Glu Asn Ser
 470 475 480 485

 tgaaccgcgc acgaatcgcg acc 1578

<210> 18

<211> 485

<212> PRT

<213> Corynebacterium glutamicum

<400> 18

Met Asp Asp Ser Asn Ser Phe Val Val Val Ala Asn Arg Leu Pro Val
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Asp Met Thr Val His Pro Asp Gly Ser Tyr Ser Ile Ser Pro Ser Pro
 20 25 30

Gly Gly Leu Val Thr Gly Leu Ser Pro Val Leu Glu Gln His Arg Gly

35					40					45					
Cys	Trp	Val	Gly	Trp	Pro	Gly	Thr	Val	Asp	Val	Ala	Pro	Glu	Pro	Phe
50					55					60					
Arg	Thr	Asp	Thr	Gly	Val	Leu	Leu	His	Pro	Val	Val	Leu	Thr	Ala	Ser
65					70					75					80
Asp	Tyr	Glu	Gly	Phe	Tyr	Glu	Gly	Phe	Ser	Asn	Ala	Thr	Leu	Trp	Pro
				85					90					95	
Leu	Phe	His	Asp	Leu	Ile	Val	Thr	Pro	Val	Tyr	Asn	Thr	Asp	Trp	Trp
			100					105					110		
His	Ala	Phe	Arg	Glu	Val	Asn	Leu	Lys	Phe	Ala	Glu	Ala	Val	Ser	Gln
		115					120					125			
Val	Ala	Ala	His	Gly	Ala	Thr	Val	Trp	Val	Gln	Asp	Tyr	Gln	Leu	Leu
	130					135					140				
Leu	Val	Pro	Gly	Ile	Leu	Arg	Gln	Met	Arg	Pro	Asp	Leu	Lys	Ile	Gly
145					150					155					160
Phe	Phe	Leu	His	Ile	Pro	Phe	Pro	Ser	Pro	Asp	Leu	Phe	Arg	Gln	Leu
			165						170					175	
Pro	Trp	Arg	Glu	Glu	Ile	Val	Arg	Gly	Met	Leu	Gly	Ala	Asp	Leu	Val
			180					185					190		
Gly	Phe	His	Leu	Val	Gln	Asn	Ala	Glu	Asn	Phe	Leu	Ala	Leu	Thr	Gln
		195					200					205			
Gln	Val	Ala	Gly	Thr	Ala	Gly	Ser	His	Val	Gly	Gln	Pro	Asp	Thr	Leu
	210					215					220				
Gln	Val	Ser	Gly	Glu	Ala	Leu	Val	Arg	Glu	Ile	Gly	Ala	His	Val	Glu
225					230					235					240
Thr	Ala	Asp	Gly	Arg	Arg	Val	Ser	Val	Gly	Ala	Phe	Pro	Ile	Ser	Ile
				245					250					255	
Asp	Val	Glu	Met	Phe	Gly	Glu	Ala	Ser	Lys	Ser	Ala	Val	Leu	Asp	Leu
			260					265					270		
Leu	Lys	Thr	Leu	Asp	Glu	Pro	Glu	Thr	Val	Phe	Leu	Gly	Val	Asp	Arg
		275					280					285			
Leu	Asp	Tyr	Thr	Lys	Gly	Ile	Leu	Gln	Arg	Leu	Leu	Ala	Phe	Glu	Glu
	290					295					300				
Leu	Leu	Glu	Ser	Gly	Ala	Leu	Glu	Ala	Asp	Lys	Ala	Val	Leu	Leu	Gln
305					310					315					320
Val	Ala	Thr	Pro	Ser	Arg	Glu	Arg	Ile	Asp	His	Tyr	Arg	Val	Ser	Arg
				325					330					335	
Ser	Gln	Val	Glu	Glu	Ala	Val	Gly	Arg	Ile	Asn	Gly	Arg	Phe	Gly	Arg
			340					345					350		
Met	Gly	Arg	Pro	Val	Val	His	Tyr	Leu	His	Arg	Ser	Leu	Ser	Lys	Asn
		355					360					365			

Asp Leu Gln Val Leu Tyr Thr Ala Ala Asp Val Met Leu Val Thr Pro
 370 375 380
 Phe Lys Asp Gly Met Asn Leu Val Ala Lys Glu Phe Val Ala Asn His
 385 390 395 400
 Arg Asp Gly Thr Gly Ala Leu Val Leu Ser Glu Phe Ala Gly Ala Ala
 405 410 415
 Thr Glu Leu Thr Gly Ala Tyr Leu Cys Asn Pro Phe Asp Val Glu Ser
 420 425 430
 Ile Lys Arg Gln Met Val Ala Ala Val His Asp Leu Lys His Asn Pro
 435 440 445
 Glu Ser Ala Ala Thr Arg Met Lys Thr Asn Ser Glu Gln Val Tyr Thr
 450 455 460
 His Asp Val Asn Val Trp Ala Asn Ser Phe Leu Asp Cys Leu Ala Gln
 465 470 475 480
 Ser Gly Glu Asn Ser
 485

<210> 19
 <211> 1546
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1546)
 <223> FRXA00351

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 cgcaaagaag accacaaaga agtcttaagc cggatcttat atg gat gat tcc aat 115
 Met Asp Asp Ser Asn
 1 5
 agc ttt gta gtt gtt gct aac cgt ctg cca gtg gat atg act gtc cac 163
 Ser Phe Val Val Val Ala Asn Arg Leu Pro Val Asp Met Thr Val His
 10 15 20
 cca gat ggt agc tat agc atc tcc ccc agc ccc ggt ggc ctt gtc acg 211
 Pro Asp Gly Ser Tyr Ser Ile Ser Pro Ser Pro Gly Gly Leu Val Thr
 25 30 35
 ggg ctt tcc ccc gtt ctg gaa caa cat cgt gga tgt tgg gtc gga tgg 259
 Gly Leu Ser Pro Val Leu Glu Gln His Arg Gly Cys Trp Val Gly Trp
 40 45 50
 cct gga act gta gat gtt gca ccc gaa cca ttt cga aca gat acg ggt 307
 Pro Gly Thr Val Asp Val Ala Pro Glu Pro Phe Arg Thr Asp Thr Gly
 55 60 65
 gtt ttg ctg cac cct gtt gtc ctc act gca agt gac tat gaa ggc ttc 355
 Val Leu Leu His Pro Val Val Leu Thr Ala Ser Asp Tyr Glu Gly Phe

70	75	80	85	
tac gag ggc ttt tca aac gca acg ctg tgg cct ctt ttc cac gat ctg				403
Tyr Glu Gly Phe Ser Asn Ala Thr Leu Trp Pro Leu Phe His Asp Leu	90	95	100	
att gtt act ccg gtg tac aac acc gat tgg tgg cat gcg ttt cgg gag				451
Ile Val Thr Pro Val Tyr Asn Thr Asp Trp Trp His Ala Phe Arg Glu	105	110	115	
gta aac ctc aag ttc gct gaa gcc gtg agc caa gtg gcg gca cac ggt				499
Val Asn Leu Lys Phe Ala Glu Ala Val Ser Gln Val Ala Ala His Gly	120	125	130	
gcc act gtg tgg gtg cag gac tat cag ctg ttg ctg gtt cct ggc att				547
Ala Thr Val Trp Val Gln Asp Tyr Gln Leu Leu Leu Val Pro Gly Ile	135	140	145	
ttg cgc cag atg cgc cct gat ttg aag atc ggt ttc ttc ctc cac att				595
Leu Arg Gln Met Arg Pro Asp Leu Lys Ile Gly Phe Phe Leu His Ile	150	155	160	165
ccc ttc cct tcc cct gat ctg ttc cgt cag ctg ccg tgg cgt gaa gag				643
Pro Phe Pro Ser Pro Asp Leu Phe Arg Gln Leu Pro Trp Arg Glu Glu	170	175	180	
att gtt cga ggc atg ctg ggc gca gat ttg gtg gga ttc cat ttg gtt				691
Ile Val Arg Gly Met Leu Gly Ala Asp Leu Val Gly Phe His Leu Val	185	190	195	
caa aac gca gaa aac ttc ctt gcg tta acc cag cag gtt gcc ggc act				739
Gln Asn Ala Glu Asn Phe Leu Ala Leu Thr Gln Gln Val Ala Gly Thr	200	205	210	
gcc ggg tct cat gtg ggt cag ccg gac acc ttg cag gtc agt ggt gaa				787
Ala Gly Ser His Val Gly Gln Pro Asp Thr Leu Gln Val Ser Gly Glu	215	220	225	
gca ttg gtg cgt gag att ggc gct cat gtt gaa acc gct gac gga agg				835
Ala Leu Val Arg Glu Ile Gly Ala His Val Glu Thr Ala Asp Gly Arg	230	235	240	245
cga gtt agc gtc ggg gcg ttc ccg atc tcg att gat gtt gaa atg ttt				883
Arg Val Ser Val Gly Ala Phe Pro Ile Ser Ile Asp Val Glu Met Phe	250	255	260	
ggg gag gcg tcg aaa agc gcc gtt ctt gat ctt tta aaa acg ctc gac				931
Gly Glu Ala Ser Lys Ser Ala Val Leu Asp Leu Leu Lys Thr Leu Asp	265	270	275	
gag ccg gaa acc gta ttc ctg ggc gtt gac cga ctg gac tac acc aag				979
Glu Pro Glu Thr Val Phe Leu Gly Val Asp Arg Leu Asp Tyr Thr Lys	280	285	290	
ggc att ttg cag gcg ctg ctt gcg ttt gag gaa ctg ctg gaa tcc ggc				1027
Gly Ile Leu Gln Arg Leu Leu Ala Phe Glu Glu Leu Leu Glu Ser Gly	295	300	305	
gcg ttg gag gcc gac aaa gct gtg ttg ctg cag gtc gcg acg cct tcg				1075
Ala Leu Glu Ala Asp Lys Ala Val Leu Leu Gln Val Ala Thr Pro Ser	310	315	320	325

cgt gag cgc att gat cac tat cgt gtg tcg cgt tcg cag gtc gag gaa 1123
 Arg Glu Arg Ile Asp His Tyr Arg Val Ser Arg Ser Gln Val Glu Glu
 330 335 340

 gcc gtc ggc cgt atc aat ggt cgt ttc ggt cgc atg ggg cgt ccc gtg 1171
 Ala Val Gly Arg Ile Asn Gly Arg Phe Gly Arg Met Gly Arg Pro Val
 345 350 355

 gtg cat tat cta cac agg tca ttg agc aaa aat gat ctc cag gtg ctg 1219
 Val His Tyr Leu His Arg Ser Leu Ser Lys Asn Asp Leu Gln Val Leu
 360 365 370

 tat acc gca gcc gat gtc atg ctg gtt acg cct ttt aaa gac ggt atg 1267
 Tyr Thr Ala Ala Asp Val Met Leu Val Thr Pro Phe Lys Asp Gly Met
 375 380 385

 aac ttg gtg gct aaa gaa ttc gtg gcc aac cac cgc gac ggc act ggt 1315
 Asn Leu Val Ala Lys Glu Phe Val Ala Asn His Arg Asp Gly Thr Gly
 390 395 400 405

 gct ttg gtg ctg tcc gaa ttt gcc ggc gcg gcc act gag ctg acc ggt 1363
 Ala Leu Val Leu Ser Glu Phe Ala Gly Ala Ala Thr Glu Leu Thr Gly
 410 415 420

 gcg tat tta tgc aac cca ttt gat gtg gaa tcc atc aaa cgg caa atg 1411
 Ala Tyr Leu Cys Asn Pro Phe Asp Val Glu Ser Ile Lys Arg Gln Met
 425 430 435

 gtg gca gct gtc cat gat ttg aag cac aat ccg gaa tct gcg gca acg 1459
 Val Ala Ala Val His Asp Leu Lys His Asn Pro Glu Ser Ala Ala Thr
 440 445 450

 cga atg aaa acg aac agc gag cag gtc tat acc cac gac gtc aac gtg 1507
 Arg Met Lys Thr Asn Ser Glu Gln Val Tyr Thr His Asp Val Asn Val
 455 460 465

 tgg gct aat agt ttc ctg gat tgt ttg gca cag tcg gga 1546
 Trp Ala Asn Ser Phe Leu Asp Cys Leu Ala Gln Ser Gly
 470 475 480

<210> 20

<211> 482

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 20

Met Asp Asp Ser Asn Ser Phe Val Val Val Ala Asn Arg Leu Pro Val
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Asp Met Thr Val His Pro Asp Gly Ser Tyr Ser Ile Ser Pro Ser Pro
 20 25 30

Gly Gly Leu Val Thr Gly Leu Ser Pro Val Leu Glu Gln His Arg Gly
 35 40 45

Cys Trp Val Gly Trp Pro Gly Thr Val Asp Val Ala Pro Glu Pro Phe
 50 55 60

Arg Thr Asp Thr Gly Val Leu Leu His Pro Val Val Leu Thr Ala Ser

65		70		75		80
Asp Tyr Glu Gly Phe Tyr Glu Gly Phe Ser Asn Ala Thr Leu Trp Pro						
		85		90		95
Leu Phe His Asp Leu Ile Val Thr Pro Val Tyr Asn Thr Asp Trp Trp						
	100		105		110	
His Ala Phe Arg Glu Val Asn Leu Lys Phe Ala Glu Ala Val Ser Gln						
	115		120		125	
Val Ala Ala His Gly Ala Thr Val Trp Val Gln Asp Tyr Gln Leu Leu						
	130		135		140	
Leu Val Pro Gly Ile Leu Arg Gln Met Arg Pro Asp Leu Lys Ile Gly						
145		150		155		160
Phe Phe Leu His Ile Pro Phe Pro Ser Pro Asp Leu Phe Arg Gln Leu						
	165		170		175	
Pro Trp Arg Glu Glu Ile Val Arg Gly Met Leu Gly Ala Asp Leu Val						
	180		185		190	
Gly Phe His Leu Val Gln Asn Ala Glu Asn Phe Leu Ala Leu Thr Gln						
	195		200		205	
Gln Val Ala Gly Thr Ala Gly Ser His Val Gly Gln Pro Asp Thr Leu						
	210		215		220	
Gln Val Ser Gly Glu Ala Leu Val Arg Glu Ile Gly Ala His Val Glu						
225		230		235		240
Thr Ala Asp Gly Arg Arg Val Ser Val Gly Ala Phe Pro Ile Ser Ile						
	245		250		255	
Asp Val Glu Met Phe Gly Glu Ala Ser Lys Ser Ala Val Leu Asp Leu						
	260		265		270	
Leu Lys Thr Leu Asp Glu Pro Glu Thr Val Phe Leu Gly Val Asp Arg						
	275		280		285	
Leu Asp Tyr Thr Lys Gly Ile Leu Gln Arg Leu Leu Ala Phe Glu Glu						
	290		295		300	
Leu Leu Glu Ser Gly Ala Leu Glu Ala Asp Lys Ala Val Leu Leu Gln						
305		310		315		320
Val Ala Thr Pro Ser Arg Glu Arg Ile Asp His Tyr Arg Val Ser Arg						
	325		330		335	
Ser Gln Val Glu Glu Ala Val Gly Arg Ile Asn Gly Arg Phe Gly Arg						
	340		345		350	
Met Gly Arg Pro Val Val His Tyr Leu His Arg Ser Leu Ser Lys Asn						
	355		360		365	
Asp Leu Gln Val Leu Tyr Thr Ala Ala Asp Val Met Leu Val Thr Pro						
	370		375		380	
Phe Lys Asp Gly Met Asn Leu Val Ala Lys Glu Phe Val Ala Asn His						
385		390		395		400

Arg Asp Gly Thr Gly Ala Leu Val Leu Ser Glu Phe Ala Gly Ala Ala
 405 410 415

Thr Glu Leu Thr Gly Ala Tyr Leu Cys Asn Pro Phe Asp Val Glu Ser
 420 425 430

Ile Lys Arg Gln Met Val Ala Ala Val His Asp Leu Lys His Asn Pro
 435 440 445

Glu Ser Ala Ala Thr Arg Met Lys Thr Asn Ser Glu Gln Val Tyr Thr
 450 455 460

His Asp Val Asn Val Trp Ala Asn Ser Phe Leu Asp Cys Leu Ala Gln
 465 470 475 480

Ser Gly

<210> 21
 <211> 779
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(756)
 <223> RXA00873

<400> 21
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 Thr Ala Gln Trp Gly Ile Phe Leu Arg Asn His Asp Glu Leu Thr Leu
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gaa atg gtc tcc gat gag gaa cgc agc tac atg tac tcc caa ttc gcc 96
 Glu Met Val Ser Asp Glu Glu Arg Ser Tyr Met Tyr Ser Gln Phe Ala
 20 25 30

tcc gaa cct cgc atg cgc gcc aac gta gga atc cgc agg cgc ctt tcc 144
 Ser Glu Pro Arg Met Arg Ala Asn Val Gly Ile Arg Arg Arg Leu Ser
 35 40 45

cca ctg ctt gaa ggc gac cgc aac cag ctg gaa ctc ctt cac ggt ttg 192
 Pro Leu Leu Glu Gly Asp Arg Asn Gln Leu Glu Leu Leu His Gly Leu
 50 55 60

ttg ctg tct cta cct ggc tca ccc gtg ttg tat tac ggt gat gaa att 240
 Leu Leu Ser Leu Pro Gly Ser Pro Val Leu Tyr Tyr Gly Asp Glu Ile
 65 70 75 80

ggc atg ggc gac aat atc tgg ctc cac gac cgc gac gga gtg cgc acc 288
 Gly Met Gly Asp Asn Ile Trp Leu His Asp Arg Asp Gly Val Arg Thr
 85 90 95

ccc atg cag tgg tcc aac gac cgc aac ggt ggt ttc tcc aaa gct gat 336
 Pro Met Gln Trp Ser Asn Asp Arg Asn Gly Gly Phe Ser Lys Ala Asp
 100 105 110

cct gaa cgc ctg tac ctt cca gcg atc caa aat gat caa tac ggc tac 384
 Pro Glu Arg Leu Tyr Leu Pro Ala Ile Gln Asn Asp Gln Tyr Gly Tyr

115	120	125	
gcc caa gta aac gtg gaa agc caa ctc aac cgc gaa aac tcc ctg ctg			432
Ala Gln Val Asn Val Glu Ser Gln Leu Asn Arg Glu Asn Ser Leu Leu			
130	135	140	
cgc tgg ctc cga aac caa atc ctt atc cgc aag cag tac cgc gca ttt			480
Arg Trp Leu Arg Asn Gln Ile Leu Ile Arg Lys Gln Tyr Arg Ala Phe			
145	150	155	160
ggt gcc gga acc tac cgt gaa gtg tcc tcc acc aat gag tca gtg ttg			528
Gly Ala Gly Thr Tyr Arg Glu Val Ser Ser Thr Asn Glu Ser Val Leu			
165	170	175	
aca ttt tta cga gaa cac aag ggc caa acc att ttg tgt gtc aac aac			576
Thr Phe Leu Arg Glu His Lys Gly Gln Thr Ile Leu Cys Val Asn Asn			
180	185	190	
atg agc aaa tat cct cag gca gtc tcg ctt gat ttg cgt gaa ttt gca			624
Met Ser Lys Tyr Pro Gln Ala Val Ser Leu Asp Leu Arg Glu Phe Ala			
195	200	205	
gga cac acc cct cga gag atg tcg ggc ggg cag ctg ttc cct acc att			672
Gly His Thr Pro Arg Glu Met Ser Gly Gly Gln Leu Phe Pro Thr Ile			
210	215	220	
gct gaa cgg gag tgg att gtc act tta gcc cct cac gga ttc ttc tgg			720
Ala Glu Arg Glu Trp Ile Val Thr Leu Ala Pro His Gly Phe Phe Trp			
225	230	235	240
ttt gat ctc acc gcc gat gaa aag gac gat atg gaa tgagcattgg			766
Phe Asp Leu Thr Ala Asp Glu Lys Asp Asp Met Glu			
245	250		
ccaacacatc atc			779
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<211> 252			
<212> PRT			
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<400> 22			
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Glu Met Val Ser Asp Glu Glu Arg Ser Tyr Met Tyr Ser Gln Phe Ala			
20	25	30	
Ser Glu Pro Arg Met Arg Ala Asn Val Gly Ile Arg Arg Arg Leu Ser			
35	40	45	
Pro Leu Leu Glu Gly Asp Arg Asn Gln Leu Glu Leu Leu His Gly Leu			
50	55	60	
Leu Leu Ser Leu Pro Gly Ser Pro Val Leu Tyr Tyr Gly Asp Glu Ile			
65	70	75	80
Gly Met Gly Asp Asn Ile Trp Leu His Asp Arg Asp Gly Val Arg Thr			
85	90	95	

Pro Met Gln Trp Ser Asn Asp Arg Asn Gly Gly Phe Ser Lys Ala Asp
 100 105 110

Pro Glu Arg Leu Tyr Leu Pro Ala Ile Gln Asn Asp Gln Tyr Gly Tyr
 115 120 125

Ala Gln Val Asn Val Glu Ser Gln Leu Asn Arg Glu Asn Ser Leu Leu
 130 135 140

Arg Trp Leu Arg Asn Gln Ile Leu Ile Arg Lys Gln Tyr Arg Ala Phe
 145 150 155 160

Gly Ala Gly Thr Tyr Arg Glu Val Ser Ser Thr Asn Glu Ser Val Leu
 165 170 175

Thr Phe Leu Arg Glu His Lys Gly Gln Thr Ile Leu Cys Val Asn Asn
 180 185 190

Met Ser Lys Tyr Pro Gln Ala Val Ser Leu Asp Leu Arg Glu Phe Ala
 195 200 205

Gly His Thr Pro Arg Glu Met Ser Gly Gly Gln Leu Phe Pro Thr Ile
 210 215 220

Ala Glu Arg Glu Trp Ile Val Thr Leu Ala Pro His Gly Phe Phe Trp
 225 230 235 240

Phe Asp Leu Thr Ala Asp Glu Lys Asp Asp Met Glu
 245 250

<210> 23

<211> 1102

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1102)

<223> RXA00891

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 Val Leu Gln Thr Ser
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tgg cat ttc tct atc ctg gca ggc atg act gat acc tct ccg ttg aat 163
 Trp His Phe Ser Ile Leu Ala Gly Met Thr Asp Thr Ser Pro Leu Asn
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 Ser Gln Pro Ser Ala Asp His His Pro Asp His Ala Ala Arg Pro Val
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ctt gat gcc cac ggc ttg atc gtt gag cac gaa tcg gaa gag ttt cca 259
 Leu Asp Ala His Gly Leu Ile Val Glu His Glu Ser Glu Glu Phe Pro
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gtc ccc gca ccc gct ccc ggt gaa cag ccc tgg gag aag aaa aac cgc 307

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Glu	Trp	Tyr	Lys	Asp	Ala	Val	Phe	Tyr	Glu	Val	Leu	Val	Arg	Ala	Phe	
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Tyr	Asp	Pro	Glu	Gly	Asn	Gly	Val	Gly	Ser	Leu	Lys	Gly	Leu	Thr	Glu	
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Lys	Leu	Asp	Tyr	Ile	Gln	Trp	Leu	Gly	Val	Asp	Cys	Ile	Trp	Ile	Pro	
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Pro	Phe	Tyr	Asp	Ser	Pro	Leu	Arg	Asp	Gly	Gly	Tyr	Asp	Ile	Arg	Asn	
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Phe	Arg	Glu	Ile	Leu	Pro	Glu	Phe	Gly	Thr	Val	Asp	Asp	Phe	Val	Glu	
	135					140					145					
ctc	gtt	gac	cac	gcc	cac	cgc	cgt	ggc	ctg	cgt	gtt	atc	acc	gac	ttg	595
Leu	Val	Asp	His	Ala	His	Arg	Arg	Gly	Leu	Arg	Val	Ile	Thr	Asp	Leu	
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Val	Met	Asn	His	Thr	Ser	Asp	Gln	His	Ala	Trp	Phe	Gln	Glu	Ser	Arg	
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cgc	gac	cca	acc	ggc	ccc	tac	gga	gat	ttc	tat	gtg	tgg	agc	gat	gat	691
Arg	Asp	Pro	Thr	Gly	Pro	Tyr	Gly	Asp	Phe	Tyr	Val	Trp	Ser	Asp	Asp	
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ccc	acc	ctg	tac	aac	gaa	gcc	cgc	atc	atc	ttt	gta	gat	aca	gaa	gaa	739
Pro	Thr	Leu	Tyr	Asn	Glu	Ala	Arg	Ile	Ile	Phe	Val	Asp	Thr	Glu	Glu	
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Ser	Asn	Trp	Thr	Tyr	Asp	Pro	Val	Arg	Gly	Gln	Tyr	Phe	Trp	His	Arg	
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Phe	Phe	Ser	His	Gln	Pro	Asp	Leu	Asn	Tyr	Asp	Asn	Pro	Ala	Val	Gln	
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Gly	Phe	Arg	Leu	Asp	Ala	Val	Pro	Tyr	Leu	Phe	Glu	Arg	Glu	Gly	Thr	
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Asn	Gly	Glu	Asn	Leu	Lys	Glu	Thr	His	Asp	Phe	Leu	Lys	Leu	Cys	Arg	
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Ser	Val	Ile	Glu	Lys	Glu	Tyr	Pro	Gly	Arg	Ile	Leu	Leu	Ala	Glu	Ala	

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 Asn Gln Trp Pro Gln Asp Val Val Glu Tyr Phe Gly Glu Lys Asp Lys
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Ala Ala Arg Pro Val Leu Asp Ala His Gly Leu Ile Val Glu His Glu
 35 40 45

Ser Glu Glu Phe Pro Val Pro Ala Pro Ala Pro Gly Glu Gln Pro Trp
 50 55 60

Glu Lys Lys Asn Arg Glu Trp Tyr Lys Asp Ala Val Phe Tyr Glu Val
 65 70 75 80

Leu Val Arg Ala Phe Tyr Asp Pro Glu Gly Asn Gly Val Gly Ser Leu
 85 90 95

Lys Gly Leu Thr Glu Lys Leu Asp Tyr Ile Gln Trp Leu Gly Val Asp
 100 105 110

Cys Ile Trp Ile Pro Pro Phe Tyr Asp Ser Pro Leu Arg Asp Gly Gly
 115 120 125

Tyr Asp Ile Arg Asn Phe Arg Glu Ile Leu Pro Glu Phe Gly Thr Val
 130 135 140

Asp Asp Phe Val Glu Leu Val Asp His Ala His Arg Arg Gly Leu Arg
 145 150 155 160

Val Ile Thr Asp Leu Val Met Asn His Thr Ser Asp Gln His Ala Trp
 165 170 175

Phe Gln Glu Ser Arg Arg Asp Pro Thr Gly Pro Tyr Gly Asp Phe Tyr
 180 185 190

Val Trp Ser Asp Asp Pro Thr Leu Tyr Asn Glu Ala Arg Ile Ile Phe
 195 200 205

Val Asp Thr Glu Glu Ser Asn Trp Thr Tyr Asp Pro Val Arg Gly Gln
 210 215 220

Tyr Phe Trp His Arg Phe Phe Ser His Gln Pro Asp Leu Asn Tyr Asp
 225 230 235 240

Asn Pro Ala Val Gln Glu Ala Met Leu Asp Val Leu Arg Phe Trp Leu
 245 250 255

Asp Leu Gly Leu Asp Gly Phe Arg Leu Asp Ala Val Pro Tyr Leu Phe
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Glu Arg Glu Gly Thr Asn Gly Glu Asn Leu Lys Glu Thr His Asp Phe
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Leu Lys Leu Cys Arg Ser Val Ile Glu Lys Glu Tyr Pro Gly Arg Ile
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 Val Ala Leu Val Val
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cag aaa tat ggc ggt tcc tcg ctt gag agt gcg gaa cgc att aga aac 163
 Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala Glu Arg Ile Arg Asn
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 Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala Gly Asn Asp Val Val
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 Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp Glu Leu Leu Glu Leu
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gca gcg gca gtg aat ccc gtt ccg cca gct cgt gaa atg gat atg ctc 307
 Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg Glu Met Asp Met Leu
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ctg act gct ggt gag cgt att tct aac gct ctc gtc gcc atg gct att 355
 Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu Val Ala Met Ala Ile
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gag tcc ctt ggc gca gaa gcc caa tct ttc acg ggc tct cag gct ggt 403
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Phe	Glu	Glu	Met	Leu	Glu	Leu	Ala	Ala	Val	Gly	Ser	Lys	Ile	Leu	Val	
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Leu	Arg	Ser	Val	Glu	Tyr	Ala	Arg	Ala	Phe	Asn	Val	Pro	Leu	Arg	Val	
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Glu	Ala	Ala	Lys	Val	Phe	Arg	Ala	Leu	Ala	Asp	Ala	Glu	Ile	Asn	Ile	
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Asp	Met	Val	Leu	Gln	Asn	Val	Ser	Ser	Val	Glu	Asp	Gly	Thr	Thr	Asp	
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atc	acc	ttc	acc	tgc	cct	cgt	tcc	gac	ggc	cgc	cgc	gcg	atg	gag	atc	1075
Ile	Thr	Phe	Thr	Cys	Pro	Arg	Ser	Asp	Gly	Arg	Arg	Ala	Met	Glu	Ile	
310					315					320					325	
ttg	aag	aag	ctt	cag	gtt	cag	ggc	aac	tgg	acc	aat	gtg	ctt	tac	gac	1123
Leu	Lys	Lys	Leu	Gln	Val	Gln	Gly	Asn	Trp	Thr	Asn	Val	Leu	Tyr	Asp	
			330					335						340		
gac	cag	gtc	ggc	aaa	gtc	tcc	ctc	gtg	ggt	gct	ggc	atg	aag	tct	cac	1171

Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala Gly Met Lys Ser His
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 cca ggt gtt acc gca gag ttc atg gaa gct ctg cgc gat gtc aac gtg 1219
 Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu Arg Asp Val Asn Val
 360 365 370
 aac atc gaa ttg att tcc acc tct gag att cgt att tcc gtg ctg atc 1267
 Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg Ile Ser Val Leu Ile
 375 380 385
 cgt gaa gat gat ctg gat gct gct gca cgt gca ttg cat gag cag ttc 1315
 Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala Leu His Glu Gln Phe
 390 395 400 405
 cag ctg ggc ggc gaa gac gaa gcc gtc gtt tat gca ggc acc gga cgc 1363
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 Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
 35 40 45
 Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg
 50 55 60
 Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
 65 70 75 80
 Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
 85 90 95
 Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
 100 105 110
 Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
 115 120 125
 Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
 130 135 140
 Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala
 145 150 155 160
 Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
 165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
 180 185 190
 Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
 195 200 205
 Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
 210 215 220
 Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
 225 230 235 240
 Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
 245 250 255
 Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile
 260 265 270
 Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
 275 280 285
 Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
 290 295 300
 Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ser Asp Gly Arg
 305 310 315 320
 Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr
 325 330 335
 Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala
 340 345 350
 Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
 355 360 365
 Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
 370 375 380
 Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
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<212> DNA

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<222> (101)..(1132)

<223> RXA00533

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Val	Val	Gly	Ala	Thr	Gly	Gln	Val	Gly	Gln	Val	Met	Arg	Thr	Leu	Leu		
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gaa	gag	cgc	aat	ttc	cca	gct	gac	act	gtt	cgt	ttc	ttt	gct	tcc	cca		211
Glu	Glu	Arg	Asn	Phe	Pro	Ala	Asp	Thr	Val	Arg	Phe	Phe	Ala	Ser	Pro		
			25					30					35				
cgt	tcc	gca	ggc	cgt	aag	att	gaa	ttc	cgt	ggc	acg	gaa	atc	gag	gta		259
Arg	Ser	Ala	Gly	Arg	Lys	Ile	Glu	Phe	Arg	Gly	Thr	Glu	Ile	Glu	Val		
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gaa	gac	att	act	cag	gca	acc	gag	gag	tcc	ctc	aag	gac	atc	gac	gtt		307
Glu	Asp	Ile	Thr	Gln	Ala	Thr	Glu	Glu	Ser	Leu	Lys	Asp	Ile	Asp	Val		
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Ala	Leu	Phe	Ser	Ala	Gly	Gly	Thr	Ala	Ser	Lys	Gln	Tyr	Ala	Pro	Leu		
	70				75					80					85		
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Lys	Asp	Asp	Glu	Val	Pro	Leu	Ile	Val	Ser	Glu	Val	Asn	Pro	Ser	Asp		
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aag	gat	tcc	ctg	gtc	aag	ggc	att	att	gcg	aac	cct	aac	tgc	acc	acc		499
Lys	Asp	Ser	Leu	Val	Lys	Gly	Ile	Ile	Ala	Asn	Pro	Asn	Cys	Thr	Thr		
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atg	gct	gcg	atg	cca	gtg	ctg	aag	cca	ctt	cac	gat	gcc	gct	ggt	ctt		547
Met	Ala	Ala	Met	Pro	Val	Leu	Lys	Pro	Leu	His	Asp	Ala	Ala	Gly	Leu		
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gta	aag	ctt	cac	gtt	tcc	tct	tac	cag	gct	gtt	tcc	ggt	tct	ggt	ctt		595
Val	Lys	Leu	His	Val	Ser	Ser	Tyr	Gln	Ala	Val	Ser	Gly	Ser	Gly	Leu		
	150				155					160					165		
gca	ggt	gtg	gaa	acc	ttg	gca	aag	cag	gtt	gct	gca	ggt	gga	gac	cac		643
Ala	Gly	Val	Glu	Thr	Leu	Ala	Lys	Gln	Val	Ala	Ala	Val	Gly	Asp	His		
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aac	gtt	gag	ttc	gtc	cat	gat	gga	cag	gct	gct	gac	gca	ggc	gat	gtc		691
Asn	Val	Glu	Phe	Val	His	Asp	Gly	Gln	Ala	Ala	Asp	Ala	Gly	Asp	Val		
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cgc aac gaa tcc cgc aag att ctc ggt ctc cca gac ctc aag gtc tca 835
 Arg Asn Glu Ser Arg Lys Ile Leu Gly Leu Pro Asp Leu Lys Val Ser
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 ggc acc tgc gtc cgc gtg ccg gtt ttc acc ggc cac acg ctg acc att 883
 Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly His Thr Leu Thr Ile
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 cac gcc gaa ttc gac aag gca atc acc gtg gac cag gcg cag gag atc 931
 His Ala Glu Phe Asp Lys Ala Ile Thr Val Asp Gln Ala Gln Glu Ile
 265 270 275

 ttg ggt gcc gct tca ggc gtc aag ctt gtc gac gtc cca acc cca ctt 979
 Leu Gly Ala Ala Ser Gly Val Lys Leu Val Asp Val Pro Thr Pro Leu
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 gca gct gcc ggc att gac gaa tcc ctc gtt gga cgc atc cgt cag gac 1027
 Ala Ala Ala Gly Ile Asp Glu Ser Leu Val Gly Arg Ile Arg Gln Asp
 295 300 305

 tcc act gtc gac gat aac cgc ggt ctg gtt ctc gtc gta tct ggc gac 1075
 Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu Val Val Ser Gly Asp
 310 315 320 325

 aac ctc cgc aag ggt gct gcg cta aac acc atc cag atc gct gag ctg 1123
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<212> PRT

<213> Corynebacterium glutamicum

<400> 28

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 35 40 45

 Thr Glu Ile Glu Val Glu Asp Ile Thr Gln Ala Thr Glu Glu Ser Leu
 50 55 60

 Lys Asp Ile Asp Val Ala Leu Phe Ser Ala Gly Gly Thr Ala Ser Lys
 65 70 75 80

 Gln Tyr Ala Pro Leu Phe Ala Ala Ala Gly Ala Thr Val Val Asp Asn
 85 90 95

 Ser Ser Ala Trp Arg Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu
 100 105 110

 Val Asn Pro Ser Asp Lys Asp Ser Leu Val Lys Gly Ile Ile Ala Asn

115					120					125						
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Asp	Ala	Gly	Asp	Val	Gly	Pro	Tyr	Val	Ser	Pro	Ile	Ala	Tyr	Asn	Val	
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Leu	Pro	Phe	Ala	Gly	Asn	Leu	Val	Asp	Asp	Gly	Thr	Phe	Glu	Thr	Asp	
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Glu	Glu	Gln	Lys	Leu	Arg	Asn	Glu	Ser	Arg	Lys	Ile	Leu	Gly	Leu	Pro	
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Asp	Leu	Lys	Val	Ser	Gly	Thr	Cys	Val	Arg	Val	Pro	Val	Phe	Thr	Gly	
245					250					255						
His	Thr	Leu	Thr	Ile	His	Ala	Glu	Phe	Asp	Lys	Ala	Ile	Thr	Val	Asp	
260					265					270						
Gln	Ala	Gln	Glu	Ile	Leu	Gly	Ala	Ala	Ser	Gly	Val	Lys	Leu	Val	Asp	
275					280					285						
Val	Pro	Thr	Pro	Leu	Ala	Ala	Ala	Gly	Ile	Asp	Glu	Ser	Leu	Val	Gly	
290					295					300						
Arg	Ile	Arg	Gln	Asp	Ser	Thr	Val	Asp	Asp	Asn	Arg	Gly	Leu	Val	Leu	
305					310					315					320	
Val	Val	Ser	Gly	Asp	Asn	Leu	Arg	Lys	Gly	Ala	Ala	Leu	Asn	Thr	Ile	
325					330					335						
Gln	Ile	Ala	Glu	Leu	Leu	Val	Lys									
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 <213> Corynebacterium glutamicum

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Met	Thr	Thr	Ala	Ser	Ala	Thr	Gly	Ile	Ala	Thr	Leu	Thr	Ser	
1					5				10					

acc ggc gac gtc ctg gac gtg tgg tat cca gaa atc ggg tcc acc gac 158
 Thr Gly Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp
 15 20 25 30

cag tcc gcg ctc aca cct cta gaa ggc gtc gat gaa gat cga aac gtc 206
 Gln Ser Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val
 35 40 45

acc cgc aaa atc gtg acg aca act atc gac acc gac gca gcc ccc acc 254
 Thr Arg Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr
 50 55 60

gac acc tac gat gca tgg ctg cgc ctt cac ctc ctc tcc cac cgc gtt 302
 Asp Thr Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val
 65 70 75

ttc cgc cct cac acc atc aac cta gac ggc att ttc ggc ctc ctc aac 350
 Phe Arg Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn
 80 85 90

aat gtc gtg tgg acc aac ttc gga ccg tgc gca gtt gac ggt ttc gca 398
 Asn Val Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala
 95 100 105 110

ctc acc cgc gcg cgc ctg tca cgc cga ggc caa gtt acg gtt tat agc 446
 Leu Thr Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser
 115 120 125

gtc gac aag ttc cca cgc atg gtc gac tat gtg gtt ccc tcg ggc gtg 494
 Val Asp Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val
 130 135 140

cgc atc ggt gac gcc gac cgc gtc cga ctt ggc gcg tac ctg gca gat 542
 Arg Ile Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp
 145 150 155

ggc acc acc gtg atg cat gag ggc ttc gtg aac ttc aac gct ggc acg 590
 Gly Thr Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr
 160 165 170

ctc ggc gct tcc atg gtt 608
 Leu Gly Ala Ser Met Val
 175 180

<210> 30

<211> 180

<212> PRT

<213> Corynebacterium glutamicum

<400> 30

Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser Thr Gly
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 20 25 30

Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val Thr Arg
 35 40 45

Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr Asp Thr
 50 55 60
 Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val Phe Arg
 65 70 75 80
 Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn Asn Val
 85 90 95
 Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala Leu Thr
 100 105 110
 Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser Val Asp
 115 120 125
 Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val Arg Ile
 130 135 140
 Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp Gly Thr
 145 150 155 160
 Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr Leu Gly
 165 170 175
 Ala Ser Met Val
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 Val Asn Ser Glu Leu
 1 5
 aaa cca gga tta gat ctc ctc ggc gac cca att gtc ctt act caa cgt 163
 Lys Pro Gly Leu Asp Leu Leu Gly Asp Pro Ile Val Leu Thr Gln Arg
 10 15 20
 ttg gta gat ata ccg agt ccg tcg ggt cag gaa aag cag att gct gat 211
 Leu Val Asp Ile Pro Ser Pro Ser Gly Gln Glu Lys Gln Ile Ala Asp
 25 30 35
 gaa att gaa gat gcc ctt cgg aac ctt aat cta cct ggt gta gag gtc 259
 Glu Ile Glu Asp Ala Leu Arg Asn Leu Asn Leu Pro Gly Val Glu Val
 40 45 50
 ttc cgc ttc aac aac aac gtt ctt gct cgc acg aac agg gga ttg gcc 307
 Phe Arg Phe Asn Asn Asn Val Leu Ala Arg Thr Asn Arg Gly Leu Ala
 55 60 65

tcg agg gtc atg ctt gct ggt cat atc gat aca gtg ccg atc gcg gac	355
Ser Arg Val Met Leu Ala Gly His Ile Asp Thr Val Pro Ile Ala Asp	
70 75 80 85	
aat ctg cca agc cgt gtg gaa gac ggc atc atg tat ggc tgt ggc acc	403
Asn Leu Pro Ser Arg Val Glu Asp Gly Ile Met Tyr Gly Cys Gly Thr	
90 95 100	
gtc gat atg aaa tct ggg ttg gcg gtg tat ttg cat act ttt gcc acc	451
Val Asp Met Lys Ser Gly Leu Ala Val Tyr Leu His Thr Phe Ala Thr	
105 110 115	
ttg gcc acg tcg act gag ctt aaa cat gat ctg acg ctg att gcg tat	499
Leu Ala Thr Ser Thr Glu Leu Lys His Asp Leu Thr Leu Ile Ala Tyr	
120 125 130	
gag tgc gag gaa gtt gct gat cac ctc aat ggt ttg ggc cac att cgc	547
Glu Cys Glu Glu Val Ala Asp His Leu Asn Gly Leu Gly His Ile Arg	
135 140 145	
gat gag cat ccg gag tgg ttg gcg gct gat ttg gcg ttg ttg ggt gag	595
Asp Glu His Pro Glu Trp Leu Ala Ala Asp Leu Ala Leu Leu Gly Glu	
150 155 160 165	
cct act ggc ggc tgg att gag gcg ggc tgc cag ggc aat ctg cgc atc	643
Pro Thr Gly Gly Trp Ile Glu Ala Gly Cys Gln Gly Asn Leu Arg Ile	
170 175 180	
aag gtg acg gcg cat ggt gtg cgt gcc cat tcg gcg aga agc tgg ttg	691
Lys Val Thr Ala His Gly Val Arg Ala His Ser Ala Arg Ser Trp Leu	
185 190 195	
ggt gat aat gcg atg cat aag ttg tcg ccg atc att tcg aag gtt gct	739
Gly Asp Asn Ala Met His Lys Leu Ser Pro Ile Ile Ser Lys Val Ala	
200 205 210	
gcg tat aag gcc gca gaa gtc aac att gat ggc ttg acc tac cgt gaa	787
Ala Tyr Lys Ala Ala Glu Val Asn Ile Asp Gly Leu Thr Tyr Arg Glu	
215 220 225	
ggc ctc aac atc gtt ttc tgc gaa tcg ggc gtg gca aac aac gtc att	835
Gly Leu Asn Ile Val Phe Cys Glu Ser Gly Val Ala Asn Asn Val Ile	
230 235 240 245	
cca gac ctc gcg tgg atg aac ctc aac ttc cgt ttc gcg ccg aat cgc	883
Pro Asp Leu Ala Trp Met Asn Leu Asn Phe Arg Phe Ala Pro Asn Arg	
250 255 260	
gat ctc aac gag gcg atc gag cat gtc gtc gaa acg ctt gag ctt gac	931
Asp Leu Asn Glu Ala Ile Glu His Val Val Glu Thr Leu Glu Leu Asp	
265 270 275	
ggt caa gac ggc atc gaa tgg gcc gta gaa gac ggg gca ggc ggt gcc	979
Gly Gln Asp Gly Ile Glu Trp Ala Val Glu Asp Gly Ala Gly Gly Ala	
280 285 290	
ctt cca ggc ttg ggg cag cag gtg aca agc ggg ctt atc gac gcc gtc	1027
Leu Pro Gly Leu Gly Gln Gln Val Thr Ser Gly Leu Ile Asp Ala Val	
295 300 305	
ggc cgc gaa aaa atc cgc gca aaa ttc ggc tgg acc gat gtc tca cgt	1075

Gly Arg Glu Lys Ile Arg Ala Lys Phe Gly Trp Thr Asp Val Ser Arg
 310 315 320 325

ttt tca gcc atg gga att cca gcc cta aac ttt ggc gct ggt gat cca 1123
 Phe Ser Ala Met Gly Ile Pro Ala Leu Asn Phe Gly Ala Gly Asp Pro
 330 335 340

agt ttc gcg cat aaa cgc gac gag cag tgc cca gtg gag caa atc acg 1171
 Ser Phe Ala His Lys Arg Asp Glu Gln Cys Pro Val Glu Gln Ile Thr
 345 350 355

gat gtg gca gca att ttg aag cag tac ctg agc gag taaccgcatt 1217
 Asp Val Ala Ala Ile Leu Lys Gln Tyr Leu Ser Glu
 360 365

cgggggttatc gtg 1230

<210> 32
 <211> 369
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 32
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Val Leu Thr Gln Arg Leu Val Asp Ile Pro Ser Pro Ser Gly Gln Glu
 20 25 30

Lys Gln Ile Ala Asp Glu Ile Glu Asp Ala Leu Arg Asn Leu Asn Leu
 35 40 45

Pro Gly Val Glu Val Phe Arg Phe Asn Asn Asn Val Leu Ala Arg Thr
 50 55 60

Asn Arg Gly Leu Ala Ser Arg Val Met Leu Ala Gly His Ile Asp Thr
 65 70 75 80

Val Pro Ile Ala Asp Asn Leu Pro Ser Arg Val Glu Asp Gly Ile Met
 85 90 95

Tyr Gly Cys Gly Thr Val Asp Met Lys Ser Gly Leu Ala Val Tyr Leu
 100 105 110

His Thr Phe Ala Thr Leu Ala Thr Ser Thr Glu Leu Lys His Asp Leu
 115 120 125

Thr Leu Ile Ala Tyr Glu Cys Glu Glu Val Ala Asp His Leu Asn Gly
 130 135 140

Leu Gly His Ile Arg Asp Glu His Pro Glu Trp Leu Ala Ala Asp Leu
 145 150 155 160

Ala Leu Leu Gly Glu Pro Thr Gly Gly Trp Ile Glu Ala Gly Cys Gln
 165 170 175

Gly Asn Leu Arg Ile Lys Val Thr Ala His Gly Val Arg Ala His Ser
 180 185 190

Ala Arg Ser Trp Leu Gly Asp Asn Ala Met His Lys Leu Ser Pro Ile

195					200					205					
Ile	Ser	Lys	Val	Ala	Ala	Tyr	Lys	Ala	Ala	Glu	Val	Asn	Ile	Asp	Gly
210					215					220					
Leu	Thr	Tyr	Arg	Glu	Gly	Leu	Asn	Ile	Val	Phe	Cys	Glu	Ser	Gly	Val
225					230					235					240
Ala	Asn	Asn	Val	Ile	Pro	Asp	Leu	Ala	Trp	Met	Asn	Leu	Asn	Phe	Arg
				245					250					255	
Phe	Ala	Pro	Asn	Arg	Asp	Leu	Asn	Glu	Ala	Ile	Glu	His	Val	Val	Glu
			260					265					270		
Thr	Leu	Glu	Leu	Asp	Gly	Gln	Asp	Gly	Ile	Glu	Trp	Ala	Val	Glu	Asp
		275					280					285			
Gly	Ala	Gly	Gly	Ala	Leu	Pro	Gly	Leu	Gly	Gln	Gln	Val	Thr	Ser	Gly
290					295					300					
Leu	Ile	Asp	Ala	Val	Gly	Arg	Glu	Lys	Ile	Arg	Ala	Lys	Phe	Gly	Trp
305					310					315					320
Thr	Asp	Val	Ser	Arg	Phe	Ser	Ala	Met	Gly	Ile	Pro	Ala	Leu	Asn	Phe
				325					330					335	
Gly	Ala	Gly	Asp	Pro	Ser	Phe	Ala	His	Lys	Arg	Asp	Glu	Gln	Cys	Pro
			340					345					350		
Val	Glu	Gln	Ile	Thr	Asp	Val	Ala	Ala	Ile	Leu	Lys	Gln	Tyr	Leu	Ser
		355					360					365			

Glu

<210> 33
 <211> 1059
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1036)
 <223> RXA00044

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ttctcacccg cactcggttcc ctcaaccac aaggagcacc atg gct tcc gca act 115
 Met Ala Ser Ala Thr
 1 5

ttc acc ggc gtg atc cca ccc gta atg acc cca ctc cac gcc gac ggc 163
 Phe Thr Gly Val Ile Pro Pro Val Met Thr Pro Leu His Ala Asp Gly
 10 15 20

agt gtg gat gta gaa agc ctc cgc aag ctc gtt gac cac ctc atc aat 211
 Ser Val Asp Val Glu Ser Leu Arg Lys Leu Val Asp His Leu Ile Asn
 25 30 35

ggt ggc gtc gac gga ctt ttc gca ctg ggc tcc tca ggc gaa gcg gca	259
Gly Gly Val Asp Gly Leu Phe Ala Leu Gly Ser Ser Gly Glu Ala Ala	
40 45 50	
ttc ctc acc cgc gcc cag cgc aaa ctc gca ctg acc acc atc atc gag	307
Phe Leu Thr Arg Ala Gln Arg Lys Leu Ala Leu Thr Thr Ile Ile Glu	
55 60 65	
cac acc gca ggc cgc gtt ccc gta act gct ggt gtc att gaa acc acc	355
His Thr Ala Gly Arg Val Pro Val Thr Ala Gly Val Ile Glu Thr Thr	
70 75 80 85	
act gct cgc gtg att gag ctc gtg gaa gat gcc ctg gag gct ggt gcc	403
Thr Ala Arg Val Ile Glu Leu Val Glu Asp Ala Leu Glu Ala Gly Ala	
90 95 100	
gaa ggc ctc gtt gcc act gca cct ttc tac acc cgc acc cac gat gtg	451
Glu Gly Leu Val Ala Thr Ala Pro Phe Tyr Thr Arg Thr His Asp Val	
105 110 115	
gaa att gaa gaa cac ttc cgc aag atc cac gcc gcc gct cca gag ctt	499
Glu Ile Glu Glu His Phe Arg Lys Ile His Ala Ala Ala Pro Glu Leu	
120 125 130	
cca ctg ttt gcc tac aac atc cca gtg tcg gtg cac tcc aac ctc aac	547
Pro Leu Phe Ala Tyr Asn Ile Pro Val Ser Val His Ser Asn Leu Asn	
135 140 145	
cca gtc atg ctt ttg acg ctg gcc aag gat ggc gtt ctt gca ggc acc	595
Pro Val Met Leu Leu Thr Leu Ala Lys Asp Gly Val Leu Ala Gly Thr	
150 155 160 165	
aag gat tcc agt ggc aat gat ggc gca atc cgc tca ctg atc gaa gct	643
Lys Asp Ser Ser Gly Asn Asp Gly Ala Ile Arg Ser Leu Ile Glu Ala	
170 175 180	
cgt gat gat gct gga ctc act gag cag ttc aag atc ctc acc ggc agc	691
Arg Asp Asp Ala Gly Leu Thr Glu Gln Phe Lys Ile Leu Thr Gly Ser	
185 190 195	
gaa acc acc gtt gat ttc gcc tac ctt gcg ggt gcc gat gga gtt gtc	739
Glu Thr Thr Val Asp Phe Ala Tyr Leu Ala Gly Ala Asp Gly Val Val	
200 205 210	
cca ggc ctg ggc aat gtt gat cct gca gca tac gca gct tta gca aaa	787
Pro Gly Leu Gly Asn Val Asp Pro Ala Ala Tyr Ala Ala Leu Ala Lys	
215 220 225	
ctc tgc ctc gat gga aag tgg gca gaa gct gct gct ttg cag aag cgc	835
Leu Cys Leu Asp Gly Lys Trp Ala Glu Ala Ala Ala Leu Gln Lys Arg	
230 235 240 245	
atc aac cac ctc ttc cac atc gtc ttc gtg gga gac acc tcc cat atg	883
Ile Asn His Leu Phe His Ile Val Phe Val Gly Asp Thr Ser His Met	
250 255 260	
tcc gga tcc agc gct ggt ttg ggc ggt ttc aag aca gca ctc gca cac	931
Ser Gly Ser Ser Ala Gly Leu Gly Gly Phe Lys Thr Ala Leu Ala His	
265 270 275	
ctt ggc att att gaa tcc aat gcg atg gca gtt cct cac cag agc ctc	979

Leu Gly Ile Ile Glu Ser Asn Ala Met Ala Val Pro His Gln Ser Leu
 280 285 290

agc gac gaa gaa act gct cgc att cac gcc att gtt gat gaa ttc ctg 1027
 Ser Asp Glu Glu Thr Ala Arg Ile His Ala Ile Val Asp Glu Phe Leu
 295 300 305

tac acc gct taaggccac acctcatgac tga 1059
 Tyr Thr Ala
 310

<210> 34

<211> 312

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 34

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Leu His Ala Asp Gly Ser Val Asp Val Glu Ser Leu Arg Lys Leu Val
 20 25 30

Asp His Leu Ile Asn Gly Gly Val Asp Gly Leu Phe Ala Leu Gly Ser
 35 40 45

Ser Gly Glu Ala Ala Phe Leu Thr Arg Ala Gln Arg Lys Leu Ala Leu
 50 55 60

Thr Thr Ile Ile Glu His Thr Ala Gly Arg Val Pro Val Thr Ala Gly
 65 70 75 80

Val Ile Glu Thr Thr Thr Ala Arg Val Ile Glu Leu Val Glu Asp Ala
 85 90 95

Leu Glu Ala Gly Ala Glu Gly Leu Val Ala Thr Ala Pro Phe Tyr Thr
 100 105 110

Arg Thr His Asp Val Glu Ile Glu Glu His Phe Arg Lys Ile His Ala
 115 120 125

Ala Ala Pro Glu Leu Pro Leu Phe Ala Tyr Asn Ile Pro Val Ser Val
 130 135 140

His Ser Asn Leu Asn Pro Val Met Leu Leu Thr Leu Ala Lys Asp Gly
 145 150 155 160

Val Leu Ala Gly Thr Lys Asp Ser Ser Gly Asn Asp Gly Ala Ile Arg
 165 170 175

Ser Leu Ile Glu Ala Arg Asp Asp Ala Gly Leu Thr Glu Gln Phe Lys
 180 185 190

Ile Leu Thr Gly Ser Glu Thr Thr Val Asp Phe Ala Tyr Leu Ala Gly
 195 200 205

Ala Asp Gly Val Val Pro Gly Leu Gly Asn Val Asp Pro Ala Ala Tyr
 210 215 220

Ala Ala Leu Ala Lys Leu Cys Leu Asp Gly Lys Trp Ala Glu Ala Ala

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<212> DNA
<213> Corynebacterium glutamicum
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Met Gly Ile Lys Val															
1 5															
ggc gtt ctc gga gcc aaa ggc cgt gtt ggt caa act att gtg gca gca															163
Gly Val Leu Gly Ala Lys Gly Arg Val Gly Gln Thr Ile Val Ala Ala															
10 15 20															
gtc aat gag tcc gac gat ctg gag ctt gtt gca gag atc ggc gtc gac															211
Val Asn Glu Ser Asp Asp Leu Glu Leu Val Ala Glu Ile Gly Val Asp															
25 30 35															
gat gat ttg agc ctt ctg gta gac aac ggc gct gaa gtt gtc gtt gac															259
Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala Glu Val Val Val Asp															
40 45 50															
ttc acc act cct aac gct gtg atg ggc aac ctg gag ttc tgc atc aac															307
Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu Glu Phe Cys Ile Asn															
55 60 65															
aac ggc att tct gcg gtt gtt gga acc acg ggc ttc gat gat gct cgt															355
Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly Phe Asp Asp Ala Arg															
70 75 80 85															
ttg gag cag gtt cgc gac tgg ctt gaa gga aaa gac aat gtc ggt gtt															403
Leu Glu Gln Val Arg Asp Trp Leu Glu Gly Lys Asp Asn Val Gly Val															
90 95 100															
ctg atc gca cct aac ttt gct atc tct gcg gtg ttg acc atg gtc ttt															451
Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val Leu Thr Met Val Phe															

105					110					115					
tcc aag cag gct gcc cgc ttc ttc gaa tca gct gaa gtt att gag ctg	499														
Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala Glu Val Ile Glu Leu															
120 125 130															
cac cac ccc aac aag ctg gat gca cct tca ggc acc gcg atc cac act	547														
His His Pro Asn Lys Leu Asp Ala Pro Ser Gly Thr Ala Ile His Thr															
135 140 145															
gct cag ggc att gct gcg gca cgc aaa gaa gca ggc atg gac gca cag	595														
Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala Gly Met Asp Ala Gln															
150 155 160 165															
cca gat gcg acc gag cag gca ctt gag ggt tcc cgt ggc gca agc gta	643														
Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser Arg Gly Ala Ser Val															
170 175 180															
gat gga atc ccg gtt cat gca gtc cgc atg tcc ggc atg gtt gct cac	691														
Asp Gly Ile Pro Val His Ala Val Arg Met Ser Gly Met Val Ala His															
185 190 195															
gag caa gtt atc ttt ggc acc cag ggt cag acc ttg acc atc aag cag	739														
Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr Leu Thr Ile Lys Gln															
200 205 210															
gac tcc tat gat cgc aac tca ttt gca cca ggt gtc ttg gtg ggt gtg	787														
Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly Val Leu Val Gly Val															
215 220 225															
cgc aac att gca cag cac cca ggc cta gtc gta gga ctt gag cat tac	835														
Arg Asn Ile Ala Gln His Pro Gly Leu Val Val Gly Leu Glu His Tyr															
230 235 240 245															
cta ggc ctg taaaggctca tttcagcagc ggg	867														
Leu Gly Leu															

<210> 36

<211> 248

<212> PRT

<213> Corynebacterium glutamicum

<400> 36

Met Gly Ile Lys Val Gly Val Leu Gly Ala Lys Gly Arg Val Gly Gln
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Thr Ile Val Ala Ala Val Asn Glu Ser Asp Asp Leu Glu Leu Val Ala
20 25 30

Glu Ile Gly Val Asp Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala
35 40 45

Glu Val Val Val Asp Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu
50 55 60

Glu Phe Cys Ile Asn Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly
65 70 75 80

Phe Asp Asp Ala Arg Leu Glu Gln Val Arg Asp Trp Leu Glu Gly Lys

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<210> 37
<211> 873
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101) .. (850)  
<223> RXA00864
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<400> 37

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agcagcgggt ggaattttttt aaaaggagcg tttaaaggct gtg gcc gaa caa gtt 115
Val Ala Glu Gln Val
1 5

aaa ttg agc gtg gag ttg ata gcg tgc agt tct ttt act cca ccc gct 163
Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser Phe Thr Pro Pro Ala
10 15 20

gat gtt gag tgg tca act gat gtt gag ggc gcg gaa gca ctc gtc gag 211
Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala Glu Ala Leu Val Glu
25 30 35

ttt gcg ggt cgt gcc tgc tac gaa act ttt gat aag ccg aac cct cga 259
Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp Lys Pro Asn Pro Arg
40 45 50

act gct tcc aat gct gcg tat ctg cgc cac atc atg gaa gtg ggg cac 307
 Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile Met Glu Val Gly His
 55 60 65

act gct ttg ctt gag cat gcc aat gcc acg atg tat atc cga ggc att 355
 Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met Tyr Ile Arg Gly Ile
 70 75 80 85

tct cgg tcc gcg acc cat gaa ttg gtc cga cac cgc cat ttt tcc ttc 403
 Ser Arg Ser Ala Thr His Glu Leu Val Arg His Arg His Phe Ser Phe
 90 95 100

tct caa ctg tct cag cgt ttc gtg cac agc gga gaa tcg gaa gta gtg 451
 Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly Glu Ser Glu Val Val
 105 110 115

gtg ccc act ctc atc gat gaa gat ccg cag ttg cgt gaa ctt ttc atg 499
 Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu Arg Glu Leu Phe Met
 120 125 130

cac gcc atg gat gag tct cgg ttc gct ttc aat gag ctg ctt aat gcg 547
 His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn Glu Leu Leu Asn Ala
 135 140 145

ctg gaa gaa aaa ctt ggc gat gaa ccg aat gca ctt tta agg aaa aag 595
 Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala Leu Leu Arg Lys Lys
 150 155 160 165

cag gct cgt caa gca gct cgc gct gtg ctg ccc aac gct aca gag tcc 643
 Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro Asn Ala Thr Glu Ser
 170 175 180

aga atc gtg gtg tct gga aac ttc cgc acc tgg agg cat ttc att ggc 691
 Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp Arg His Phe Ile Gly
 185 190 195

atg cga gcc agt gaa cat gca gac gtc gaa atc cgc gaa gta gcg gta 739
 Met Arg Ala Ser Glu His Ala Asp Val Glu Ile Arg Glu Val Ala Val
 200 205 210

gaa tgt tta aga aag ctg cag gta gca gcg cca act gtt ttc ggt gat 787
 Glu Cys Leu Arg Lys Leu Gln Val Ala Ala Pro Thr Val Phe Gly Asp
 215 220 225

ttt gag att gaa act ttg gca gac gga tcg caa atg gca aca agc ccg 835
 Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln Met Ala Thr Ser Pro
 230 235 240 245

tat gtc atg gac ttt taacgcaaag ctcacaccca cga 873
 Tyr Val Met Asp Phe
 250

<210> 38

<211> 250

<212> PRT

<213> Corynebacterium glutamicum

<400> 38

Val Ala Glu Gln Val Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser

1	5	10	15
Phe Thr Pro Pro Ala Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala	20	25	30
Glu Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp	35	40	45
Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile	50	55	60
Met Glu Val Gly His Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met	65	70	75
Tyr Ile Arg Gly Ile Ser Arg Ser Ala Thr His Glu Leu Val Arg His	85	90	95
Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly	100	105	110
Glu Ser Glu Val Val Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu	115	120	125
Arg Glu Leu Phe Met His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn	130	135	140
Glu Leu Leu Asn Ala Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala	145	150	155
Leu Leu Arg Lys Lys Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro	165	170	175
Asn Ala Thr Glu Ser Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp	180	185	190
Arg His Phe Ile Gly Met Arg Ala Ser Glu His Ala Asp Val Glu Ile	195	200	205
Arg Glu Val Ala Val Glu Cys Leu Arg Lys Leu Gln Val Ala Ala Pro	210	215	220
Thr Val Phe Gly Asp Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln	225	230	235
Met Ala Thr Ser Pro Tyr Val Met Asp Phe	245	250	

<210> 39

<211> 608

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (69)..(608)

<223> RXA02843

<400> 39

cccattgcgc ggaggtcgca ccccttccga cttgaactga taggcgata gaaattattc 60

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tggacgtcatg act act gct tcc gca acc gga att gca aca ctg acc tcc 110
      Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser
          1              5              10

acc ggc gac gtc ctg gac gtg tgg tat cca gaa atc ggg tcc acc gac 158
Thr Gly Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp
  15              20              25              30

cag tcc gcg ctc aca cct cta gaa ggc gtc gat gaa gat cga aac gtc 206
Gln Ser Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val
          35              40              45

acc cgc aaa atc gtg acg aca act atc gac acc gac gca gcc ccc acc 254
Thr Arg Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr
          50              55              60

gac acc tac gat gca tgg ctg cgc ctt cac ctc ctc tcc cac cgc gtt 302
Asp Thr Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val
          65              70              75

ttc cgc cct cac acc atc aac cta gac ggc att ttc ggc ctc ctc aac 350
Phe Arg Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn
          80              85              90

aat gtc gtg tgg acc aac ttc gga ccg tgc gca gtt gac ggt ttc gca 398
Asn Val Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala
  95              100              105              110

ctc acc cgc gcg cgc ctg tca cgc cga ggc caa gtt acg gtt tat agc 446
Leu Thr Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser
          115              120              125

gtc gac aag ttc cca cgc atg gtc gac tat gtg gtt ccc tcg ggc gtg 494
Val Asp Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val
          130              135              140

cgc atc ggt gac gcc gac cgc gtc cga ctt ggc gcg tac ctg gca gat 542
Arg Ile Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp
          145              150              155

ggc acc acc gtg atg cat gag ggc ttc gtg aac ttc aac gct ggc acg 590
Gly Thr Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr
          160              165              170

ctc ggc gct tcc atg gtt
Leu Gly Ala Ser Met Val
175              180

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<210> 40

<211> 180

<212> PRT

<213> Corynebacterium glutamicum

<400> 40

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Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser Thr Gly
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Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp Gln Ser
          20              25              30

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Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val Thr Arg
 35 40 45

Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr Asp Thr
 50 55 60

Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val Phe Arg
 65 70 75 80

Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn Asn Val
 85 90 95

Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala Leu Thr
 100 105 110

Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser Val Asp
 115 120 125

Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val Arg Ile
 130 135 140

Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp Gly Thr
 145 150 155 160

Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr Leu Gly
 165 170 175

Ala Ser Met Val
 180

<210> 41
 <211> 1143
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1120)
 <223> RXN00355

<400> 41
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ggtcctgatg aaagagatgt ccctgaatca tcactaagt atg cat ctc ggt aag 115
 Met His Leu Gly Lys
 1 5

ctc gac cag gac agt gcc acc aca att ttg gag gat tac aag aac atg 163
 Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu Asp Tyr Lys Asn Met
 10 15 20

acc aac atc cgc gta gct atc gtg ggc tac gga aac ctg gga cgc agc 211
 Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly Asn Leu Gly Arg Ser
 25 30 35

gtc gaa aag ctt att gcc aag cag ccc gac atg gac ctt gta gga atc 259
 Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met Asp Leu Val Gly Ile
 40 45 50

ttc tcg cgc cgg gcc acc ctc gac aca aag acg cca gtc ttt gat gtc 307

Phe	Ser	Arg	Arg	Ala	Thr	Leu	Asp	Thr	Lys	Thr	Pro	Val	Phe	Asp	Val	
55						60					65					
gcc	gac	gtg	gac	aag	cac	gcc	gac	gac	gtg	gac	gtg	ctg	ttc	ctg	tgc	355
Ala	Asp	Val	Asp	Lys	His	Ala	Asp	Asp	Val	Asp	Val	Leu	Phe	Leu	Cys	
70					75				80						85	
atg	ggc	tcc	gcc	acc	gac	atc	cct	gag	cag	gca	cca	aag	ttc	gcg	cag	403
Met	Gly	Ser	Ala	Thr	Asp	Ile	Pro	Glu	Gln	Ala	Pro	Lys	Phe	Ala	Gln	
				90				95					100			
ttc	gcc	tgc	acc	gta	gac	acc	tac	gac	aac	cac	cgc	gac	atc	cca	cgc	451
Phe	Ala	Cys	Thr	Val	Asp	Thr	Tyr	Asp	Asn	His	Arg	Asp	Ile	Pro	Arg	
			105					110					115			
cac	cgc	cag	gtc	atg	aac	gaa	gcc	gcc	acc	gca	gcc	ggc	aac	gtt	gca	499
His	Arg	Gln	Val	Met	Asn	Glu	Ala	Ala	Thr	Ala	Ala	Gly	Asn	Val	Ala	
			120				125					130				
ctg	gtc	tct	acc	ggc	tgg	gat	cca	gga	atg	ttc	tcc	atc	aac	cgc	gtc	547
Leu	Val	Ser	Thr	Gly	Trp	Asp	Pro	Gly	Met	Phe	Ser	Ile	Asn	Arg	Val	
	135					140					145					
tac	gca	gcg	gca	gtc	tta	gcc	gag	cac	cag	cag	cac	acc	ttc	tgg	ggc	595
Tyr	Ala	Ala	Ala	Val	Leu	Ala	Glu	His	Gln	Gln	His	Thr	Phe	Trp	Gly	
150					155				160						165	
cca	ggt	ttg	tca	cag	ggc	cac	tcc	gat	gct	ttg	cga	cgc	atc	cct	ggc	643
Pro	Gly	Leu	Ser	Gln	Gly	His	Ser	Asp	Ala	Leu	Arg	Arg	Ile	Pro	Gly	
				170				175					180			
gtt	caa	aag	gca	gtc	cag	tac	acc	ctc	cca	tcc	gaa	gac	gcc	ctg	gaa	691
Val	Gln	Lys	Ala	Val	Gln	Tyr	Thr	Leu	Pro	Ser	Glu	Asp	Ala	Leu	Glu	
			185					190					195			
aag	gcc	cgc	cgc	ggc	gaa	gcc	ggc	gac	ctt	acc	gga	aag	caa	acc	cac	739
Lys	Ala	Arg	Arg	Gly	Glu	Ala	Gly	Asp	Leu	Thr	Gly	Lys	Gln	Thr	His	
		200					205					210				
aag	cgc	caa	tgc	ttc	gtg	gtt	gcc	gac	gcg	gcc	gat	cac	gag	cgc	atc	787
Lys	Arg	Gln	Cys	Phe	Val	Val	Ala	Asp	Ala	Ala	Asp	His	Glu	Arg	Ile	
	215					220					225					
gaa	aac	gac	atc	cgc	acc	atg	cct	gat	tac	ttc	gtt	ggc	tac	gaa	gtc	835
Glu	Asn	Asp	Ile	Arg	Thr	Met	Pro	Asp	Tyr	Phe	Val	Gly	Tyr	Glu	Val	
230					235					240					245	
gaa	gtc	aac	ttc	atc	gac	gaa	gca	acc	ttc	gac	tcc	gag	cac	acc	ggc	883
Glu	Val	Asn	Phe	Ile	Asp	Glu	Ala	Thr	Phe	Asp	Ser	Glu	His	Thr	Gly	
				250					255					260		
atg	cca	cac	ggt	ggc	cac	gtg	att	acc	acc	ggc	gac	acc	ggt	ggc	ttc	931
Met	Pro	His	Gly	Gly	His	Val	Ile	Thr	Thr	Gly	Asp	Thr	Gly	Gly	Phe	
			265					270					275			
aac	cac	acc	gtg	gaa	tac	atc	ctc	aag	ctg	gac	cga	aac	cca	gat	ttc	979
Asn	His	Thr	Val	Glu	Tyr	Ile	Leu	Lys	Leu	Asp	Arg	Asn	Pro	Asp	Phe	
		280					285					290				
acc	gct	tcc	tca	cag	atc	gct	ttc	ggt	cgc	gca	gct	cac	cgc	atg	aag	1027
Thr	Ala	Ser	Ser	Gln	Ile	Ala	Phe	Gly	Arg	Ala	Ala	His	Arg	Met	Lys	

295	300	305	
cag cag ggc caa agc gga gct ttc acc gtc ctc gaa gtt gct cca tac			1075
Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu Glu Val Ala Pro Tyr			
310	315	320	325
ctg ctc tcc cca gag aac ttg gac gat ctg atc gca cgc gac gtc			1120
Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile Ala Arg Asp Val			
	330	335	340
taatttagct cgaggggcaa gga			1143

<210> 42

<211> 340

<212> PRT

<213> Corynebacterium glutamicum

<400> 42

Met His Leu Gly Lys Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu			
1	5	10	15
Asp Tyr Lys Asn Met Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly			
	20	25	30
Asn Leu Gly Arg Ser Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met			
	35	40	45
Asp Leu Val Gly Ile Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr			
	50	55	60
Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp			
	65	70	75
Val Leu Phe Leu Cys Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala			
	85	90	95
Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His			
	100	105	110
Arg Asp Ile Pro Arg His Arg Gln Val Met Asn Glu Ala Ala Thr Ala			
	115	120	125
Ala Gly Asn Val Ala Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe			
	130	135	140
Ser Ile Asn Arg Val Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln			
	145	150	155
His Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu			
	165	170	175
Arg Arg Ile Pro Gly Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser			
	180	185	190
Glu Asp Ala Leu Glu Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr			
	195	200	205
Gly Lys Gln Thr His Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala			
	210	215	220

Asp His Glu Arg Ile Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe
 225 230 235 240
 Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp
 245 250 255
 Ser Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly
 260 265 270
 Asp Thr Gly Gly Phe Asn His Thr Val Glu Tyr Ile Leu Lys Leu Asp
 275 280 285
 Arg Asn Pro Asp Phe Thr Ala Ser Ser Gln Ile Ala Phe Gly Arg Ala
 290 295 300
 Ala His Arg Met Lys Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu
 305 310 315 320
 Glu Val Ala Pro Tyr Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile
 325 330 335
 Ala Arg Asp Val
 340

<210> 43
 <211> 958
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(958)
 <223> FRXA00352

<400> 43
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 ggtcctgatg aaagagatgt ccctgaatca tcactaagt atg cat ctc ggt aag 115
 Met His Leu Gly Lys
 1 5
 ctc gac cag gac agt gcc acc aca att ttg gag gat tac aag aac atg 163
 Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu Asp Tyr Lys Asn Met
 10 15 20
 acc aac atc cgc gta gct atc gtg ggc tac gga aac ctg gga cgc agc 211
 Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly Asn Leu Gly Arg Ser
 25 30 35
 gtc gaa aag ctt att gcc aag cag ccc gac atg gac ctt gta gga atc 259
 Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met Asp Leu Val Gly Ile
 40 45 50
 ttc tcg cgc cgg gcc acc ctc gac aca aag acg cca gtc ttt gat gtc 307
 Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr Pro Val Phe Asp Val
 55 60 65
 gcc gac gtg gac aag cac gcc gac gac gtg gac gtg ctg ttc ctg tgc 355
 Ala Asp Val Asp Lys His Ala Asp Asp Val Asp Val Leu Phe Leu Cys
 70 75 80 85

atg ggc tcc gcc acc gac atc cct gag cag gca cca aag ttc gcg cag	403
Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala Pro Lys Phe Ala Gln	
90 95 100	
ttc gcc tgc acc gta gac acc tac gac aac cac cgc gac atc cca cgc	451
Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His Arg Asp Ile Pro Arg	
105 110 115	
cac cgc cag gtc atg aac gaa gcc gcc acc gca gcc ggc aac gtt gca	499
His Arg Gln Val Met Asn Glu Ala Ala Thr Ala Ala Gly Asn Val Ala	
120 125 130	
ctg gtc tct acc ggc tgg gat cca gga atg ttc tcc atc aac cgc gtc	547
Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe Ser Ile Asn Arg Val	
135 140 145	
tac gca gcg gca gtc tta gcc gag cac cag cag cac acc ttc tgg ggc	595
Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln His Thr Phe Trp Gly	
150 155 160 165	
cca ggt ttg tca cag ggc cac tcc gat gct ttg cga cgc atc cct ggc	643
Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu Arg Arg Ile Pro Gly	
170 175 180	
gtt caa aag gca gtc cag tac acc ctc cca tcc gaa gac gcc ctg gaa	691
Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser Glu Asp Ala Leu Glu	
185 190 195	
aag gcc cgc cgc ggc gaa gcc ggc gac ctt acc gga aag caa acc cac	739
Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr Gly Lys Gln Thr His	
200 205 210	
aag cgc caa tgc ttc gtg gtt gcc gac gcg gcc gat cac gag cgc atc	787
Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala Asp His Glu Arg Ile	
215 220 225	
gaa aac gac atc cgc acc atg cct gat tac ttc gtt ggc tac gaa gtc	835
Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe Val Gly Tyr Glu Val	
230 235 240 245	
gaa gtc aac ttc atc gac gaa gca acc ttc gac tcc gag cac acc ggc	883
Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp Ser Glu His Thr Gly	
250 255 260	
atg cca cac ggt ggc cac gtg att acc acc ggc gac acc ggt ggc ttc	931
Met Pro His Gly Gly His Val Ile Thr Thr Gly Asp Thr Gly Gly Phe	
265 270 275	
aac cac acc gtg gaa tac atc ctc aag	958
Asn His Thr Val Glu Tyr Ile Leu Lys	
280 285	

<210> 44

<211> 286

<212> PRT

<213> Corynebacterium glutamicum

<400> 44

Met His Leu Gly Lys Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu

1	5	10	15
Asp Tyr Lys Asn Met Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly	20	25	30
Asn Leu Gly Arg Ser Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met	35	40	45
Asp Leu Val Gly Ile Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr	50	55	60
Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp	65	70	75
Val Leu Phe Leu Cys Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala	85	90	95
Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His	100	105	110
Arg Asp Ile Pro Arg His Arg Gln Val Met Asn Glu Ala Ala Thr Ala	115	120	125
Ala Gly Asn Val Ala Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe	130	135	140
Ser Ile Asn Arg Val Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln	145	150	155
His Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu	165	170	175
Arg Arg Ile Pro Gly Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser	180	185	190
Glu Asp Ala Leu Glu Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr	195	200	205
Gly Lys Gln Thr His Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala	210	215	220
Asp His Glu Arg Ile Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe	225	230	235
Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp	245	250	255
Ser Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly	260	265	270
Asp Thr Gly Gly Phe Asn His Thr Val Glu Tyr Ile Leu Lys	275	280	285

<210> 45

<211> 1400

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1377)

<223> RXA00972

<400> 45

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aca gtt gaa aat ttc aat gaa ctt ccc gca cac gta tgg cca cgc aat	96
Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro Arg Asn	
20 25 30	
gcc gtg cgc caa gaa gac ggc gtt gtc acc gtc gct ggt gtg cct ctg	144
Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val Pro Leu	
35 40 45	
cct gac ctc gct gaa gaa tac gga acc cca ctg ttc gta gtc gac gag	192
Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val Asp Glu	
50 55 60	
gac gat ttc cgt tcc cgc tgt cgc gac atg gct acc gca ttc ggt gga	240
Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe Gly Gly	
65 70 75 80	
cca ggc aat gtg cac tac gca tct aaa gcg ttc ctg acc aag acc att	288
Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys Thr Ile	
85 90 95	
gca cgt tgg gtt gat gaa gag ggg ctg gca ctg gac att gca tcc atc	336
Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala Ser Ile	
100 105 110	
aac gaa ctg ggc att gcc ctg gcc gct ggt ttc ccc gcc agc cgt atc	384
Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser Arg Ile	
115 120 125	
acc gcg cac ggc aac aac aaa ggc gta gag ttc ctg cgc gcg ttg gtt	432
Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala Leu Val	
130 135 140	
caa aac ggt gtg gga cac gtg gtg ctg gac tcc gca cag gaa cta gaa	480
Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu Leu Glu	
145 150 155 160	
ctg ttg gat tac gtt gcc gct ggt gaa ggc aag att cag gac gtg ttg	528
Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp Val Leu	
165 170 175	
atc cgc gta aag cca ggc atc gaa gca cac acc cac gag ttc atc gcc	576
Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe Ile Ala	
180 185 190	
act agc cac gaa gac cag aag ttc gga ttc tcc ctg gca tcc ggt tcc	624
Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser Gly Ser	
195 200 205	
gca ttc gaa gca gca aaa gcc gcc aac aac gca gaa aac ctg aac ctg	672
Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu Asn Leu	
210 215 220	
gtt ggc ctg cac tgc cac gtt ggt tcc cag gtg ttc gac gcc gaa ggc	720

Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala Glu Gly	
225 230 235 240	
ttc aag ctg gca gca gaa cgc gtg ttg ggc ctg tac tca cag atc cac	768
Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln Ile His	
245 250 255	
agc gaa ctg ggc gtt gcc ctt cct gaa ctg gat ctc ggt ggc gga tac	816
Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly Tyr	
260 265 270	
ggc att gcc tat acc gca gct gaa gaa cca ctc aac gtc gca gaa gtt	864
Gly Ile Ala Tyr Thr Ala Ala Glu Glu Pro Leu Asn Val Ala Glu Val	
275 280 285	
gcc tcc gac ctg ctc acc gca gtc gga aaa atg gca gcg gaa cta ggc	912
Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu Leu Gly	
290 295 300	
atc gac gca cca acc gtg ctt gtt gag ccc ggc cgc gct atc gca ggc	960
Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile Ala Gly	
305 310 315 320	
ccc tcc acc gtg acc atc tac gaa gtc ggc acc acc aaa gac gtc cac	1008
Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asp Val His	
325 330 335	
gta gac gac gac aaa acc cgc cgt tac atc gcc gtg gac gga ggc atg	1056
Val Asp Asp Asp Lys Thr Arg Arg Tyr Ile Ala Val Asp Gly Gly Met	
340 345 350	
tcc gac aac atc cgc cca gca ctc tac ggg tcc gaa tac gac gcc cgc	1104
Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp Ala Arg	
355 360 365	
gta gta tcc cgc ttc gcc gaa gga gac cca gta agc acc cgc atc gtg	1152
Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg Ile Val	
370 375 380	
ggc tcc cac tgc gaa tcc ggc gat atc ctg atc aac gat gaa atc tac	1200
Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu Ile Tyr	
385 390 395 400	
cca tct gac atc acc agc ggc gac ttc ctt gca ctc gca gcc acc ggc	1248
Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala Thr Gly	
405 410 415	
gca tac tgc tac gcc atg agc tcc cgc tac aac gcc ttc aca cgg ccc	1296
Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr Arg Pro	
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Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu Arg Arg	
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gaa acg ctc gac gac atc ctc tca cta gag gca taacgctttt cgacgcctga	1397
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Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val Asp Glu
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Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe Gly Gly
          65           70           75           80

Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys Thr Ile
          85           90           95

Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala Ser Ile
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Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser Arg Ile
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Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala Leu Val
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Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu Leu Glu
          145          150          155          160

Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp Val Leu
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Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe Ile Ala
          180          185          190

Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser Gly Ser
          195          200          205

Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu Asn Leu
          210          215          220

Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala Glu Gly
          225          230          235          240

Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln Ile His
          245          250          255

Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly Gly Tyr
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Gly Ile Ala Tyr Thr Ala Ala Glu Glu Pro Leu Asn Val Ala Glu Val
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Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu Leu Gly
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Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile Ala Gly
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Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asp Val His
 325 330 335

Val Asp Asp Asp Lys Thr Arg Arg Tyr Ile Ala Val Asp Gly Gly Met
 340 345 350

Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp Ala Arg
 355 360 365

Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg Ile Val
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Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu Ile Tyr
 385 390 395 400

Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala Thr Gly
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Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr Arg Pro
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 Met Ile Pro Lys Pro
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 Asp Val Thr Asp Leu Tyr Leu Glu Asp Leu Leu Asn Glu Gly Ser Glu
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aag att cgg tcc gcc aag gat ctt tcc gaa ctt agg aca gtt cta aaa 211
 Lys Ile Arg Ser Ala Lys Asp Leu Ser Glu Leu Arg Thr Val Leu Lys
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gag gtt tcc tcc caa att cag gaa cga gct ggg aaa aaa gat gaa gaa 259
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cgc	gct	tcc	tac	gaa	ggg	cgt	gac	agc	cta	atc	gga	ttt	gat	cac	tta	355
Arg	Ala	Ser	Tyr	Glu	Gly	Arg	Asp	Ser	Leu	Ile	Gly	Phe	Asp	His	Leu	
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Pro	Gly	Thr	Arg	Gly	Leu	Asp	Val	Ala	Ala	Asp	Gly	Thr	Val	Gln	Gly	
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Gln	Arg	His	Leu	Ala	Ala	Val	Gly	Arg	Met	Thr	Glu	Asp	Val	Val	Leu	
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Thr	Ser	Asp	Pro	Ala	Thr	Cys	Arg	His	Leu	Ile	Glu	Glu	Phe	Gly	Ser	
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Lys	Pro	Asp	Arg	Leu	Leu	Ala	Leu	Ala	Ile	Glu	Asn	Gly	Val	Ile	Ile	
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Ser	Val	Asp	Ser	Arg	Asp	Glu	Leu	Asp	Arg	Ile	Ser	Ala	Leu	Val	Gly	
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Phe	Tyr	Gln	Thr	Pro	Val	Arg	Gly	Asn	Trp	Leu	Lys	Asp	Val	Leu	Ser	
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gct atg aac cga acg cag tgc cgg act aca tcc gat gat ttt ctc att 1843
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 Asp Pro Leu His Ile Thr Asp Gly Asp Val Gly Glu Glu Ile Glu Ala
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tat cta gtg ggt gcc tac tgc atc gaa gat gag ctg att tta cgc cgg 1939
 Tyr Leu Val Gly Ala Tyr Cys Ile Glu Asp Glu Leu Ile Leu Arg Arg
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cga atc cgc ttc ccg aga gga gtc aaa cca gga gat atc atc gga att 1987
 Arg Ile Arg Phe Pro Arg Gly Val Lys Pro Gly Asp Ile Ile Gly Ile
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cct aac acc gca gga tac ttc atg cat atc ttg gaa agt gca tcg cac 2035
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 630 635 640 645

caa atc ccg ttg gcg aaa aat gta gtg tgg ccg gag ggg cag tta gac 2083
 Gln Ile Pro Leu Ala Lys Asn Val Val Trp Pro Glu Gly Gln Leu Asp
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 Lys Lys Asp Glu Glu Trp Gly Met Gly Ala Thr Trp Arg Glu Leu Tyr
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 Pro Ser Ile Val Glu Arg Ala Ser Tyr Glu Gly Arg Asp Ser Leu Ile
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 Gly Phe Asp His Leu Ala Arg Glu Met Glu Arg Leu Ala Phe Gly Pro
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Pro Ser Glu Ser Phe Glu Tyr Leu Gln Glu Leu Val Lys Ser Gly Val
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 Val Asp Ile Thr His Leu His Arg Gly Arg Glu Pro Leu Thr Asp Leu
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 Val Arg Glu Leu Glu Ile Thr Val Val Ile Asp Ala Val Leu Pro Pro
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 Pro Gly Val Val Pro Gly Thr Leu Val His Asn Leu Val Lys Glu Gly
 145 150 155 160
 Tyr Ala Arg Met Arg Pro Gly Thr Arg Gly Leu Asp Val Ala Ala Asp
 165 170 175
 Gly Thr Val Gln Gly Gln Arg His Leu Ala Ala Val Gly Arg Met Thr
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 Glu Asp Val Val Leu Gly Asn Asp Thr Leu Ser Arg Ser Leu His Asp
 195 200 205
 Ile Ile Pro Lys Trp Ala Arg Arg Val Ile Arg Asp Ala Ser Thr Tyr
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 Pro Asp Arg Val His Gly Thr Pro Pro Leu Pro Ala Arg Leu Glu Pro
 225 230 235 240
 Trp Ala Glu Lys Leu Thr Ser Asp Pro Ala Thr Cys Arg His Leu Ile
 245 250 255
 Glu Glu Phe Gly Ser Pro Val Asn Val Leu His Ser Gly Ser Met Pro
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 Arg Asn Ile Asn Glu Leu Val Asp Ala Gly Ile Gln Met Gly Val Asp
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 Thr Arg Ile Phe Phe Ala Arg Lys Ala Asn Lys Gly Leu Thr Phe Val
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 Asp Ala Val Lys Asp Thr Gly His Gly Val Asp Val Ala Ser Glu Arg
 305 310 315 320
 Glu Leu Ser Gln Val Leu Asn Arg Gly Val Pro Gly Glu Arg Ile Ile
 325 330 335
 Leu Ser Ala Ala Ile Lys Pro Asp Arg Leu Leu Ala Leu Ala Ile Glu
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 Asn Gly Val Ile Ile Ser Val Asp Ser Arg Asp Glu Leu Asp Arg Ile
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 Ser Ala Leu Val Gly Asp Arg Val Ala Arg Val Ala Pro Arg Val Ala
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 Pro Asp Pro Ala Val Leu Pro Pro Thr Arg Phe Gly Glu Arg Ala Ala
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 Asp Trp Gly Asn Arg Leu Thr Glu Val Ile Pro Gly Val Asp Ile Val
 405 410 415
 Gly Leu His Val His Leu His Gly Tyr Ala Ala Lys Asp Arg Ala Leu

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His	Ser	Pro	Gln	Phe	Ile	Asp	Leu	Gly	Gly	Gly	Val	Pro	Met	Ser	Tyr
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Leu	Arg	Leu	His	Ile	Glu	Pro	Gly	Arg	Ser	Leu	Leu	Asp	Gly	Cys	Gly
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Val	Thr	Leu	Ala	Glu	Val	Ala	Phe	Val	Lys	Thr	Arg	Ser	Asp	Gly	Leu
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Pro	Leu	Val	Gly	Leu	Ala	Met	Asn	Arg	Thr	Gln	Cys	Arg	Thr	Thr	Ser
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Asp	Asp	Phe	Leu	Ile	Asp	Pro	Leu	His	Ile	Thr	Asp	Gly	Asp	Val	Gly
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<222> (101)..(970)

<223> RXA01393

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	Met Asn Pro Ile Gln	
	1 5	
ctg gac act ttg ctc tca atc att gat gaa ggc agc ttc gaa ggc gcc	163	
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Ser Leu Ala Leu Ser Ile Ser Pro Ser Ala Val Ser Gln Arg Val Lys		
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Ala Leu Glu His His Val Gly Arg Val Leu Val Ser Arg Thr Gln Pro		
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Ala Lys Ala Thr Glu Ala Gly Glu Val Leu Val Gln Ala Ala Arg Lys		
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Trp Phe Pro Pro Val Phe Asn Glu Val Ala Ser Trp Gly Gly Ala Thr		
105 110 115		
ctc acg ctg cgc ttg gaa gat gaa gcg cac aca tta tcc ttg ctg cgg	499	
Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr Leu Ser Leu Leu Arg		
120 125 130		
cgt gga gat gtt tta gga gcg gta acc cgt gaa gct aat ccc gtg gcg	547	
Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu Ala Asn Pro Val Ala		
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gga tgt gaa gta gta gaa ctt gga acc atg cgc cac ttg gcc att gca	595	
Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg His Leu Ala Ile Ala		
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acc ccc tca ttg cgg gat gcc tac atg gtt gat ggg aaa cta gat tgg	643	
Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp Gly Lys Leu Asp Trp		
170 175 180		
gct gcg atg ccc gtc tta cgc ttc ggt ccc aaa gat gtg ctt caa gac	691	
Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys Asp Val Leu Gln Asp		
185 190 195		
cgt gac ctg gac ggg cgc gtc gat ggt cct gtg ggg cgc agg cgc gta	739	
Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val Gly Arg Arg Arg Val		
200 205 210		
tcc att gtc ccg tcg gcg gaa ggt ttt ggt gag gca att cgc cga ggc	787	
Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu Ala Ile Arg Arg Gly		
215 220 225		
ctt ggt tgg gga ctt ctt ccc gaa acc caa gct gct ccc atg cta aaa	835	

Leu Gly Trp Gly Leu Leu Pro Glu Thr Gln Ala Ala Pro Met Leu Lys
 230 235 240 245
 gca gga gaa gtg atc ctc ctc gat gag ata ccc att gac aca ccg atg 883
 Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro Ile Asp Thr Pro Met
 250 255 260
 tat tgg caa cga tgg cgc ctg gaa tct aga tct cta gct aga ctc aca 931
 Tyr Trp Gln Arg Trp Arg Leu Glu Ser Arg Ser Leu Ala Arg Leu Thr
 265 270 275
 gac gcc gtc gtt gat gca gca atc gag gga ttg cgg cct tagttacttc 980
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<212> PRT

<213> *Corynebacterium glutamicum*

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 Ser Gln Arg Val Lys Ala Leu Glu His His Val Gly Arg Val Leu Val
 35 40 45
 Ser Arg Thr Gln Pro Ala Lys Ala Thr Glu Ala Gly Glu Val Leu Val
 50 55 60
 Gln Ala Ala Arg Lys Met Val Leu Leu Gln Ala Glu Thr Lys Ala Gln
 65 70 75 80
 Leu Ser Gly Arg Leu Ala Glu Ile Pro Leu Thr Ile Ala Ile Asn Ala
 85 90 95
 Asp Ser Leu Ser Thr Trp Phe Pro Pro Val Phe Asn Glu Val Ala Ser
 100 105 110
 Trp Gly Gly Ala Thr Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr
 115 120 125
 Leu Ser Leu Leu Arg Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu
 130 135 140
 Ala Asn Pro Val Ala Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg
 145 150 155 160
 His Leu Ala Ile Ala Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp
 165 170 175
 Gly Lys Leu Asp Trp Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys
 180 185 190
 Asp Val Leu Gln Asp Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val

195	200	205
Gly Arg Arg Arg Val Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu		
210	215	220
Ala Ile Arg Arg Gly Leu Gly Trp Gly Leu Leu Pro Glu Thr Gln Ala		
225	230	235 240
Ala Pro Met Leu Lys Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro		
	245	250 255
Ile Asp Thr Pro Met Tyr Trp Gln Arg Trp Arg Leu Glu Ser Arg Ser		
	260	265 270
Leu Ala Arg Leu Thr Asp Ala Val Val Asp Ala Ala Ile Glu Gly Leu		
	275	280 285
Arg Pro		
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<210> 51
 <211> 1626
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1603)
 <223> RXA00241

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 Val Asn Thr Gln Ser
 1 5
 gat tct gcg ggg tct caa ggt gca gcg gcc aca agt cgt act gta tct 163
 Asp Ser Ala Gly Ser Gln Gly Ala Ala Ala Thr Ser Arg Thr Val Ser
 10 15 20
 att aga acc ctc atc gcg ctg atc atc gga tcg acc gtc ggc gcg gga 211
 Ile Arg Thr Leu Ile Ala Leu Ile Ile Gly Ser Thr Val Gly Ala Gly
 25 30 35
 att ttc tcc atc cct caa aac atc ggc tca gtc gca ggt ccc ggc gcg 259
 Ile Phe Ser Ile Pro Gln Asn Ile Gly Ser Val Ala Gly Pro Gly Ala
 40 45 50
 atg ctc atc ggc tgg ctg atc gcc ggt gtg ggc atg ttg tcc gta gcg 307
 Met Leu Ile Gly Trp Leu Ile Ala Gly Val Gly Met Leu Ser Val Ala
 55 60 65
 ttc gtg ttc cat gtt ctt gcc cgc cgt aaa cct cac ctc gat tct ggc 355
 Phe Val Phe His Val Leu Ala Arg Arg Lys Pro His Leu Asp Ser Gly
 70 75 80 85
 gtc tac gca tat gcg cgt gtt gga ttg ggc gat tat gta ggt ttc tcc 403
 Val Tyr Ala Tyr Ala Arg Val Gly Leu Gly Asp Tyr Val Gly Phe Ser
 90 95 100

tcc gct tgg ggt tat tgg ctg ggt tca gtc atc gcc caa gtt ggc tac	451
Ser Ala Trp Gly Tyr Trp Leu Gly Ser Val Ile Ala Gln Val Gly Tyr	
105 110 115	
gca acg tta ttt ttc tcc acg ttg ggc cac tac gta ccg ctg ttt tcc	499
Ala Thr Leu Phe Phe Ser Thr Leu Gly His Tyr Val Pro Leu Phe Ser	
120 125 130	
caa gat cat cca ttt gtg tca gcg ttg gca gtt agc gct ttg acc tgg	547
Gln Asp His Pro Phe Val Ser Ala Leu Ala Val Ser Ala Leu Thr Trp	
135 140 145	
ctg gtg ttt gga gtt gtt tcc cga gga att agc caa gct gct ttc ttg	595
Leu Val Phe Gly Val Val Ser Arg Gly Ile Ser Gln Ala Ala Phe Leu	
150 155 160 165	
aca acg gtc acc acc gtg gcc aaa att ctg cct ctg ttg tgc ttc atc	643
Thr Thr Val Thr Thr Val Ala Lys Ile Leu Pro Leu Leu Cys Phe Ile	
170 175 180	
atc ctt gtt gca ttc ttg ggc ttt agc tgg gag aag ttc act gtt gat	691
Ile Leu Val Ala Phe Leu Gly Phe Ser Trp Glu Lys Phe Thr Val Asp	
185 190 195	
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Leu Trp Ala Arg Asp Gly Gly Val Gly Ser Ile Phe Asp Gln Val Arg	
200 205 210	
ggc atc atg gtg tac acc gtg tgg gtg ttc atc ggt atc gaa ggt gca	787
Gly Ile Met Val Tyr Thr Val Trp Val Phe Ile Gly Ile Glu Gly Ala	
215 220 225	
tcg gta tat tcc cgc cag gca cgc tca cgc agt gat gtc agc cga gct	835
Ser Val Tyr Ser Arg Gln Ala Arg Ser Arg Ser Asp Val Ser Arg Ala	
230 235 240 245	
acc gtg att ggt ttt gtg gct gtt ctc ctt ttg ctg gtg tcg att tct	883
Thr Val Ile Gly Phe Val Ala Val Leu Leu Leu Leu Val Ser Ile Ser	
250 255 260	
tcg ctg agc ttc ggt gta ctg acc caa caa gag ctc gct gcg tta cca	931
Ser Leu Ser Phe Gly Val Leu Thr Gln Gln Glu Leu Ala Ala Leu Pro	
265 270 275	
gat aat tcc atg gcg tcg gtg ctc gaa gct gtt gtt ggt cca tgg ggt	979
Asp Asn Ser Met Ala Ser Val Leu Glu Ala Val Val Gly Pro Trp Gly	
280 285 290	
gcc gca ttg att tcg ttg ggt ctg tgt ctt tcg gtt ctt ggg gcc tat	1027
Ala Ala Leu Ile Ser Leu Gly Leu Cys Leu Ser Val Leu Gly Ala Tyr	
295 300 305	
gtg tcc tgg cag atg ctc tgc gca gaa cca ctg gcg ttg atg gca atg	1075
Val Ser Trp Gln Met Leu Cys Ala Glu Pro Leu Ala Leu Met Ala Met	
310 315 320 325	
gat ggc ctc att cca agc aaa atc ggg gcc atc aac agc cgc ggt gct	1123
Asp Gly Leu Ile Pro Ser Lys Ile Gly Ala Ile Asn Ser Arg Gly Ala	
330 335 340	

gcc tgg atg gct cag ctg atc tcc acc atc gtg att cag att ttc atc 1171
 Ala Trp Met Ala Gln Leu Ile Ser Thr Ile Val Ile Gln Ile Phe Ile
 345 350 355

atc att ttc ttc ctc aac gag acc acc tac gtc tcc atg gtg caa ttg 1219
 Ile Ile Phe Phe Leu Asn Glu Thr Thr Tyr Val Ser Met Val Gln Leu
 360 365 370

gct acc aac cta tac ttg gtg cct tac ctg ttc tct gcc ttt tat ctg 1267
 Ala Thr Asn Leu Tyr Leu Val Pro Tyr Leu Phe Ser Ala Phe Tyr Leu
 375 380 385

gtc atg ctg gca aca cgt gga aaa gga atc acc cac cca cat gcc ggc 1315
 Val Met Leu Ala Thr Arg Gly Lys Gly Ile Thr His Pro His Ala Gly
 390 395 400 405

aca cgt ttt gat gat tcc ggt cca gag ata tcc cgc cga gaa aac cgc 1363
 Thr Arg Phe Asp Asp Ser Gly Pro Glu Ile Ser Arg Arg Glu Asn Arg
 410 415 420

aaa cac ctc atc gtc ggt tta gta gca acg gtg tat tca gtg tgg ctg 1411
 Lys His Leu Ile Val Gly Leu Val Ala Thr Val Tyr Ser Val Trp Leu
 425 430 435

ttt tac gct gca gaa ccg cag ttt gtc ctc ttc gga gcc atg gcg atg 1459
 Phe Tyr Ala Ala Glu Pro Gln Phe Val Leu Phe Gly Ala Met Ala Met
 440 445 450

ctt ccc ggc tta atc ccc tat gtg tgg aca agg att tat cgt ggc gaa 1507
 Leu Pro Gly Leu Ile Pro Tyr Val Trp Thr Arg Ile Tyr Arg Gly Glu
 455 460 465

cag gtg ttt aac cgc ttt gaa atc ggc gtg gtt gtt gtc ctg gtc gtt 1555
 Gln Val Phe Asn Arg Phe Glu Ile Gly Val Val Val Val Leu Val Val
 470 475 480 485

gct gcc agc gcg ggc gtt att ggt ttg gtc aac gga tca cta tcg ctt 1603
 Ala Ala Ser Ala Gly Val Ile Gly Leu Val Asn Gly Ser Leu Ser Leu
 490 495 500

taaacaccga aaccttctg cta 1626

<210> 52

<211> 501

<212> PRT

<213> Corynebacterium glutamicum

<400> 52

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 20 25 30

Thr Val Gly Ala Gly Ile Phe Ser Ile Pro Gln Asn Ile Gly Ser Val
 35 40 45

Ala Gly Pro Gly Ala Met Leu Ile Gly Trp Leu Ile Ala Gly Val Gly
 50 55 60

Met Leu Ser Val Ala Phe Val Phe His Val Leu Ala Arg Arg Lys Pro
 65 70 75 80
 His Leu Asp Ser Gly Val Tyr Ala Tyr Ala Arg Val Gly Leu Gly Asp
 85 90 95
 Tyr Val Gly Phe Ser Ser Ala Trp Gly Tyr Trp Leu Gly Ser Val Ile
 100 105 110
 Ala Gln Val Gly Tyr Ala Thr Leu Phe Phe Ser Thr Leu Gly His Tyr
 115 120 125
 Val Pro Leu Phe Ser Gln Asp His Pro Phe Val Ser Ala Leu Ala Val
 130 135 140
 Ser Ala Leu Thr Trp Leu Val Phe Gly Val Val Ser Arg Gly Ile Ser
 145 150 155 160
 Gln Ala Ala Phe Leu Thr Thr Val Thr Thr Val Ala Lys Ile Leu Pro
 165 170 175
 Leu Leu Cys Phe Ile Ile Leu Val Ala Phe Leu Gly Phe Ser Trp Glu
 180 185 190
 Lys Phe Thr Val Asp Leu Trp Ala Arg Asp Gly Gly Val Gly Ser Ile
 195 200 205
 Phe Asp Gln Val Arg Gly Ile Met Val Tyr Thr Val Trp Val Phe Ile
 210 215 220
 Gly Ile Glu Gly Ala Ser Val Tyr Ser Arg Gln Ala Arg Ser Arg Ser
 225 230 235 240
 Asp Val Ser Arg Ala Thr Val Ile Gly Phe Val Ala Val Leu Leu Leu
 245 250 255
 Leu Val Ser Ile Ser Ser Leu Ser Phe Gly Val Leu Thr Gln Gln Glu
 260 265 270
 Leu Ala Ala Leu Pro Asp Asn Ser Met Ala Ser Val Leu Glu Ala Val
 275 280 285
 Val Gly Pro Trp Gly Ala Ala Leu Ile Ser Leu Gly Leu Cys Leu Ser
 290 295 300
 Val Leu Gly Ala Tyr Val Ser Trp Gln Met Leu Cys Ala Glu Pro Leu
 305 310 315 320
 Ala Leu Met Ala Met Asp Gly Leu Ile Pro Ser Lys Ile Gly Ala Ile
 325 330 335
 Asn Ser Arg Gly Ala Ala Trp Met Ala Gln Leu Ile Ser Thr Ile Val
 340 345 350
 Ile Gln Ile Phe Ile Ile Ile Phe Phe Leu Asn Glu Thr Thr Tyr Val
 355 360 365
 Ser Met Val Gln Leu Ala Thr Asn Leu Tyr Leu Val Pro Tyr Leu Phe
 370 375 380
 Ser Ala Phe Tyr Leu Val Met Leu Ala Thr Arg Gly Lys Gly Ile Thr

385		390		395		400									
His	Pro	His	Ala	Gly	Thr	Arg	Phe	Asp	Asp	Ser	Gly	Pro	Glu	Ile	Ser
				405					410					415	
Arg	Arg	Glu	Asn	Arg	Lys	His	Leu	Ile	Val	Gly	Leu	Val	Ala	Thr	Val
			420					425					430		
Tyr	Ser	Val	Trp	Leu	Phe	Tyr	Ala	Ala	Glu	Pro	Gln	Phe	Val	Leu	Phe
		435					440					445			
Gly	Ala	Met	Ala	Met	Leu	Pro	Gly	Leu	Ile	Pro	Tyr	Val	Trp	Thr	Arg
	450					455					460				
Ile	Tyr	Arg	Gly	Glu	Gln	Val	Phe	Asn	Arg	Phe	Glu	Ile	Gly	Val	Val
465					470					475					480
Val	Val	Leu	Val	Val	Ala	Ala	Ser	Ala	Gly	Val	Ile	Gly	Leu	Val	Asn
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Gly	Ser	Leu	Ser	Leu											
			500												

<210> 53
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(799)
 <223> RXA01394

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 Met Glu Ile Phe Ile
 1 5
 aca ggt ctg ctt ttg ggg gcc agt ctt tta ctg tcc atc gga ccg cag 163
 Thr Gly Leu Leu Leu Gly Ala Ser Leu Leu Ser Ile Gly Pro Gln
 10 15 20
 aat gta ctg gtg att aaa caa gga att aag cgc gaa gga ctc att gcg 211
 Asn Val Leu Val Ile Lys Gln Gly Ile Lys Arg Glu Gly Leu Ile Ala
 25 30 35
 gtt ctt ctc gtg tgt tta att tct gac gtc ttt ttg ttc atc gcc ggc 259
 Val Leu Leu Val Cys Leu Ile Ser Asp Val Phe Leu Phe Ile Ala Gly
 40 45 50
 acc ttg ggc gtt gat ctt ttg tcc aat gcc gcg ccg atc gtg ctc gat 307
 Thr Leu Gly Val Asp Leu Leu Ser Asn Ala Ala Pro Ile Val Leu Asp
 55 60 65
 att atg cgc tgg ggt ggc atc gct tac ctg tta tgg ttt gcc gtc atg 355
 Ile Met Arg Trp Gly Gly Ile Ala Tyr Leu Leu Trp Phe Ala Val Met
 70 75 80 85

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<400> 54
Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser Leu Leu Leu
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Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly Ile Lys Arg
      20             25             30

Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser Asp Val Phe
      35             40             45

Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser Asn Ala Ala
  50             55             60

Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala Tyr Leu Leu
  65             70             75             80

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Trp	Phe	Ala	Val	Met	Ala	Ala	Lys	Asp	Ala	Met	Thr	Asn	Lys	Val	Glu	
				85					90					95		
Ala	Pro	Gln	Ile	Ile	Glu	Glu	Thr	Glu	Pro	Thr	Val	Pro	Asp	Asp	Thr	
				100					105					110		
Pro	Leu	Gly	Gly	Ser	Ala	Val	Ala	Thr	Asp	Thr	Arg	Asn	Arg	Val	Arg	
				115					120					125		
Val	Glu	Val	Ser	Val	Asp	Lys	Gln	Arg	Val	Trp	Val	Lys	Pro	Met	Leu	
				130					135					140		
Met	Ala	Ile	Val	Leu	Thr	Trp	Leu	Asn	Pro	Asn	Ala	Tyr	Leu	Asp	Ala	
				145					150					155		
Phe	Val	Phe	Ile	Gly	Gly	Val	Gly	Ala	Gln	Tyr	Gly	Asp	Thr	Gly	Arg	
				165					170					175		
Trp	Ile	Phe	Ala	Ala	Gly	Ala	Phe	Ala	Ala	Ser	Leu	Ile	Trp	Phe	Pro	
				180					185					190		
Leu	Val	Gly	Phe	Gly	Ala	Ala	Ala	Leu	Ser	Arg	Pro	Leu	Ser	Ser	Pro	
				195					200					205		
Lys	Val	Trp	Arg	Trp	Ile	Asn	Val	Val	Val	Ala	Val	Val	Met	Thr	Ala	
				210					215					220		
Leu	Ala	Ile	Lys	Leu	Met	Leu	Met	Gly								
				225					230							

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<210> 55
<211> 1026
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(1003)
<223> RXA00865
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																				Met	Ser	Thr	Gly	Leu		
																				1					5	
aca	gct	aag	acc	gga	gta	gag	cac	ttc	ggc	acc	ggt	gga	gta	gca	atg	163										
Thr	Ala	Lys	Thr	Gly	Val	Glu	His	Phe	Gly	Thr	Val	Gly	Val	Ala	Met											
				10					15					20												
ggt	act	cca	ttc	acg	gaa	tcc	gga	gac	atc	gat	atc	gct	gct	ggc	cgc	211										
Val	Thr	Pro	Phe	Thr	Glu	Ser	Gly	Asp	Ile	Asp	Ile	Ala	Ala	Gly	Arg											
				25					30					35												
gaa	gtc	gcg	gct	tat	ttg	gtt	gat	aag	ggc	ttg	gat	tct	ttg	gtt	ctc	259										
Glu	Val	Ala	Ala	Tyr	Leu	Val	Asp	Lys	Gly	Leu	Asp	Ser	Leu	Val	Leu											
				40					45					50												

gcg ggc acc act ggt gaa tcc cca acg aca acc gcc gct gaa aaa cta	307
Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr Ala Ala Glu Lys Leu	
55 60 65	
gaa ctg ctc aag gcc gtt cgt gag gaa gtt ggg gat cgg gcg aag ctc	355
Glu Leu Leu Lys Ala Val Arg Glu Glu Val Gly Asp Arg Ala Lys Leu	
70 75 80 85	
atc gcc ggt gtc gga acc aac aac acg cgg aca tct gtg gaa ctt gcg	403
Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr Ser Val Glu Leu Ala	
90 95 100	
gaa gct gct gct tct gct ggc gca gac ggc ctt tta gtt gta act cct	451
Glu Ala Ala Ala Ser Ala Gly Ala Asp Gly Leu Leu Val Val Thr Pro	
105 110 115	
tat tac tcc aag ccg agc caa gag gga ttg ctg gcg cac ttc ggt gca	499
Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu Leu Ala His Phe Gly Ala	
120 125 130	
att gct gca gca aca gag gtt cca att tgt ctc tat gac att cct ggt	547
Ile Ala Ala Ala Thr Glu Val Pro Ile Cys Leu Tyr Asp Ile Pro Gly	
135 140 145	
cgg tca ggt att cca att gag tct gat acc atg aga cgc ctg agt gaa	595
Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met Arg Arg Leu Ser Glu	
150 155 160 165	
tta cct acg att ttg gcg gtc aag gac gcc aag ggt gac ctc gtt gca	643
Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys Gly Asp Leu Val Ala	
170 175 180	
gcc acg tca ttg atc aaa gaa acg gga ctt gcc tgg tat tca ggc gat	691
Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala Trp Tyr Ser Gly Asp	
185 190 195	
gac cca cta aac ctt gtt tgg ctt gct ttg ggc gga tca ggt ttc att	739
Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly Gly Ser Gly Phe Ile	
200 205 210	
tcc gta att gga cat gca gcc ccc aca gca tta cgt gag ttg tac aca	787
Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu Arg Glu Leu Tyr Thr	
215 220 225	
agc ttc gag gaa ggc gac ctc gtc cgt gcg cgg gaa atc aac gcc aaa	835
Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg Glu Ile Asn Ala Lys	
230 235 240 245	
cta tca ccg ctg gta gct gcc caa ggt cgc ttg ggt gga gtc agc ttg	883
Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu Gly Gly Val Ser Leu	
250 255 260	
gca aaa gct gct ctg cgt ctg cag ggc atc aac gta gga gat cct cga	931
Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn Val Gly Asp Pro Arg	
265 270 275	
ctt cca att atg gct cca aat gag cag gaa ctt gag gct ctc cga gaa	979
Leu Pro Ile Met Ala Pro Asn Glu Gln Glu Leu Glu Ala Leu Arg Glu	
280 285 290	
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295 300

<210> 56

<211> 301

<212> PRT

<213> Corynebacterium glutamicum

<400> 56

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Ile Ala Ala Gly Arg Glu Val Ala Ala Tyr Leu Val Asp Lys Gly Leu
35 40 45

Asp Ser Leu Val Leu Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr
50 55 60

Ala Ala Glu Lys Leu Glu Leu Leu Lys Ala Val Arg Glu Glu Val Gly
65 70 75 80

Asp Arg Ala Lys Leu Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr
85 90 95

Ser Val Glu Leu Ala Glu Ala Ala Ala Ser Ala Gly Ala Asp Gly Leu
100 105 110

Leu Val Val Thr Pro Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu Leu
115 120 125

Ala His Phe Gly Ala Ile Ala Ala Ala Thr Glu Val Pro Ile Cys Leu
130 135 140

Tyr Asp Ile Pro Gly Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met
145 150 155 160

Arg Arg Leu Ser Glu Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys
165 170 175

Gly Asp Leu Val Ala Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala
180 185 190

Trp Tyr Ser Gly Asp Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly
195 200 205

Gly Ser Gly Phe Ile Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu
210 215 220

Arg Glu Leu Tyr Thr Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg
225 230 235 240

Glu Ile Asn Ala Lys Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu
245 250 255

Gly Gly Val Ser Leu Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn
260 265 270

Glu Ala Leu Arg Glu Asp Met Lys Lys Ala Gly Val Leu
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<210> 57
<211> 1071
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(1048)
<223> RXS02021
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Met Ser Glu Asn Ile																5
1																
cgc gga gcc caa gca gtt gga atc gca aat atc gcc atg gac ggg acc																163
Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile Ala Met Asp Gly Thr																20
10																
15																
atc ctg gac acg tgg tac cca gaa ccc caa att ttc aac ccg gat cag																211
Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile Phe Asn Pro Asp Gln																35
25																
30																
35																
tgg gct gaa cgc tac cca ttg gaa gtg ggc acc aca cgc ctc gga gca																259
Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr Thr Arg Leu Gly Ala																40
45																
50																
aac gaa ctc acc cca cgg atg ctg cag ttg gta aaa ctg gac caa gat																307
Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val Lys Leu Asp Gln Asp																55
60																
65																
cgc ctc gtc gaa cag gta gca gtc cgc acc gtt atc ccc gat ctg tct																355
Arg Leu Val Glu Gln Val Ala Val Arg Thr Val Ile Pro Asp Leu Ser																70
75																
80																
85																
caa cct cca gta gac gcg cac gat gtt tac ctg cgc ctc cac ctg ctt																403
Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu Arg Leu His Leu Leu																90
95																
100																
tcc cac cgg ctg gtc cgc ccc cac gaa atg cac atg caa aac acc ttg																451
Ser His Arg Leu Val Arg Pro His Glu Met His Met Gln Asn Thr Leu																105
110																
115																
gag ctg ctg tcc gac gtg gtg tgg aca aac aag ggc cct tgc ctt cct																499
Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys Gly Pro Cys Leu Pro																120
125																
130																
gaa aac ttt gag tgg gtg cgt ggt gct ctg cgg tcc cgc gga ctc atc																547
Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg Ser Arg Gly Leu Ile																135
140																
145																
cac gtc tac tgt gtg gac cgt ctt ccc cgc atg gtc gac tat gtg gtt																595

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His Val Tyr Cys Val Asp Arg Leu Pro Arg Met Val Asp Tyr Val Val
150                      155                      160                      165

ccc cct gga gtc cgc atc tcc gaa gca gaa cgc gtg cgc cta ggt gca 643
Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg Val Arg Leu Gly Ala
                      170                      175                      180

tac ctt gct ccg ggt acc tct gtg ctg cgt gaa ggt ttc gtg tct ttc 691
Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu Gly Phe Val Ser Phe
                      185                      190                      195

aac tcc ggc acc ttg ggt gcc gca aag gtg gaa ggc cgc ctg agt tcc 739
Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu Gly Arg Leu Ser Ser
                      200                      205                      210

ggt gtg gtc atc ggt gaa ggt tcc gag att gga ctg tct tct act att 787
Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly Leu Ser Ser Thr Ile
                      215                      220                      225

cag tcc ccg aga gat gaa cag cgc cgc cgt ttg ccg ttg agc atc ggc 835
Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu Pro Leu Ser Ile Gly
230                      235                      240                      245

caa aac tgc aac ttt ggt gtc agc tcc gga atc atc gga gtc agt ctg 883
Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile Ile Gly Val Ser Leu
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gga gac aat tgc gac atc gga aat aac att gtc ttg gat gga gat acc 931
Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val Leu Asp Gly Asp Thr
                      265                      270                      275

ccc att tgg ttc gca gcc gat gag gag tta cgc act atc gac tcc atc 979
Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg Thr Ile Asp Ser Ile
                      280                      285                      290

gaa ggc caa gca aat tgg tca atc aag cgt gaa tcc ggc ttc cat gag 1027
Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu Ser Gly Phe His Glu
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Pro Val Ala Arg Leu Lys Ala
310                      315

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<210> 58

<211> 316

<212> PRT

<213> Corynebacterium glutamicum

<400> 58

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Met Ser Glu Asn Ile Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile
 1                      5                      10                      15

Ala Met Asp Gly Thr Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile
 20                      25                      30

Phe Asn Pro Asp Gln Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr
 35                      40                      45

Thr Arg Leu Gly Ala Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val
 50                      55                      60

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Lys Leu Asp Gln Asp Arg Leu Val Glu Gln Val Ala Val Arg Thr Val
 65                               70                               75                               80

Ile Pro Asp Leu Ser Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu
                               85                               90                               95

Arg Leu His Leu Leu Ser His Arg Leu Val Arg Pro His Glu Met His
                               100                              105                              110

Met Gln Asn Thr Leu Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys
                               115                              120                              125

Gly Pro Cys Leu Pro Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg
 130                              135                              140

Ser Arg Gly Leu Ile His Val Tyr Cys Val Asp Arg Leu Pro Arg Met
 145                              150                              155                              160

Val Asp Tyr Val Val Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg
                               165                              170                              175

Val Arg Leu Gly Ala Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu
                               180                              185                              190

Gly Phe Val Ser Phe Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu
 195                              200                              205

Gly Arg Leu Ser Ser Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly
 210                              215                              220

Leu Ser Ser Thr Ile Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu
 225                              230                              235                              240

Pro Leu Ser Ile Gly Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile
                               245                              250                              255

Ile Gly Val Ser Leu Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val
 260                              265                              270

Leu Asp Gly Asp Thr Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg
 275                              280                              285

Thr Ile Asp Ser Ile Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu
 290                              295                              300

Ser Gly Phe His Glu Pro Val Ala Arg Leu Lys Ala
 305                              310                              315

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<210> 59

<211> 1296

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1273)

<223> RXS02157

<400> 59

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caccgttttt																agaaaagacg				acaagggatgg				ggaactgtaa				atg		agc		acg		ctg		gaa		115										
																								Met		Ser		Thr		Leu		Glu		5														
act																tgg		cca		cag		gtc		att		att		aat		acg		tac		ggc		acc		cca		cca		gtt		gag		163		
Thr																Trp		Pro		Gln		Val		Ile		Ile		Asn		Thr		Tyr		Gly		Thr		Pro		Pro		Val		Glu		20		
																						10																										
ctg																gtg		tcc		ggc		aag		ggc		gca		acc		gtc		act		gat		gac		cag		ggc		aat		gtc		21		
Leu																Val		Ser		Gly		Lys		Gly		Ala		Thr		Val		Thr		Asp		Asp		Gln		Gly		Asn		Val		30		
																				25																										35		
tac																atc		gac		ttg		ctc		gcg		ggc		atc		gca		gtc		aac		gcg		ttg		ggc		cac		gcc		259		
Tyr																Ile		Asp		Leu		Leu		Ala		Gly		Ile		Ala		Val		Asn		Ala		Leu		Gly		His		Ala		40		
																												45																		50		
cac																ccg		gcg		atc		atc		gag		gcg		gtc		acc		aac		cag		atc		ggc		caa		ctt		ggc		307		
His																Pro		Ala		Ile		Ile		Glu		Ala		Val		Thr		Asn		Gln		Ile		Gly		Gln		Leu		Gly		55		
																										60																				65		
cac																gtc		tca		aac		ttg		ttc		gca		tcc		agg		ccc		gtc		gtc		gag		gtc		gcc		gag		355		
His																Val		Ser		Asn		Leu		Phe		Ala		Ser		Arg		Pro		Val		Val		Glu		Val		Ala		Glu		70		
																								75										80												85		
gag																ctc		atc		aag		cgt		ttt		tcg		ctt		gac		gac		gcc		acc		ctc		gcc		gcg		caa		403		
Glu																Leu		Ile		Lys		Arg		Phe		Ser		Leu		Asp		Asp		Ala		Thr		Leu		Ala		Ala		Gln		90		
																				90																												100
acc																cgg		gtt		ttc		ttc		tgc		aac		tcg		ggc		gcc		gaa		gca		aac		gag		gct		gct		451		
Thr																Arg		Val		Phe		Phe		Cys		Asn		Ser		Gly		Ala		Glu		Ala		Asn		Glu		Ala		Ala		105		
																				105								110																		115		
ttc																aag		att		gca		cgc		ttg		act		ggc		cgt		tcc		cgg		att		ctg		gct		gca		gtt		499		
Phe																Lys		Ile		Ala		Arg		Leu		Thr		Gly		Arg		Ser		Arg		Ile		Leu		Ala		Ala		Val		120		
																										125																				130		
cat																ggc		ttc		cac		ggc		cgc		acc		atg		ggc		tcc		ctc														

gtt ggc cgt acc ggc gat ttc ttt gca cat cag cac gat ggc gtt gtt 835
 Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln His Asp Gly Val Val
 230 235 240 245

 ccc gat gtg gtg acc atg gcc aag gga ctt ggc ggc ggt ctt ccc atc 883
 Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly Gly Gly Leu Pro Ile
 250 255 260

 ggt gct tgt ttg gcc act ggc cgt gca gct gaa ttg atg acc cca ggc 931
 Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu Leu Met Thr Pro Gly
 265 270 275

 aag cac ggc acc act ttc ggt ggc aac cca gtt gct tgt gca gct gcc 979
 Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val Ala Cys Ala Ala Ala
 280 285 290

 aag gca gtg ctg tct gtt gtc gat gac gct ttc tgc gca gaa gtt gcc 1027
 Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe Cys Ala Glu Val Ala
 295 300 305

 cgc aag ggc gag ctg ttc aag gaa ctt ctt gcc aag gtt gac ggc gtt 1075
 Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala Lys Val Asp Gly Val
 310 315 320 325

 gta gac gtc cgt ggc agg ggc ttg atg ttg ggc gtg gtg ctg gag cgc 1123
 Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly Val Val Leu Glu Arg
 330 335 340

 gac gtc gca aag caa gct gtt ctt gat ggt ttt aag cac ggc gtt att 1171
 Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe Lys His Gly Val Ile
 345 350 355

 ttg aat gca ccg gcg gac aac att atc cgt ttg acc ccg ccg ctg gtg 1219
 Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu Thr Pro Pro Leu Val
 360 365 370

 atc acc gac gaa gaa atc gca gac gca gtc aag gct att gcc gag aca 1267
 Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys Ala Ile Ala Glu Thr
 375 380 385

 atc gca taaaggactc aaacttatga ctt 1296
 Ile Ala
 390

<210> 60

<211> 391

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 60

Met Ser Thr Leu Glu Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly
 1 5 10 15

Thr Pro Pro Val Glu Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp
 20 25 30

Asp Gln Gly Asn Val Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn
 35 40 45

Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln
 50 55 60
 Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val
 65 70 75 80
 Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala
 85 90 95
 Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu
 100 105 110
 Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg
 115 120 125
 Ile Leu Ala Ala Val His Gly Phe His Gly Arg Thr Met Gly Ser Leu
 130 135 140
 Ala Leu Thr Gly Gln Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro
 145 150 155 160
 Ser Gly Val Glu Phe Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys
 165 170 175
 Met Val Glu Thr Asn Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro
 180 185 190
 Ile Gln Gly Glu Thr Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys
 195 200 205
 Ala Val Arg Glu Leu Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp
 210 215 220
 Glu Val Gln Thr Gly Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln
 225 230 235 240
 His Asp Gly Val Val Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly
 245 250 255
 Gly Gly Leu Pro Ile Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu
 260 265 270
 Leu Met Thr Pro Gly Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val
 275 280 285
 Ala Cys Ala Ala Ala Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe
 290 295 300
 Cys Ala Glu Val Ala Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala
 305 310 315 320
 Lys Val Asp Gly Val Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly
 325 330 335
 Val Val Leu Glu Arg Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe
 340 345 350
 Lys His Gly Val Ile Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu
 355 360 365
 Thr Pro Pro Leu Val Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys

370

375

380

Ala Ile Ala Glu Thr Ile Ala
385 390

<210> 61
<211> 1008
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(985)
<223> RXC00733

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gtgaaattgt tgaatcccaa gagactgcgc aggcgcaatc atg agt aat act gca 115
Met Ser Asn Thr Ala
1 5
ggc ccc cgc ggg cgt tcc cat cag gca gac gcc gcg ccg aat caa aag 163
Gly Pro Arg Gly Arg Ser His Gln Ala Asp Ala Ala Pro Asn Gln Lys
10 15 20
gca cag aat ttc gga cca tct gcc aaa agg ctt ttc gga att cta ggc 211
Ala Gln Asn Phe Gly Pro Ser Ala Lys Arg Leu Phe Gly Ile Leu Gly
25 30 35
cat gac cgt aac acc tta att ttt gtt atc ttc cta gcc gtc ctg agc 259
His Asp Arg Asn Thr Leu Ile Phe Val Ile Phe Leu Ala Val Leu Ser
40 45 50
gtt gga ctt acc gtc ttg ggc cca tgg ttg ctg ggt aaa gcc acc aac 307
Val Gly Leu Thr Val Leu Gly Pro Trp Leu Leu Gly Lys Ala Thr Asn
55 60 65
gtg gtg ttt gaa gga ttc cta tct aag cgc atg ccg gct ggt gcg tca 355
Val Val Phe Glu Gly Phe Leu Ser Lys Arg Met Pro Ala Gly Ala Ser
70 75 80 85
aag gaa gat atc atc gcg cag ttg cag gct gca ggt aaa cat aat cag 403
Lys Glu Asp Ile Ile Ala Gln Leu Gln Ala Ala Gly Lys His Asn Gln
90 95 100
gct tcc atg atg gaa gac atg aac ctt gtt cca ggc tca ggc att gat 451
Ala Ser Met Met Glu Asp Met Asn Leu Val Pro Gly Ser Gly Ile Asp
105 110 115
ttt gaa aaa tta gcc atg atc ctc gga ctg gtg atc ggt gct tat ctc 499
Phe Glu Lys Leu Ala Met Ile Leu Gly Leu Val Ile Gly Ala Tyr Leu
120 125 130
atc ggt agc ctg ttg tcg ttg ttc cag gcg cgg atg ctc aac cgc atc 547
Ile Gly Ser Leu Leu Ser Leu Phe Gln Ala Arg Met Leu Asn Arg Ile
135 140 145
gtg caa agt gcc atg cac cgg ctg cgc atg gag gtg gag gaa aaa atc 595
Val Gln Ser Ala Met His Arg Leu Arg Met Glu Val Glu Glu Lys Ile

150	155	160	165	
cac cgc cta ccg ctg agc tat ttc gat tcc atc aaa cgt ggt gat ctg				643
His Arg Leu Pro Leu Ser Tyr Phe Asp Ser Ile Lys Arg Gly Asp Leu	170	175	180	
ctt agc cgt gtg acc aac gat gtg gat aat atc ggt caa tcc ctg caa				691
Leu Ser Arg Val Thr Asn Asp Val Asp Asn Ile Gly Gln Ser Leu Gln	185	190	195	
caa acc ttg tca cag gcg atc act tcc cta ctg acc gtc atc ggt gtg				739
Gln Thr Leu Ser Gln Ala Ile Thr Ser Leu Leu Thr Val Ile Gly Val	200	205	210	
ttg gtg atg atg ttt atc atc tcc cca ctg ctc gca ctc gtg gcg ctg				787
Leu Val Met Met Phe Ile Ile Ser Pro Leu Leu Ala Leu Val Ala Leu	215	220	225	
gta tcc att ccg gtc acc atc gtg gtc act gtg gtg gtt gcg agc cgt				835
Val Ser Ile Pro Val Thr Ile Val Val Thr Val Val Val Ala Ser Arg	230	235	240	245
tcc cag aaa ctc ttt gcg gaa cag tgg aag cag acc ggt att ttg aat				883
Ser Gln Lys Leu Phe Ala Glu Gln Trp Lys Gln Thr Gly Ile Leu Asn	250	255	260	
gcg cgc ctg gag gaa acc tac tct ggc cac gcc gtg gtt aag gtt ttc				931
Ala Arg Leu Glu Glu Thr Tyr Ser Gly His Ala Val Val Lys Val Phe	265	270	275	
gga cac caa aag gat gtt caa gaa gca ttc gag gaa gaa aat caa gct				979
Gly His Gln Lys Asp Val Gln Glu Ala Phe Glu Glu Glu Asn Gln Ala	280	285	290	
tgt gta taaggccagc tttggtgccc agt				1008
Cys Val	295			

<210> 62

<211> 295

<212> PRT

<213> Corynebacterium glutamicum

<400> 62

Met Ser Asn Thr Ala Gly Pro Arg Gly Arg Ser His Gln Ala Asp Ala
1 5 10 15

Ala Pro Asn Gln Lys Ala Gln Asn Phe Gly Pro Ser Ala Lys Arg Leu
20 25 30

Phe Gly Ile Leu Gly His Asp Arg Asn Thr Leu Ile Phe Val Ile Phe
35 40 45

Leu Ala Val Leu Ser Val Gly Leu Thr Val Leu Gly Pro Trp Leu Leu
50 55 60

Gly Lys Ala Thr Asn Val Val Phe Glu Gly Phe Leu Ser Lys Arg Met
65 70 75 80

Pro Ala Gly Ala Ser Lys Glu Asp Ile Ile Ala Gln Leu Gln Ala Ala

85								90					95			
Gly	Lys	His	Asn	Gln	Ala	Ser	Met	Met	Glu	Asp	Met	Asn	Leu	Val	Pro	
100								105					110			
Gly	Ser	Gly	Ile	Asp	Phe	Glu	Lys	Leu	Ala	Met	Ile	Leu	Gly	Leu	Val	
115								120					125			
Ile	Gly	Ala	Tyr	Leu	Ile	Gly	Ser	Leu	Leu	Ser	Leu	Phe	Gln	Ala	Arg	
130								135					140			
Met	Leu	Asn	Arg	Ile	Val	Gln	Ser	Ala	Met	His	Arg	Leu	Arg	Met	Glu	
145								150					155			
Val	Glu	Glu	Lys	Ile	His	Arg	Leu	Pro	Leu	Ser	Tyr	Phe	Asp	Ser	Ile	
165								170					175			
Lys	Arg	Gly	Asp	Leu	Leu	Ser	Arg	Val	Thr	Asn	Asp	Val	Asp	Asn	Ile	
180								185					190			
Gly	Gln	Ser	Leu	Gln	Gln	Thr	Leu	Ser	Gln	Ala	Ile	Thr	Ser	Leu	Leu	
195								200					205			
Thr	Val	Ile	Gly	Val	Leu	Val	Met	Met	Phe	Ile	Ile	Ser	Pro	Leu	Leu	
210								215					220			
Ala	Leu	Val	Ala	Leu	Val	Ser	Ile	Pro	Val	Thr	Ile	Val	Val	Thr	Val	
225								230					235			
Val	Val	Ala	Ser	Arg	Ser	Gln	Lys	Leu	Phe	Ala	Glu	Gln	Trp	Lys	Gln	
245								250					255			
Thr	Gly	Ile	Leu	Asn	Ala	Arg	Leu	Glu	Glu	Thr	Tyr	Ser	Gly	His	Ala	
260								265					270			
Val	Val	Lys	Val	Phe	Gly	His	Gln	Lys	Asp	Val	Gln	Glu	Ala	Phe	Glu	
275								280					285			
Glu	Glu	Asn	Gln	Ala	Cys	Val										
290								295								

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<210> 63
<211> 426
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (1) .. (426)  
<223> RXC00861
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Met	Ala	Pro	His	Lys	Val	Met	Leu	Ile	Thr	Thr	Gly	Thr	Gln	Gly	Glu	
1				5					10					15		
cct	atg	gct	gcg	ctg	tct	cgc	atg	gcg	cgt	cgt	gag	cac	cga	cag	atc	96
Pro	Met	Ala	Ala	Leu	Ser	Arg	Met	Ala	Arg	Arg	Glu	His	Arg	Gln	Ile	
			20					25					30			

act gtc cgt gat gga gac ttg att atc ctt tct tcc tcc ctg gtt cca 144
 Thr Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro
 35 40 45

ggt aac gaa gaa gca gtg ttc ggt gtc atc aac atg ctg gct cag atc 192
 Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile
 50 55 60

ggt gca act gtt gtt acc ggt cgc gac gcc aag gtg cac acc tcg ggc 240
 Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly
 65 70 75 80

cac ggc tac tcc gga gag ctg ttg ttc ttg tac aac gcc gct cgt ccg 288
 His Gly Tyr Ser Gly Glu Leu Leu Phe Leu Tyr Asn Ala Ala Arg Pro
 85 90 95

aag aac gct atg cct gtc cac ggc gag tgg cgc cac ctg cgc gcc aac 336
 Lys Asn Ala Met Pro Val His Gly Glu Trp Arg His Leu Arg Ala Asn
 100 105 110

aag gaa ctg gct atc tcc act ggt gtt aac cgc gac aac gtt gtg ctt 384
 Lys Glu Leu Ala Ile Ser Thr Gly Val Asn Arg Asp Asn Val Val Leu
 115 120 125

gca caa aac ggt gtt gtg gtt gat atg gtc aac ggt cgc gca 426
 Ala Gln Asn Gly Val Val Val Asp Met Val Asn Gly Arg Ala
 130 135 140

<210> 64

<211> 142

<212> PRT

<213> Corynebacterium glutamicum

<400> 64

Met Ala Pro His Lys Val Met Leu Ile Thr Thr Gly Thr Gln Gly Glu
 1 5 10 15

Pro Met Ala Ala Leu Ser Arg Met Ala Arg Arg Glu His Arg Gln Ile
 20 25 30

Thr Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro
 35 40 45

Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile
 50 55 60

Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly
 65 70 75 80

His Gly Tyr Ser Gly Glu Leu Leu Phe Leu Tyr Asn Ala Ala Arg Pro
 85 90 95

Lys Asn Ala Met Pro Val His Gly Glu Trp Arg His Leu Arg Ala Asn
 100 105 110

Lys Glu Leu Ala Ile Ser Thr Gly Val Asn Arg Asp Asn Val Val Leu
 115 120 125

Ala Gln Asn Gly Val Val Val Asp Met Val Asn Gly Arg Ala
 130 135 140

<210> 65
 <211> 1066
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1066)
 <223> RXC00866

<400> 65
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 ctctccgaga agacatgaaa aaagctggag ttctataaat atg aat gat tcc cga 115
 Met Asn Asp Ser Arg
 1 5
 aat cgc ggc cgg aag gtt acc cgc aag gcg ggc cca cca gaa gct ggt 163
 Asn Arg Gly Arg Lys Val Thr Arg Lys Ala Gly Pro Pro Glu Ala Gly
 10 15 20
 cag gaa aac cat ctg gat acc cct gtc ttt cag gca cca gat gct tcc 211
 Gln Glu Asn His Leu Asp Thr Pro Val Phe Gln Ala Pro Asp Ala Ser
 25 30 35
 tct aac cag agc gct gta aaa gct gag acc gcc gga aac gac aat cgg 259
 Ser Asn Gln Ser Ala Val Lys Ala Glu Thr Ala Gly Asn Asp Asn Arg
 40 45 50
 gat gct gcg caa ggt gct caa gga tcc caa gat tct cag ggt tcc cag 307
 Asp Ala Ala Gln Gly Ala Gln Gly Ser Gln Asp Ser Gln Gly Ser Gln
 55 60 65
 aac gct caa ggt tcc cag aac cgc gag tcc gga aac aac aac cgc aac 355
 Asn Ala Gln Gly Ser Gln Asn Arg Glu Ser Gly Asn Asn Asn Arg Asn
 70 75 80 85
 cgt tcc aac aac aac cgt cgc ggt ggt cgt gga cgt cgt gga tcc gga 403
 Arg Ser Asn Asn Asn Arg Arg Gly Gly Arg Gly Arg Arg Gly Ser Gly
 90 95 100
 aac gcc aat gag ggc gcg aac aac aac agc ggt aac cag aac cgt cag 451
 Asn Ala Asn Glu Gly Ala Asn Asn Asn Ser Gly Asn Gln Asn Arg Gln
 105 110 115
 ggc gga aac cgt ggc aac cgc ggt ggc gga cgc cga aac gtt gtt aag 499
 Gly Gly Asn Arg Gly Asn Arg Gly Gly Gly Arg Arg Asn Val Val Lys
 120 125 130
 tcg atg cag ggt gcg gat ctg acc cag cgc ctg cca gag cca cca aag 547
 Ser Met Gln Gly Ala Asp Leu Thr Gln Arg Leu Pro Glu Pro Pro Lys
 135 140 145
 gca ccg gca aac ggt ctg cgt att tac gca ctt ggt ggc att tcc gaa 595
 Ala Pro Ala Asn Gly Leu Arg Ile Tyr Ala Leu Gly Gly Ile Ser Glu
 150 155 160 165
 atc ggt cgc aac atg acc gtg ttt gag tac aac aac cgt ctg ctc atc 643
 Ile Gly Arg Asn Met Thr Val Phe Glu Tyr Asn Asn Arg Leu Leu Ile

170										175					180					
gtg	gac	tgt	ggt	gtg	ctc	ttc	cca	tct	tca	ggt	gag	cca	ggc	gtt	gac	691				
Val	Asp	Cys	Gly	Val	Leu	Phe	Pro	Ser	Ser	Gly	Glu	Pro	Gly	Val	Asp					
			185				190						195							
ctg	att	ctt	cct	gac	ttc	ggc	cca	att	gag	gat	cac	ctg	cac	cgc	gtc	739				
Leu	Ile	Leu	Pro	Asp	Phe	Gly	Pro	Ile	Glu	Asp	His	Leu	His	Arg	Val					
			200				205						210							
gat	gca	ttg	gtg	gtt	act	cac	gga	cac	gaa	gac	cac	att	ggt	gct	att	787				
Asp	Ala	Leu	Val	Val	Thr	His	Gly	His	Glu	Asp	His	Ile	Gly	Ala	Ile					
			215				220						225							
ccc	tgg	ctg	ctg	aag	ctg	cgc	aac	gat	atc	cca	atc	ttg	gca	tcc	cgt	835				
Pro	Trp	Leu	Leu	Lys	Leu	Arg	Asn	Asp	Ile	Pro	Ile	Leu	Ala	Ser	Arg					
			230				235						240							
ttc	acc	ttg	gct	ctg	att	gca	gct	aag	tgt	aag	gaa	cac	cgt	cag	cgt	883				
Phe	Thr	Leu	Ala	Leu	Ile	Ala	Ala	Lys	Cys	Lys	Glu	His	Arg	Gln	Arg					
			250							255			260							
ccg	aag	ctg	atc	gag	gtc	aac	gag	cag	tcc	aat	gag	gac	cgc	gga	ccg	931				
Pro	Lys	Leu	Ile	Glu	Val	Asn	Glu	Gln	Ser	Asn	Glu	Asp	Arg	Gly	Pro					
			265							270			275							
ttc	aac	att	cgc	ttc	tgg	gct	gtt	aac	cac	tcc	atc	cca	gac	tgc	ctt	979				
Phe	Asn	Ile	Arg	Phe	Trp	Ala	Val	Asn	His	Ser	Ile	Pro	Asp	Cys	Leu					
			280				285						290							
ggt	ctt	gct	atc	aag	act	cct	gct	ggt	ttg	gtc	atc	cac	acc	ggt	gac	1027				
Gly	Leu	Ala	Ile	Lys	Thr	Pro	Ala	Gly	Leu	Val	Ile	His	Thr	Gly	Asp					
			295				300						305							
atc	aag	ctg	gat	cag	act	cct	cct	gat	gga	cgc	cca	act				1066				
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<210> 66

<211> 322

<212> PRT

<213> Corynebacterium glutamicum

<400> 66

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Pro	Pro	Glu	Ala	Gly	Gln	Glu	Asn	His	Leu	Asp	Thr	Pro	Val	Phe	Gln
		20						25					30		

Ala	Pro	Asp	Ala	Ser	Ser	Asn	Gln	Ser	Ala	Val	Lys	Ala	Glu	Thr	Ala
		35					40					45			

Gly	Asn	Asp	Asn	Arg	Asp	Ala	Ala	Gln	Gly	Ala	Gln	Gly	Ser	Gln	Asp
	50					55					60				

Ser	Gln	Gly	Ser	Gln	Asn	Ala	Gln	Gly	Ser	Gln	Asn	Arg	Glu	Ser	Gly
65					70				75					80	

Asn	Asn	Asn	Arg	Asn	Arg	Ser	Asn	Asn	Asn	Arg	Arg	Gly	Gly	Arg	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

85					90					95					
Arg	Arg	Gly	Ser	Gly	Asn	Ala	Asn	Glu	Gly	Ala	Asn	Asn	Asn	Ser	Gly
		100						105					110		
Asn	Gln	Asn	Arg	Gln	Gly	Gly	Asn	Arg	Gly	Asn	Arg	Gly	Gly	Gly	Arg
		115					120					125			
Arg	Asn	Val	Val	Lys	Ser	Met	Gln	Gly	Ala	Asp	Leu	Thr	Gln	Arg	Leu
		130				135						140			
Pro	Glu	Pro	Pro	Lys	Ala	Pro	Ala	Asn	Gly	Leu	Arg	Ile	Tyr	Ala	Leu
					150					155					160
Gly	Gly	Ile	Ser	Glu	Ile	Gly	Arg	Asn	Met	Thr	Val	Phe	Glu	Tyr	Asn
				165					170					175	
Asn	Arg	Leu	Leu	Ile	Val	Asp	Cys	Gly	Val	Leu	Phe	Pro	Ser	Ser	Gly
			180					185						190	
Glu	Pro	Gly	Val	Asp	Leu	Ile	Leu	Pro	Asp	Phe	Gly	Pro	Ile	Glu	Asp
			195				200						205		
His	Leu	His	Arg	Val	Asp	Ala	Leu	Val	Val	Thr	His	Gly	His	Glu	Asp
						215					220				
His	Ile	Gly	Ala	Ile	Pro	Trp	Leu	Leu	Lys	Leu	Arg	Asn	Asp	Ile	Pro
					230					235					240
Ile	Leu	Ala	Ser	Arg	Phe	Thr	Leu	Ala	Leu	Ile	Ala	Ala	Lys	Cys	Lys
				245					250					255	
Glu	His	Arg	Gln	Arg	Pro	Lys	Leu	Ile	Glu	Val	Asn	Glu	Gln	Ser	Asn
				260				265						270	
Glu	Asp	Arg	Gly	Pro	Phe	Asn	Ile	Arg	Phe	Trp	Ala	Val	Asn	His	Ser
			275				280					285			
Ile	Pro	Asp	Cys	Leu	Gly	Leu	Ala	Ile	Lys	Thr	Pro	Ala	Gly	Leu	Val
						295					300				
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Pro Thr

<210> 67

<211> 1527

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1504)

<223> RXC02095

<400> 67

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	Met Lys Thr Glu Gln	
	1 5	
tcc caa aaa gca caa tta gcc cct aag aaa gca cct gaa aag cca caa	163	
Ser Gln Lys Ala Gln Leu Ala Pro Lys Lys Ala Pro Glu Lys Pro Gln		
10 15 20		
cgc atc cgc caa ctt att tcc gtg gcg tgg cag cga cct tgg ctc acc	211	
Arg Ile Arg Gln Leu Ile Ser Val Ala Trp Gln Arg Pro Trp Leu Thr		
25 30 35		
tca ttc acc gta atc agc gct tta gct gca acg ttg ttt gaa ctt aca	259	
Ser Phe Thr Val Ile Ser Ala Leu Ala Ala Thr Leu Phe Glu Leu Thr		
40 45 50		
ctt cct ctt ttg acc ggt ggc gcc atc gat atc gcg ctc gga aat acc	307	
Leu Pro Leu Leu Thr Gly Gly Ala Ile Asp Ile Ala Leu Gly Asn Thr		
55 60 65		
gga gat act tta acc act gac ctg ctg gac cgg ttc act ccg agt gga	355	
Gly Asp Thr Leu Thr Thr Asp Leu Leu Asp Arg Phe Thr Pro Ser Gly		
70 75 80 85		
tta agc gtg ttg acc agc gtc att gcc ctt atc gtg ctt ctc gcg ttg	403	
Leu Ser Val Leu Thr Ser Val Ile Ala Leu Ile Val Leu Leu Ala Leu		
90 95 100		
ctt cgc tat gcc agt caa ttt gga cgg cga tac acc gca ggc aag ctc	451	
Leu Arg Tyr Ala Ser Gln Phe Gly Arg Arg Tyr Thr Ala Gly Lys Leu		
105 110 115		
agc atg ggg gta cag cat gat gtc cgg ctt aaa acg atg cgc tca ttg	499	
Ser Met Gly Val Gln His Asp Val Arg Leu Lys Thr Met Arg Ser Leu		
120 125 130		
cag aac ctc gat ggg cca ggt cag gac tct att cgc aca ggc caa gta	547	
Gln Asn Leu Asp Gly Pro Gly Gln Asp Ser Ile Arg Thr Gly Gln Val		
135 140 145		
gtc agt cgg tcc att tcg gat atc aac atg gtg caa agc ctt gtg gcg	595	
Val Ser Arg Ser Ile Ser Asp Ile Asn Met Val Gln Ser Leu Val Ala		
150 155 160 165		
atg ttg ccg atg ttg atc gga aat gtg gtc aag ctt gtg ctc act ttg	643	
Met Leu Pro Met Leu Ile Gly Asn Val Val Lys Leu Val Leu Thr Leu		
170 175 180		
gtg atc atg ctg gct att tcc ccg ccg ctg acc atc atc gct gca gtg	691	
Val Ile Met Leu Ala Ile Ser Pro Pro Leu Thr Ile Ile Ala Ala Val		
185 190 195		
ttg gtg cct ttg ctg ttg tgg gcc gtg gcc tat tcg cga aaa gcg ctt	739	
Leu Val Pro Leu Leu Leu Trp Ala Val Ala Tyr Ser Arg Lys Ala Leu		
200 205 210		
ttt gcg tcc acg tgg tcg gcc cag caa aag gct gcg gat ctg acc act	787	
Phe Ala Ser Thr Trp Ser Ala Gln Gln Lys Ala Ala Asp Leu Thr Thr		
215 220 225		
cat gtg gaa gaa act gtc acg ggt atc cgc gtg gtc aag gca ttt gcg	835	

His Val Glu Glu Thr Val Thr Gly Ile Arg Val Val Lys Ala Phe Ala	
230 235 240 245	
cag gaa gac cgc gag acc gac aaa ttg gat ctc acc gca cgt gag tta	883
Gln Glu Asp Arg Glu Thr Asp Lys Leu Asp Leu Thr Ala Arg Glu Leu	
250 255 260	
ttt gcc cag cgc atg cgc act gca cgt ctg acg gca aag ttc atc ccc	931
Phe Ala Gln Arg Met Arg Thr Ala Arg Leu Thr Ala Lys Phe Ile Pro	
265 270 275	
atg gtt gag cag ctt ccg cag ctt gct ttg gtg gtc aac att gtt ggc	979
Met Val Glu Gln Leu Pro Gln Leu Ala Leu Val Val Asn Ile Val Gly	
280 285 290	
ggt ggc tat ttg gcc atg act ggt cac atc acg gtg ggc acg ttt gtg	1027
Gly Gly Tyr Leu Ala Met Thr Gly His Ile Thr Val Gly Thr Phe Val	
295 300 305	
gcg ttt tct tcc tat ctc act agc ttg tcg gcg gtg gct agg tcc ctg	1075
Ala Phe Ser Ser Tyr Leu Thr Ser Leu Ser Ala Val Ala Arg Ser Leu	
310 315 320 325	
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Ser Gly Met Leu Met Arg Val Gln Leu Ala Leu Ser Ser Val Glu Arg	
330 335 340	
atc ttt gaa gtc att gat ctt cag cct gaa cgc acc gat cct gca cac	1171
Ile Phe Glu Val Ile Asp Leu Gln Pro Glu Arg Thr Asp Pro Ala His	
345 350 355	
ccc ctg tca ctt ccc gac act ccc ctg ggt ctg tcg ttc aac aac gta	1219
Pro Leu Ser Leu Pro Asp Thr Pro Leu Gly Leu Ser Phe Asn Asn Val	
360 365 370	
gat ttc cgt ggg att ctc aac ggt ttt gag ctg ggt gtt cag gcc ggt	1267
Asp Phe Arg Gly Ile Leu Asn Gly Phe Glu Leu Gly Val Gln Ala Gly	
375 380 385	
gaa acc gtt gtg ttg gtg ggc cct cca ggt tca ggc aag acc atg gct	1315
Glu Thr Val Val Leu Val Gly Pro Pro Gly Ser Gly Lys Thr Met Ala	
390 395 400 405	
gtg cag ctt gct gga aac ttt tat caa cca gac agc ggc cac atc gcc	1363
Val Gln Leu Ala Gly Asn Phe Tyr Gln Pro Asp Ser Gly His Ile Ala	
410 415 420	
ttt gat agc aac ggc cat cgc act cgc ttc gac gac ctc acc cac agc	1411
Phe Asp Ser Asn Gly His Arg Thr Arg Phe Asp Asp Leu Thr His Ser	
425 430 435	
gat atc cgc agg aat ctc atc gcg gtt ttt gat gag ccg ttc ttg tac	1459
Asp Ile Arg Arg Asn Leu Ile Ala Val Phe Asp Glu Pro Phe Leu Tyr	
440 445 450	
tcc tcc tcc ata ccg cga gaa cat ctc gat ggg ttt gga tgt cag	1504
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<210> 68

<211> 468

<212> PRT

<213> Corynebacterium glutamicum

<400> 68

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Arg Pro Trp Leu Thr Ser Phe Thr Val Ile Ser Ala Leu Ala Ala Thr
 35 40 45

Leu Phe Glu Leu Thr Leu Pro Leu Leu Thr Gly Gly Ala Ile Asp Ile
 50 55 60

Ala Leu Gly Asn Thr Gly Asp Thr Leu Thr Thr Asp Leu Leu Asp Arg
 65 70 75 80

Phe Thr Pro Ser Gly Leu Ser Val Leu Thr Ser Val Ile Ala Leu Ile
 85 90 95

Val Leu Leu Ala Leu Leu Arg Tyr Ala Ser Gln Phe Gly Arg Arg Tyr
 100 105 110

Thr Ala Gly Lys Leu Ser Met Gly Val Gln His Asp Val Arg Leu Lys
 115 120 125

Thr Met Arg Ser Leu Gln Asn Leu Asp Gly Pro Gly Gln Asp Ser Ile
 130 135 140

Arg Thr Gly Gln Val Val Ser Arg Ser Ile Ser Asp Ile Asn Met Val
 145 150 155 160

Gln Ser Leu Val Ala Met Leu Pro Met Leu Ile Gly Asn Val Val Lys
 165 170 175

Leu Val Leu Thr Leu Val Ile Met Leu Ala Ile Ser Pro Pro Leu Thr
 180 185 190

Ile Ile Ala Ala Val Leu Val Pro Leu Leu Leu Trp Ala Val Ala Tyr
 195 200 205

Ser Arg Lys Ala Leu Phe Ala Ser Thr Trp Ser Ala Gln Gln Lys Ala
 210 215 220

Ala Asp Leu Thr Thr His Val Glu Glu Thr Val Thr Gly Ile Arg Val
 225 230 235 240

Val Lys Ala Phe Ala Gln Glu Asp Arg Glu Thr Asp Lys Leu Asp Leu
 245 250 255

Thr Ala Arg Glu Leu Phe Ala Gln Arg Met Arg Thr Ala Arg Leu Thr
 260 265 270

Ala Lys Phe Ile Pro Met Val Glu Gln Leu Pro Gln Leu Ala Leu Val
 275 280 285

Val Asn Ile Val Gly Gly Gly Tyr Leu Ala Met Thr Gly His Ile Thr
 290 295 300

Val Gly Thr Phe Val Ala Phe Ser Ser Tyr Leu Thr Ser Leu Ser Ala
 305 310 315 320

Val Ala Arg Ser Leu Ser Gly Met Leu Met Arg Val Gln Leu Ala Leu
 325 330 335

Ser Ser Val Glu Arg Ile Phe Glu Val Ile Asp Leu Gln Pro Glu Arg
 340 345 350

Thr Asp Pro Ala His Pro Leu Ser Leu Pro Asp Thr Pro Leu Gly Leu
 355 360 365

Ser Phe Asn Asn Val Asp Phe Arg Gly Ile Leu Asn Gly Phe Glu Leu
 370 375 380

Gly Val Gln Ala Gly Glu Thr Val Val Leu Val Gly Pro Pro Gly Ser
 385 390 395 400

Gly Lys Thr Met Ala Val Gln Leu Ala Gly Asn Phe Tyr Gln Pro Asp
 405 410 415

Ser Gly His Ile Ala Phe Asp Ser Asn Gly His Arg Thr Arg Phe Asp
 420 425 430

Asp Leu Thr His Ser Asp Ile Arg Arg Asn Leu Ile Ala Val Phe Asp
 435 440 445

Glu Pro Phe Leu Tyr Ser Ser Ser Ile Pro Arg Glu His Leu Asp Gly
 450 455 460

Phe Gly Cys Gln
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<210> 69
 <211> 295
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (84)..(272)
 <223> RXC03185

<400> 69
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 Met Asn Asp Leu Ala Ala Glu Gly Glu Asn
 1 5 10

gat cct tac cgc atg gtt cag cag ctg cgc cgc aag ctc tct cgc ttc 161
 Asp Pro Tyr Arg Met Val Gln Gln Leu Arg Arg Lys Leu Ser Arg Phe
 15 20 25

gtc gag cag aag tgg aag cgc cag ccg gtc atc atg cca acc gtc att 209
 Val Glu Gln Lys Trp Lys Arg Gln Pro Val Ile Met Pro Thr Val Ile
 30 35 40

tca cgc gag tcc ctg taaaagcatt tcgcttttcg acg 295
Ser Arg Glu Ser Leu
60

aac act ggc gat ggt gcg ggc atc ctc atg cag att ccg gac ggc ttt 307
Asn Thr Gly Asp Gly Ala Gly Ile Leu Met Gln Ile Pro Asp Gly Phe
55 60 65

tat	cgt	gaa	gta	tct	ggc	att	gag	ctt	cct	gag	gca	ggg	gag	tat	gcc	355
Tyr	Arg	Glu	Val	Ser	Gly	Ile	Glu	Leu	Pro	Glu	Ala	Gly	Glu	Tyr	Ala	
70					75				80						85	
act	ggt	att	gcg	ttc	ttg	cct	cgc	ggt	cgc	atg	gcg	atg	atg	gat	gct	403
Thr	Gly	Ile	Ala	Phe	Leu	Pro	Arg	Gly	Arg	Met	Ala	Met	Met	Asp	Ala	
				90				95						100		
cag	aag	gaa	att	gag	cgc	atc	gca	aag	caa	gaa	ggg	gcc	gat	gtg	ctt	451
Gln	Lys	Glu	Ile	Glu	Arg	Ile	Ala	Lys	Gln	Glu	Gly	Ala	Asp	Val	Leu	
			105					110					115			
ggt	tgg	cgc	atg	gtt	cct	ttt	gat	tct	cgt	gat	ttg	ggg	tcc	atg	gct	499
Gly	Trp	Arg	Met	Val	Pro	Phe	Asp	Ser	Arg	Asp	Leu	Gly	Ser	Met	Ala	
		120					125					130				
gag	gag	gcg	atg	cct	agt	ttc	gcg	cag	att	ttc	ctt	act	gtg	cct	gga	547
Glu	Glu	Ala	Met	Pro	Ser	Phe	Ala	Gln	Ile	Phe	Leu	Thr	Val	Pro	Gly	
	135					140					145					
aaa	tct	ggt	gaa	gat	ctt	gac	cgt	gtg	atg	ttc	ttt	atc	cgt	aag	cgt	595
Lys	Ser	Gly	Glu	Asp	Leu	Asp	Arg	Val	Met	Phe	Phe	Ile	Arg	Lys	Arg	
150					155				160						165	
tgt	gag	cgt	gag	ctg	ggc	acc	acc	aat	ggt	cgc	gat	acg	gtg	tat	ttc	643
Cys	Glu	Arg	Glu	Leu	Gly	Thr	Thr	Asn	Gly	Arg	Asp	Thr	Val	Tyr	Phe	
				170				175						180		
ccg	tcg	cta	tct	tca	cgc	acc	atc	att	tac	aaa	ggc	atg	ttg	acc	act	691
Pro	Ser	Leu	Ser	Ser	Arg	Thr	Ile	Ile	Tyr	Lys	Gly	Met	Leu	Thr	Thr	
			185				190						195			
ctg	cag	ctt	gag	ggc	ttc	ttt	gag	gat	ctg	ggt	gat	gct	cgc	ctg	gag	739
Leu	Gln	Leu	Glu	Gly	Phe	Phe	Glu	Asp	Leu	Gly	Asp	Ala	Arg	Leu	Glu	
		200					205					210				
tcg	gcc	att	gct	att	gtg	cac	tcg	cgt	ttc	tcc	acg	aac	act	ttc	cca	787
Ser	Ala	Ile	Ala	Ile	Val	His	Ser	Arg	Phe	Ser	Thr	Asn	Thr	Phe	Pro	
	215					220					225					
agc	tgg	ccg	ctg	gcg	cac	ccg	tac	cgt	ttc	gtt	gcc	cac	aac	ggt	gag	835
Ser	Trp	Pro	Leu	Ala	His	Pro	Tyr	Arg	Phe	Val	Ala	His	Asn	Gly	Glu	
230					235				240					245		
atc	aac	act	gtg	cgt	ggc	aat	gaa	aac	tgg	atg	cgc	gcc	cgc	gag	gcg	883
Ile	Asn	Thr	Val	Arg	Gly	Asn	Glu	Asn	Trp	Met	Arg	Ala	Arg	Glu	Ala	
				250				255						260		
ctt	atc	aaa	aac	gac	aag	ctg	ggc	aat	ttg	agc	agc	gtg	ctg	cct	atc	931
Leu	Ile	Lys	Asn	Asp	Lys	Leu	Gly	Asn	Leu	Ser	Ser	Val	Leu	Pro	Ile	
			265				270						275			
tgc	acc	ccg	gag	ggc	tcg	gat	acc	gcg	cgt	ttc	gac	gag	gct	ttg	gag	979
Cys	Thr	Pro	Glu	Gly	Ser	Asp	Thr	Ala	Arg	Phe	Asp	Glu	Ala	Leu	Glu	
		280					285					290				
ctt	ttg	cac	ctg	ggc	gga	tac	tca	ctt	ccg	cat	gct	gtt	gcg	atg	atg	1027
Leu	Leu	His	Leu	Gly	Gly	Tyr	Ser	Leu	Pro	His	Ala	Val	Ala	Met	Met	
	295					300					305					

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gat ttc tac gaa tac cac tct tgt ctg atg gag cca tgg gat ggt cct Asp Phe Tyr Glu Tyr His Ser Cys Leu Met Glu Pro Trp Asp Gly Pro 330 335 340	1123
gca gcg ctg gca ttt act gac ggt cgt ttt gtg ggt gcc gtg ctg gac Ala Ala Leu Ala Phe Thr Asp Gly Arg Phe Val Gly Ala Val Leu Asp 345 350 355	1171
cgt aat ggc ctg cga cct ggg cga atc acc att act gat tcg ggt ttg Arg Asn Gly Leu Arg Pro Gly Arg Ile Thr Ile Thr Asp Ser Gly Leu 360 365 370	1219
gtt gtg atg gct tct gaa tcg gga gtg ttg gac ttg agg gag gag agc Val Val Met Ala Ser Glu Gly Val Leu Asp Leu Arg Glu Glu Ser 375 380 385	1267
gtc gta aag cgt act cgc gta cag cct gga cgc atg ttc ctt gtt gac Val Val Lys Arg Thr Arg Val Gln Pro Gly Arg Met Phe Leu Val Asp 390 395 400 405	1315
act gcc gag ggc cgc atc gtt gaa gac gag gaa atc aag cag aaa tta Thr Ala Glu Gly Arg Ile Val Glu Asp Glu Glu Ile Lys Gln Lys Leu 410 415 420	1363
agc gaa gcg cag cca tat ggt gag tgg att cgc gat aat ttt gtg cat Ser Glu Ala Gln Pro Tyr Gly Glu Trp Ile Arg Asp Asn Phe Val His 425 430 435	1411
ctg gat cgt ctg cct cag aca cgc tac aac tac atg gcg cac tct cgt Leu Asp Arg Leu Pro Gln Thr Arg Tyr Asn Tyr Met Ala His Ser Arg 440 445 450	1459
gct gtg ttg cgt cag cgt gtt ttc gga atc act gaa gaa gat gtg gat Ala Val Leu Arg Gln Arg Val Phe Gly Ile Thr Glu Glu Asp Val Asp 455 460 465	1507
ttg ttg ctg ctg ccg atg gcc cgc cag ggt gct gag gcg att ggt tcc Leu Leu Leu Leu Pro Met Ala Arg Gln Gly Ala Glu Ala Ile Gly Ser 470 475 480 485	1555
atg ggt tcg gat acg cca att gcg gcg cta tcc cag cga cca cgc atg Met Gly Ser Asp Thr Pro Ile Ala Ala Leu Ser Gln Arg Pro Arg Met 490 495 500	1603
ctt tat gat ttc ttc gcg cag cgc ttt gct cag gtg aca aac cca ccg Leu Tyr Asp Phe Phe Ala Gln Arg Phe Ala Gln Val Thr Asn Pro Pro 505 510 515	1651
ttg gac tct atc cgc gaa aag cct gtg acc agc atg ttc act ttg ttg Leu Asp Ser Ile Arg Glu Lys Pro Val Thr Ser Met Phe Thr Leu Leu 520 525 530	1699
ggt gcg cag tct gac gtg ctc aat ccg ggt cct gat gcg gcg cga cgt Gly Ala Gln Ser Asp Val Leu Asn Pro Gly Pro Asp Ala Ala Arg Arg 535 540 545	1747
atc cgt ttg gaa tcg ccg atc att gat aac cat gag ctg gcc acc ttg	1795

Ile	Arg	Leu	Glu	Ser	Pro	Ile	Ile	Asp	Asn	His	Glu	Leu	Ala	Thr	Leu		
550					555					560					565		
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Ile	Asn	Ala	Asn	Ala	His	Gly	Glu	Trp	Asp	Ser	Phe	Gly	Ala	Ala	Val		
				570					575					580			
att	tct	ggg	ttg	tac	cca	gtg	gct	cac	cat	ggg	gcc	ggc	atg	aag	gct	1891	
Ile	Ser	Gly	Leu	Tyr	Pro	Val	Ala	His	His	Gly	Ala	Gly	Met	Lys	Ala		
			585					590					595				
gcg	att	gct	cgt	gtg	cgc	cgc	gag	gtt	tct	gaa	gca	atc	cgc	aat	ggc	1939	
Ala	Ile	Ala	Arg	Val	Arg	Arg	Glu	Val	Ser	Glu	Ala	Ile	Arg	Asn	Gly		
		600					605					610					
aag	acg	ttg	atc	gtg	ctg	tcg	gat	cgt	gaa	tct	gat	gag	cgc	atg	gca	1987	
Lys	Thr	Leu	Ile	Val	Leu	Ser	Asp	Arg	Glu	Ser	Asp	Glu	Arg	Met	Ala		
	615					620					625						
cct	atc	cct	gcg	ctg	ctg	ctg	act	tcc	gct	gtg	cat	cag	tac	ttg	gtg	2035	
Pro	Ile	Pro	Ala	Leu	Leu	Leu	Thr	Ser	Ala	Val	His	Gln	Tyr	Leu	Val		
630					635					640					645		
cag	caa	cgt	acc	cgt	acc	cag	tgc	tcc	ctg	gtg	gtg	gaa	tcc	ggc	gat	2083	
Gln	Gln	Arg	Thr	Arg	Thr	Gln	Cys	Ser	Leu	Val	Val	Glu	Ser	Gly	Asp		
				650				655						660			
gcc	cgc	gag	gtt	cat	cac	ctg	gcg	atg	ctc	att	ggg	ttt	ggg	gcc	gat	2131	
Ala	Arg	Glu	Val	His	His	Leu	Ala	Met	Leu	Ile	Gly	Phe	Gly	Ala	Asp		
			665					670					675				
gcg	atc	aac	ccg	tac	atg	gca	ttt	gaa	acc	atc	gat	gag	ctg	cgc	atg	2179	
Ala	Ile	Asn	Pro	Tyr	Met	Ala	Phe	Glu	Thr	Ile	Asp	Glu	Leu	Arg	Met		
		680					685					690					
aag	ggg	cag	ttg	ggg	gat	ctt	tct	ttg	gat	gag	gca	tcc	cga	aac	tac	2227	
Lys	Gly	Gln	Leu	Gly	Asp	Leu	Ser	Leu	Asp	Glu	Ala	Ser	Arg	Asn	Tyr		
	695					700					705						
atc	aag	gca	gcc	acc	act	ggg	gtg	ctg	aag	gtg	atg	tcc	aag	atg	ggc	2275	
Ile	Lys	Ala	Ala	Thr	Thr	Gly	Val	Leu	Lys	Val	Met	Ser	Lys	Met	Gly		
710					715					720				725			
att	gca	acg	gtg	tct	tcg	tac	cgt	ggc	gcg	cag	ctt	gcc	gat	gtc	act	2323	
Ile	Ala	Thr	Val	Ser	Ser	Tyr	Arg	Gly	Ala	Gln	Leu	Ala	Asp	Val	Thr		
				730					735					740			
ggg	ctg	cac	cag	gat	ctc	ctg	gac	aac	tac	ttc	ggg	ggg	att	gct	tca	2371	
Gly	Leu	His	Gln	Asp	Leu	Leu	Asp	Asn	Tyr	Phe	Gly	Gly	Ile	Ala	Ser		
			745				750						755				
cca	att	tct	ggc	atc	ggg	ctg	gat	gaa	gtt	gca	gct	gac	gta	gaa	gct	2419	
Pro	Ile	Ser	Gly	Ile	Gly	Leu	Asp	Glu	Val	Ala	Ala	Asp	Val	Glu	Ala		
		760					765					770					
cgt	cac	cgc	agc	gca	ttt	ttg	cca	cgc	cct	gaa	gag	cac	gct	cac	cgt	2467	
Arg	His	Arg	Ser	Ala	Phe	Leu	Pro	Arg	Pro	Glu	Glu	His	Ala	His	Arg		
	775					780					785						
gaa	ttg	gat	ttg	ggg	ggg	gaa	tac	aag	tgg	cgc	cgc	gaa	ggg	gaa	tac	2515	
Glu	Leu	Asp	Leu	Gly	Gly	Glu	Tyr	Lys	Trp	Arg	Arg	Glu	Gly	Glu	Tyr		

790	795	800	805	
cac ctg ttc aac cca gaa acc atc ttc aag ctg cag cat gca acg cgt				2563
His Leu Phe Asn Pro Glu Thr Ile Phe Lys Leu Gln His Ala Thr Arg	810	815	820	
tct ggc agc tac gag att ttc aag gat tac acc cgc aag gtt gat gat				2611
Ser Gly Ser Tyr Glu Ile Phe Lys Asp Tyr Thr Arg Lys Val Asp Asp	825	830	835	
caa tcc act cgc ttg ggt act att cgt gga ctg ttt gag ttc agc acg				2659
Gln Ser Thr Arg Leu Gly Thr Ile Arg Gly Leu Phe Glu Phe Ser Thr	840	845	850	
gac cgc aag cca att tcg gtg tct gag gtg gag ccg gtc agt gag atc				2707
Asp Arg Lys Pro Ile Ser Val Ser Glu Val Glu Pro Val Ser Glu Ile	855	860	865	
gtg aag cgt ttc tcc act ggt gcg atg tct tat ggc tcg att tct gct				2755
Val Lys Arg Phe Ser Thr Gly Ala Met Ser Tyr Gly Ser Ile Ser Ala	870	875	880	885
gaa gcc cat gag gtc ttg gcc atc gcc atg aac cga ctg ggc ggt atg				2803
Glu Ala His Glu Val Leu Ala Ile Ala Met Asn Arg Leu Gly Gly Met	890	895	900	
tcc aac tcc ggc gaa ggt ggc gag gac gcc cgc cga ttt gat gtg gaa				2851
Ser Asn Ser Gly Glu Gly Gly Glu Asp Ala Arg Arg Phe Asp Val Glu	905	910	915	
ccc aac ggt gac tgg aag cgc tct gcc att aag cag gtg gcc tcg gga				2899
Pro Asn Gly Asp Trp Lys Arg Ser Ala Ile Lys Gln Val Ala Ser Gly	920	925	930	
cgt ttc ggc gtg acc agc cac tac ttg aac aac tgc acc gat att cag				2947
Arg Phe Gly Val Thr Ser His Tyr Leu Asn Asn Cys Thr Asp Ile Gln	935	940	945	
atc aag atg gca cag ggc gca aag ccc ggt gaa ggt ggc cag ctg cca				2995
Ile Lys Met Ala Gln Gly Ala Lys Pro Gly Glu Gly Gly Gln Leu Pro	950	955	960	965
cca aac aag gtg tac cca tgg gtt gca gaa gtc cgc atc acc acc cca				3043
Pro Asn Lys Val Tyr Pro Trp Val Ala Glu Val Arg Ile Thr Thr Pro	970	975	980	
ggc gtt ggt ctg att tcc cct cca cca cac cac gat att tac tcc att				3091
Gly Val Gly Leu Ile Ser Pro Pro Pro His His Asp Ile Tyr Ser Ile	985	990	995	
gag gat ctg gct cag ctg atc cac gac ctg aag aac gct aac cca cgc				3139
Glu Asp Leu Ala Gln Leu Ile His Asp Leu Lys Asn Ala Asn Pro Arg	1000	1005	1010	
gca cga atc cac gtg aag cta gtg gca gaa caa ggc gtg ggc acc gtt				3187
Ala Arg Ile His Val Lys Leu Val Ala Glu Gln Gly Val Gly Thr Val	1015	1020	1025	
gcc gca ggt gtg tcc aaa gca cac gct gat gtg gtg ctt att tcc ggc				3235
Ala Ala Gly Val Ser Lys Ala His Ala Asp Val Val Leu Ile Ser Gly	1030	1035	1040	1045

cac gat ggc gga act ggc gca tct cct ttg acc tcc ctg aag cat gcc	3283
His Asp Gly Gly Thr Gly Ala Ser Pro Leu Thr Ser Leu Lys His Ala	
1050 1055 1060	
ggt ggt cca tgg gag ttg ggc ttg gct gaa acc cag caa acg ttg ctg	3331
Gly Gly Pro Trp Glu Leu Gly Leu Ala Glu Thr Gln Gln Thr Leu Leu	
1065 1070 1075	
ctc aac ggc ctg cgc gat cgt att cgc gtg cag tgc gat ggt cag ctg	3379
Leu Asn Gly Leu Arg Asp Arg Ile Arg Val Gln Cys Asp Gly Gln Leu	
1080 1085 1090	
aaa act ggc cga gac gtg gtt atc gca gct ctt ctc ggt gcc gaa gaa	3427
Lys Thr Gly Arg Asp Val Val Ile Ala Ala Leu Leu Gly Ala Glu Glu	
1095 1100 1105	
ttc ggt ttt gcc acc gca ccg ctg gtg gtt gaa ggc tgc atc atg atg	3475
Phe Gly Phe Ala Thr Ala Pro Leu Val Val Glu Gly Cys Ile Met Met	
1110 1115 1120 1125	
cgc gtc tgc cac ctg gac acc tgc ccg gtg ggt atc gct acc cag aac	3523
Arg Val Cys His Leu Asp Thr Cys Pro Val Gly Ile Ala Thr Gln Asn	
1130 1135 1140	
ccg gat ttg cgt tcc aag ttc acc ggc aag gct gaa cac gtg gtc aac	3571
Pro Asp Leu Arg Ser Lys Phe Thr Gly Lys Ala Glu His Val Val Asn	
1145 1150 1155	
ttc ttc acc ttc atc gcc cag gaa gtc cgt gag tac ttg gca cag ctt	3619
Phe Phe Thr Phe Ile Ala Gln Glu Val Arg Glu Tyr Leu Ala Gln Leu	
1160 1165 1170	
ggt ttc cgc tct att gat gaa gcc gtc gga caa gcc cag gtg ctg cgc	3667
Gly Phe Arg Ser Ile Asp Glu Ala Val Gly Gln Ala Gln Val Leu Arg	
1175 1180 1185	
aag cgt tcc gga atc cca gct gat tcc cgc gca gca cac ctg gat ttg	3715
Lys Arg Ser Gly Ile Pro Ala Asp Ser Arg Ala Ala His Leu Asp Leu	
1190 1195 1200 1205	
agc cca att ttc cat cgc cca gaa act cca cac ttc cca act cag gat	3763
Ser Pro Ile Phe His Arg Pro Glu Thr Pro His Phe Pro Thr Gln Asp	
1210 1215 1220	
gtg cgt tgc acc aag acc cag gaa cac agc cta gaa aaa gcc ctg gac	3811
Val Arg Cys Thr Lys Thr Gln Glu His Ser Leu Glu Lys Ala Leu Asp	
1225 1230 1235	
aac gca ttt att gat aag gct tcg gac acg atc acc cgt gcc gca gcg	3859
Asn Ala Phe Ile Asp Lys Ala Ser Asp Thr Ile Thr Arg Ala Ala Ala	
1240 1245 1250	
ggt gtg gaa acc agc att gtt att gat agc tcc atc agc aac gtc aac	3907
Gly Val Glu Thr Ser Ile Val Ile Asp Ser Ser Ile Ser Asn Val Asn	
1255 1260 1265	
cgt tca gtt ggc acg atg ctg ggt tct gca gtc agc cgc gtg gct ggt	3955
Arg Ser Val Gly Thr Met Leu Gly Ser Ala Val Ser Arg Val Ala Gly	
1270 1275 1280 1285	

gcc caa ggt ttg cca gac ggc acc atc acc ttg aat ctt caa ggc tgc	4003
Ala Gln Gly Leu Pro Asp Gly Thr Ile Thr Leu Asn Leu Gln Gly Cys	
1290 1295 1300	
gcc ggt aac tcc ttt ggc gcg ttc atc cca cga ggc atc acc atc aac	4051
Ala Gly Asn Ser Phe Gly Ala Phe Ile Pro Arg Gly Ile Thr Ile Asn	
1305 1310 1315	
ctc acc ggc gat gcc aat gac ttt gtg ggc aag gga tta tct ggc gga	4099
Leu Thr Gly Asp Ala Asn Asp Phe Val Gly Lys Gly Leu Ser Gly Gly	
1320 1325 1330	
aag att gtg atc aag cct tcc gct cag gct ccg aag cag ctg aag aac	4147
Lys Ile Val Ile Lys Pro Ser Ala Gln Ala Pro Lys Gln Leu Lys Asn	
1335 1340 1345	
aat cca aat atc att gcc gga aac gtg ctt gga tac ggc gca acc agt	4195
Asn Pro Asn Ile Ile Ala Gly Asn Val Leu Gly Tyr Gly Ala Thr Ser	
1350 1355 1360 1365	
ggt gaa ttg ttc att cgt ggc cag gtc ggc gaa cgt ttc tgc gtc cgt	4243
Gly Glu Leu Phe Ile Arg Gly Gln Val Gly Glu Arg Phe Cys Val Arg	
1370 1375 1380	
aac tct ggc gcc acc gca gtg gtt gaa ggt atc gga aac cac ggt tgt	4291
Asn Ser Gly Ala Thr Ala Val Val Glu Gly Ile Gly Asn His Gly Cys	
1385 1390 1395	
gag tac atg act ggc ggc cga gtc ctg gtt ttg ggc ccg gtt ggt gag	4339
Glu Tyr Met Thr Gly Gly Arg Val Leu Val Leu Gly Pro Val Gly Glu	
1400 1405 1410	
aac ttt ggt gcc ggc atg tct ggt ggc att gca tac ctg gct aat tcc	4387
Asn Phe Gly Ala Gly Met Ser Gly Gly Ile Ala Tyr Leu Ala Asn Ser	
1415 1420 1425	
ccg gac cta aac cag aag atc aat ggc gaa ttg gtg gat gtt gtt cca	4435
Pro Asp Leu Asn Gln Lys Ile Asn Gly Glu Leu Val Asp Val Val Pro	
1430 1435 1440 1445	
ctg agc gct gac gat ctg acg tgg gct gat gag ctc att gct cgc cac	4483
Leu Ser Ala Asp Asp Leu Thr Trp Ala Asp Glu Leu Ile Ala Arg His	
1450 1455 1460	
cgc gaa ctc acc gga tcc gag acc aag ctg cgt gca caa gat ttg gtg	4531
Arg Glu Leu Thr Gly Ser Glu Thr Lys Leu Arg Ala Gln Asp Leu Val	
1465 1470 1475	
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Lys Ile Met Pro Arg Asp Phe Gln Lys Val Leu Asn Ile Ile Glu Thr	
1480 1485 1490	
gcc cac gct gag ggc caa gac cca gca atc aag atc atg gag gca gtg	4627
Ala His Ala Glu Gly Gln Asp Pro Ala Ile Lys Ile Met Glu Ala Val	
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agc taatggccga cccacaagga ttc	4653
Ser	
1510	

<210> 72
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 <213> Corynebacterium glutamicum

<400> 72

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Gly	Val	Ala	Phe	Ile	Ala	Asp	Ile	His	Gly	Arg	Pro	Ser	Arg	Ser	Ile
			20					25					30		
Val	Asp	Arg	Ala	Leu	Glu	Ala	Leu	Arg	Asn	Ile	Asp	His	Arg	Gly	Ala
		35					40					45			
Ala	Gly	Ala	Glu	Lys	Asn	Thr	Gly	Asp	Gly	Ala	Gly	Ile	Leu	Met	Gln
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Ile	Pro	Asp	Gly	Phe	Tyr	Arg	Glu	Val	Ser	Gly	Ile	Glu	Leu	Pro	Glu
65					70					75					80
Ala	Gly	Glu	Tyr	Ala	Thr	Gly	Ile	Ala	Phe	Leu	Pro	Arg	Gly	Arg	Met
				85					90					95	
Ala	Met	Met	Asp	Ala	Gln	Lys	Glu	Ile	Glu	Arg	Ile	Ala	Lys	Gln	Glu
			100					105					110		
Gly	Ala	Asp	Val	Leu	Gly	Trp	Arg	Met	Val	Pro	Phe	Asp	Ser	Arg	Asp
		115					120					125			
Leu	Gly	Ser	Met	Ala	Glu	Glu	Ala	Met	Pro	Ser	Phe	Ala	Gln	Ile	Phe
130						135						140			
Leu	Thr	Val	Pro	Gly	Lys	Ser	Gly	Glu	Asp	Leu	Asp	Arg	Val	Met	Phe
145					150					155					160
Phe	Ile	Arg	Lys	Arg	Cys	Glu	Arg	Glu	Leu	Gly	Thr	Thr	Asn	Gly	Arg
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Asp	Thr	Val	Tyr	Phe	Pro	Ser	Leu	Ser	Ser	Arg	Thr	Ile	Ile	Tyr	Lys
			180					185					190		
Gly	Met	Leu	Thr	Thr	Leu	Gln	Leu	Glu	Gly	Phe	Phe	Glu	Asp	Leu	Gly
		195					200					205			
Asp	Ala	Arg	Leu	Glu	Ser	Ala	Ile	Ala	Ile	Val	His	Ser	Arg	Phe	Ser
	210					215					220				
Thr	Asn	Thr	Phe	Pro	Ser	Trp	Pro	Leu	Ala	His	Pro	Tyr	Arg	Phe	Val
225					230					235					240
Ala	His	Asn	Gly	Glu	Ile	Asn	Thr	Val	Arg	Gly	Asn	Glu	Asn	Trp	Met
				245					250					255	
Arg	Ala	Arg	Glu	Ala	Leu	Ile	Lys	Asn	Asp	Lys	Leu	Gly	Asn	Leu	Ser
			260					265					270		
Ser	Val	Leu	Pro	Ile	Cys	Thr	Pro	Glu	Gly	Ser	Asp	Thr	Ala	Arg	Phe
		275					280					285			
Asp	Glu	Ala	Leu	Glu	Leu	Leu	His	Leu	Gly	Gly	Tyr	Ser	Leu	Pro	His

290					295					300					
Ala	Val	Ala	Met	Met	Ile	Pro	Gln	Ala	Trp	Glu	His	Asn	Lys	Thr	Leu
305					310					315					320
Ser	Pro	Glu	Leu	Arg	Asp	Phe	Tyr	Glu	Tyr	His	Ser	Cys	Leu	Met	Glu
				325					330					335	
Pro	Trp	Asp	Gly	Pro	Ala	Ala	Leu	Ala	Phe	Thr	Asp	Gly	Arg	Phe	Val
			340					345					350		
Gly	Ala	Val	Leu	Asp	Arg	Asn	Gly	Leu	Arg	Pro	Gly	Arg	Ile	Thr	Ile
		355					360					365			
Thr	Asp	Ser	Gly	Leu	Val	Val	Met	Ala	Ser	Glu	Ser	Gly	Val	Leu	Asp
	370					375					380				
Leu	Arg	Glu	Glu	Ser	Val	Val	Lys	Arg	Thr	Arg	Val	Gln	Pro	Gly	Arg
385					390					395					400
Met	Phe	Leu	Val	Asp	Thr	Ala	Glu	Gly	Arg	Ile	Val	Glu	Asp	Glu	Glu
				405					410					415	
Ile	Lys	Gln	Lys	Leu	Ser	Glu	Ala	Gln	Pro	Tyr	Gly	Glu	Trp	Ile	Arg
			420					425					430		
Asp	Asn	Phe	Val	His	Leu	Asp	Arg	Leu	Pro	Gln	Thr	Arg	Tyr	Asn	Tyr
		435					440					445			
Met	Ala	His	Ser	Arg	Ala	Val	Leu	Arg	Gln	Arg	Val	Phe	Gly	Ile	Thr
	450					455					460				
Glu	Glu	Asp	Val	Asp	Leu	Leu	Leu	Leu	Pro	Met	Ala	Arg	Gln	Gly	Ala
465					470					475					480
Glu	Ala	Ile	Gly	Ser	Met	Gly	Ser	Asp	Thr	Pro	Ile	Ala	Ala	Leu	Ser
				485					490					495	
Gln	Arg	Pro	Arg	Met	Leu	Tyr	Asp	Phe	Phe	Ala	Gln	Arg	Phe	Ala	Gln
			500					505					510		
Val	Thr	Asn	Pro	Pro	Leu	Asp	Ser	Ile	Arg	Glu	Lys	Pro	Val	Thr	Ser
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Asp	Ala	Ala	Arg	Arg	Ile	Arg	Leu	Glu	Ser	Pro	Ile	Ile	Asp	Asn	His
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Glu	Leu	Ala	Thr	Leu	Ile	Asn	Ala	Asn	Ala	His	Gly	Glu	Trp	Asp	Ser
				565					570					575	
Phe	Gly	Ala	Ala	Val	Ile	Ser	Gly	Leu	Tyr	Pro	Val	Ala	His	His	Gly
			580					585					590		
Ala	Gly	Met	Lys	Ala	Ala	Ile	Ala	Arg	Val	Arg	Arg	Glu	Val	Ser	Glu
		595					600					605			
Ala	Ile	Arg	Asn	Gly	Lys	Thr	Leu	Ile	Val	Leu	Ser	Asp	Arg	Glu	Ser
	610					615					620				

Asp	Glu	Arg	Met	Ala	Pro	Ile	Pro	Ala	Leu	Leu	Leu	Thr	Ser	Ala	Val	625	630	635	640
His	Gln	Tyr	Leu	Val	Gln	Gln	Arg	Thr	Arg	Thr	Gln	Cys	Ser	Leu	Val	645	650	655	
Val	Glu	Ser	Gly	Asp	Ala	Arg	Glu	Val	His	His	Leu	Ala	Met	Leu	Ile	660	665	670	
Gly	Phe	Gly	Ala	Asp	Ala	Ile	Asn	Pro	Tyr	Met	Ala	Phe	Glu	Thr	Ile	675	680	685	
Asp	Glu	Leu	Arg	Met	Lys	Gly	Gln	Leu	Gly	Asp	Leu	Ser	Leu	Asp	Glu	690	695	700	
Ala	Ser	Arg	Asn	Tyr	Ile	Lys	Ala	Ala	Thr	Thr	Gly	Val	Leu	Lys	Val	705	710	715	720
Met	Ser	Lys	Met	Gly	Ile	Ala	Thr	Val	Ser	Ser	Tyr	Arg	Gly	Ala	Gln	725	730	735	
Leu	Ala	Asp	Val	Thr	Gly	Leu	His	Gln	Asp	Leu	Leu	Asp	Asn	Tyr	Phe	740	745	750	
Gly	Gly	Ile	Ala	Ser	Pro	Ile	Ser	Gly	Ile	Gly	Leu	Asp	Glu	Val	Ala	755	760	765	
Ala	Asp	Val	Glu	Ala	Arg	His	Arg	Ser	Ala	Phe	Leu	Pro	Arg	Pro	Glu	770	775	780	
Glu	His	Ala	His	Arg	Glu	Leu	Asp	Leu	Gly	Gly	Glu	Tyr	Lys	Trp	Arg	785	790	795	800
Arg	Glu	Gly	Glu	Tyr	His	Leu	Phe	Asn	Pro	Glu	Thr	Ile	Phe	Lys	Leu	805	810	815	
Gln	His	Ala	Thr	Arg	Ser	Gly	Ser	Tyr	Glu	Ile	Phe	Lys	Asp	Tyr	Thr	820	825	830	
Arg	Lys	Val	Asp	Asp	Gln	Ser	Thr	Arg	Leu	Gly	Thr	Ile	Arg	Gly	Leu	835	840	845	
Phe	Glu	Phe	Ser	Thr	Asp	Arg	Lys	Pro	Ile	Ser	Val	Ser	Glu	Val	Glu	850	855	860	
Pro	Val	Ser	Glu	Ile	Val	Lys	Arg	Phe	Ser	Thr	Gly	Ala	Met	Ser	Tyr	865	870	875	880
Gly	Ser	Ile	Ser	Ala	Glu	Ala	His	Glu	Val	Leu	Ala	Ile	Ala	Met	Asn	885	890	895	
Arg	Leu	Gly	Gly	Met	Ser	Asn	Ser	Gly	Glu	Gly	Gly	Glu	Asp	Ala	Arg	900	905	910	
Arg	Phe	Asp	Val	Glu	Pro	Asn	Gly	Asp	Trp	Lys	Arg	Ser	Ala	Ile	Lys	915	920	925	
Gln	Val	Ala	Ser	Gly	Arg	Phe	Gly	Val	Thr	Ser	His	Tyr	Leu	Asn	Asn	930	935	940	

Cys Thr Asp Ile Gln Ile Lys Met Ala Gln Gly Ala Lys Pro Gly Glu
 945 950 955 960
 Gly Gly Gln Leu Pro Pro Asn Lys Val Tyr Pro Trp Val Ala Glu Val
 965 970 975
 Arg Ile Thr Thr Pro Gly Val Gly Leu Ile Ser Pro Pro Pro His His
 980 985 990
 Asp Ile Tyr Ser Ile Glu Asp Leu Ala Gln Leu Ile His Asp Leu Lys
 995 1000 1005
 Asn Ala Asn Pro Arg Ala Arg Ile His Val Lys Leu Val Ala Glu Gln
 1010 1015 1020
 Gly Val Gly Thr Val Ala Ala Gly Val Ser Lys Ala His Ala Asp Val
 1025 1030 1035 1040
 Val Leu Ile Ser Gly His Asp Gly Gly Thr Gly Ala Ser Pro Leu Thr
 1045 1050 1055
 Ser Leu Lys His Ala Gly Gly Pro Trp Glu Leu Gly Leu Ala Glu Thr
 1060 1065 1070
 Gln Gln Thr Leu Leu Leu Asn Gly Leu Arg Asp Arg Ile Arg Val Gln
 1075 1080 1085
 Cys Asp Gly Gln Leu Lys Thr Gly Arg Asp Val Val Ile Ala Ala Leu
 1090 1095 1100
 Leu Gly Ala Glu Glu Phe Gly Phe Ala Thr Ala Pro Leu Val Val Glu
 1105 1110 1115 1120
 Gly Cys Ile Met Met Arg Val Cys His Leu Asp Thr Cys Pro Val Gly
 1125 1130 1135
 Ile Ala Thr Gln Asn Pro Asp Leu Arg Ser Lys Phe Thr Gly Lys Ala
 1140 1145 1150
 Glu His Val Val Asn Phe Phe Thr Phe Ile Ala Gln Glu Val Arg Glu
 1155 1160 1165
 Tyr Leu Ala Gln Leu Gly Phe Arg Ser Ile Asp Glu Ala Val Gly Gln
 1170 1175 1180
 Ala Gln Val Leu Arg Lys Arg Ser Gly Ile Pro Ala Asp Ser Arg Ala
 1185 1190 1195 1200
 Ala His Leu Asp Leu Ser Pro Ile Phe His Arg Pro Glu Thr Pro His
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 Phe Pro Thr Gln Asp Val Arg Cys Thr Lys Thr Gln Glu His Ser Leu
 1220 1225 1230
 Glu Lys Ala Leu Asp Asn Ala Phe Ile Asp Lys Ala Ser Asp Thr Ile
 1235 1240 1245
 Thr Arg Ala Ala Ala Gly Val Glu Thr Ser Ile Val Ile Asp Ser Ser
 1250 1255 1260
 Ile Ser Asn Val Asn Arg Ser Val Gly Thr Met Leu Gly Ser Ala Val

1265	1270	1275	1280
Ser Arg Val Ala Gly Ala Gln Gly Leu Pro Asp Gly Thr Ile Thr Leu	1285	1290	1295
Asn Leu Gln Gly Cys Ala Gly Asn Ser Phe Gly Ala Phe Ile Pro Arg	1300	1305	1310
Gly Ile Thr Ile Asn Leu Thr Gly Asp Ala Asn Asp Phe Val Gly Lys	1315	1320	1325
Gly Leu Ser Gly Gly Lys Ile Val Ile Lys Pro Ser Ala Gln Ala Pro	1330	1335	1340
Lys Gln Leu Lys Asn Asn Pro Asn Ile Ile Ala Gly Asn Val Leu Gly	1345	1350	1355
			1360
Tyr Gly Ala Thr Ser Gly Glu Leu Phe Ile Arg Gly Gln Val Gly Glu	1365	1370	1375
Arg Phe Cys Val Arg Asn Ser Gly Ala Thr Ala Val Val Glu Gly Ile	1380	1385	1390
Gly Asn His Gly Cys Glu Tyr Met Thr Gly Gly Arg Val Leu Val Leu	1395	1400	1405
Gly Pro Val Gly Glu Asn Phe Gly Ala Gly Met Ser Gly Gly Ile Ala	1410	1415	1420
Tyr Leu Ala Asn Ser Pro Asp Leu Asn Gln Lys Ile Asn Gly Glu Leu	1425	1430	1435
			1440
Val Asp Val Val Pro Leu Ser Ala Asp Asp Leu Thr Trp Ala Asp Glu	1445	1450	1455
Leu Ile Ala Arg His Arg Glu Leu Thr Gly Ser Glu Thr Lys Leu Arg	1460	1465	1470
Ala Gln Asp Leu Val Lys Ile Met Pro Arg Asp Phe Gln Lys Val Leu	1475	1480	1485
Asn Ile Ile Glu Thr Ala His Ala Glu Gly Gln Asp Pro Ala Ile Lys	1490	1495	1500
Ile Met Glu Ala Val Ser	1505	1510	

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<211> 1906

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1906)

<223> FRXA00007

<400> 73

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	Met Lys Pro Gln Gly	
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ctc tac aac cct gcg cat gaa cat gac gcc tgc ggt gtg gcg ttt att	163	
Leu Tyr Asn Pro Ala His Glu His Asp Ala Cys Gly Val Ala Phe Ile		
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Ala Asp Ile His Gly Arg Pro Ser Arg Ser Ile Val Asp Arg Ala Leu		
25 30 35		
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Glu Ala Leu Arg Asn Ile Asp His Arg Gly Ala Ala Gly Ala Glu Lys		
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aac act ggc gat ggt gcg ggc atc ctc atg cag att ccg gac ggc ttt	307	
Asn Thr Gly Asp Gly Ala Gly Ile Leu Met Gln Ile Pro Asp Gly Phe		
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Tyr Arg Glu Val Ser Gly Ile Glu Leu Pro Glu Ala Gly Glu Tyr Ala		
70 75 80 85		
act ggt att gcg ttc ttg cct cgc ggt cgc atg gcg atg atg gat gct	403	
Thr Gly Ile Ala Phe Leu Pro Arg Gly Arg Met Ala Met Met Asp Ala		
90 95 100		
cag aag gaa att gag cgc atc gca aag caa gaa ggt gcc gat gtg ctt	451	
Gln Lys Glu Ile Glu Arg Ile Ala Lys Gln Glu Gly Ala Asp Val Leu		
105 110 115		
ggt tgg cgc atg gtt cct ttt gat tct cgt gat ttg ggt tcc atg gct	499	
Gly Trp Arg Met Val Pro Phe Asp Ser Arg Asp Leu Gly Ser Met Ala		
120 125 130		
gag gag gcg atg cct agt ttc gcg cag att ttc ctt act gtg cct gga	547	
Glu Glu Ala Met Pro Ser Phe Ala Gln Ile Phe Leu Thr Val Pro Gly		
135 140 145		
aaa tct ggt gaa gat ctt gac cgt gtg atg ttc ttt atc cgt aag cgt	595	
Lys Ser Gly Glu Asp Leu Asp Arg Val Met Phe Phe Ile Arg Lys Arg		
150 155 160 165		
tgt gag cgt gag ctg ggc acc acc aat ggt cgc gat acg gtg tat ttc	643	
Cys Glu Arg Glu Leu Gly Thr Thr Asn Gly Arg Asp Thr Val Tyr Phe		
170 175 180		
ccg tcg cta tct tca cgc acc atc att tac aaa ggc atg ttg acc act	691	
Pro Ser Leu Ser Ser Arg Thr Ile Ile Tyr Lys Gly Met Leu Thr Thr		
185 190 195		
ctg cag ctt gag ggc ttc ttt gag gat ctg ggt gat gct cgc ctg gag	739	
Leu Gln Leu Glu Gly Phe Phe Glu Asp Leu Gly Asp Ala Arg Leu Glu		
200 205 210		
tcg gcc att gct att gtg cac tcg cgt ttc tcc acg aac act ttc cca	787	
Ser Ala Ile Ala Ile Val His Ser Arg Phe Ser Thr Asn Thr Phe Pro		
215 220 225		
agc tgg ccg ctg gcg cac ccg tac cgt ttc gtt gcc cac aac ggt gag	835	

Ser	Trp	Pro	Leu	Ala	His	Pro	Tyr	Arg	Phe	Val	Ala	His	Asn	Gly	Glu		
230					235					240					245		
atc	aac	act	gtg	cgt	ggc	aat	gaa	aac	tgg	atg	cgc	gcc	cgc	gag	gcg		883
Ile	Asn	Thr	Val	Arg	Gly	Asn	Glu	Asn	Trp	Met	Arg	Ala	Arg	Glu	Ala		
				250					255					260			
ctt	atc	aaa	aac	gac	aag	ctg	ggc	aat	ttg	agc	agc	gtg	ctg	cct	atc		931
Leu	Ile	Lys	Asn	Asp	Lys	Leu	Gly	Asn	Leu	Ser	Ser	Val	Leu	Pro	Ile		
			265						270				275				
tgc	acc	ccg	gag	ggc	tcg	gat	acc	gcg	cgt	ttc	gac	gag	gct	ttg	gag		979
Cys	Thr	Pro	Glu	Gly	Ser	Asp	Thr	Ala	Arg	Phe	Asp	Glu	Ala	Leu	Glu		
		280						285				290					
ctt	ttg	cac	ctg	ggc	gga	tac	tca	ctt	ccg	cat	gct	gtt	gcg	atg	atg		1027
Leu	Leu	His	Leu	Gly	Gly	Tyr	Ser	Leu	Pro	His	Ala	Val	Ala	Met	Met		
			295				300				305						
atc	cct	cag	gcg	tgg	gaa	cac	aac	aag	acg	ctg	agc	cct	gag	ctg	cgt		1075
Ile	Pro	Gln	Ala	Trp	Glu	His	Asn	Lys	Thr	Leu	Ser	Pro	Glu	Leu	Arg		
310					315					320					325		
gat	ttc	tac	gaa	tac	cac	tct	tgt	ctg	atg	gag	cca	tgg	gat	ggg	cct		1123
Asp	Phe	Tyr	Glu	Tyr	His	Ser	Cys	Leu	Met	Glu	Pro	Trp	Asp	Gly	Pro		
				330						335				340			
gca	gcg	ctg	gca	ttt	act	gac	ggg	cgt	ttt	gtg	ggg	gcc	gtg	ctg	gac		1171
Ala	Ala	Leu	Ala	Phe	Thr	Asp	Gly	Arg	Phe	Val	Gly	Ala	Val	Leu	Asp		
			345					350					355				
cgt	aat	ggc	ctg	cga	cct	ggg	cga	atc	acc	att	act	gat	tcg	ggg	ttg		1219
Arg	Asn	Gly	Leu	Arg	Pro	Gly	Arg	Ile	Thr	Ile	Thr	Asp	Ser	Gly	Leu		
		360					365					370					
gtt	gtg	atg	gct	tct	gaa	tcg	gga	gtg	ttg	gac	ttg	agg	gag	gag	agc		1267
Val	Val	Met	Ala	Ser	Glu	Ser	Gly	Val	Leu	Asp	Leu	Arg	Glu	Glu	Ser		
		375				380					385						
gtc	gta	aag	cgt	act	cgc	gta	cag	cct	gga	cgc	atg	ttc	ctt	gtt	gac		1315
Val	Val	Lys	Arg	Thr	Arg	Val	Gln	Pro	Gly	Arg	Met	Phe	Leu	Val	Asp		
390					395					400					405		
act	gcc	gag	ggc	cgc	atc	gtt	gaa	gac	gag	gaa	atc	aag	cag	aaa	tta		1363
Thr	Ala	Glu	Gly	Arg	Ile	Val	Glu	Asp	Glu	Glu	Ile	Lys	Gln	Lys	Leu		
				410					415					420			
agc	gaa	gcg	cag	cca	tat	ggg	gag	tgg	att	cgc	gat	aat	ttt	gtg	cat		1411
Ser	Glu	Ala	Gln	Pro	Tyr	Gly	Glu	Trp	Ile	Arg	Asp	Asn	Phe	Val	His		
			425					430					435				
ctg	gat	cgt	ctg	cct	cag	aca	cgc	tac	aac	tac	atg	gcg	cac	tct	cgt		1459
Leu	Asp	Arg	Leu	Pro	Gln	Thr	Arg	Tyr	Asn	Tyr	Met	Ala	His	Ser	Arg		
		440					445					450					
gct	gtg	ttg	cgt	cag	cgt	gtt	ttc	gga	atc	act	gaa	gaa	gat	gtg	gat		1507
Ala	Val	Leu	Arg	Gln	Arg	Val	Phe	Gly	Ile	Thr	Glu	Glu	Asp	Val	Asp		
		455				460					465						
ttg	ttg	ctg	ctg	ccg	atg	gcc	cgc	cag	ggg	gct	gag	gcg	att	ggg	tcc		1555
Leu	Leu	Leu	Leu	Pro	Met	Ala	Arg	Gln	Gly	Ala	Glu	Ala	Ile	Gly	Ser		

470	475	480	485	
atg ggt tcg gat acg cca att gcg gcg cta tcc cag cga cca cgc atg				1603
Met Gly Ser Asp Thr Pro Ile Ala Ala Leu Ser Gln Arg Pro Arg Met				
	490	495	500	
ctt tat gat ttc ttc gcg cag cgc ttt gct cag gtg aca aac cca ccg				1651
Leu Tyr Asp Phe Phe Ala Gln Arg Phe Ala Gln Val Thr Asn Pro Pro				
	505	510	515	
ttg gac tct atc cgc gaa aag cct gtg acc agc atg ttc act ttg ttg				1699
Leu Asp Ser Ile Arg Glu Lys Pro Val Thr Ser Met Phe Thr Leu Leu				
	520	525	530	
ggt gcg cag tct gac gtg ctc aat ccg ggt cct gat gcg gcg cga cgt				1747
Gly Ala Gln Ser Asp Val Leu Asn Pro Gly Pro Asp Ala Ala Arg Arg				
	535	540	545	
att cgt ttg gaa tcg ccg atc att gat aac cat gag ctg gcc acc ttg				1795
Ile Arg Leu Glu Ser Pro Ile Ile Asp Asn His Glu Leu Ala Thr Leu				
	550	555	560	565
atc aat gcc aac gcg cat ggt gag tgg gat tcc ttt ggt gct gct gta				1843
Ile Asn Ala Asn Ala His Gly Glu Trp Asp Ser Phe Gly Ala Ala Val				
	570	575	580	
att tct ggt ttg tac cca gtg gct cac cat ggt gcc ggc atg aag gct				1891
Ile Ser Gly Leu Tyr Pro Val Ala His His Gly Ala Gly Met Lys Ala				
	585	590	595	
gcg att gct cgt gtg				1906
Ala Ile Ala Arg Val				
	600			

<210> 74

<211> 602

<212> PRT

<213> Corynebacterium glutamicum

<400> 74

Met	Lys	Pro	Gln	Gly	Leu	Tyr	Asn	Pro	Ala	His	Glu	His	Asp	Ala	Cys
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Gly	Val	Ala	Phe	Ile	Ala	Asp	Ile	His	Gly	Arg	Pro	Ser	Arg	Ser	Ile
		20						25					30		

Val	Asp	Arg	Ala	Leu	Glu	Ala	Leu	Arg	Asn	Ile	Asp	His	Arg	Gly	Ala
	35						40					45			

Ala	Gly	Ala	Glu	Lys	Asn	Thr	Gly	Asp	Gly	Ala	Gly	Ile	Leu	Met	Gln
	50					55					60				

Ile	Pro	Asp	Gly	Phe	Tyr	Arg	Glu	Val	Ser	Gly	Ile	Glu	Leu	Pro	Glu
65					70					75				80	

Ala	Gly	Glu	Tyr	Ala	Thr	Gly	Ile	Ala	Phe	Leu	Pro	Arg	Gly	Arg	Met
				85					90					95	

Ala	Met	Met	Asp	Ala	Gln	Lys	Glu	Ile	Glu	Arg	Ile	Ala	Lys	Gln	Glu
			100					105					110		

Gly Ala Asp Val Leu Gly Trp Arg Met Val Pro Phe Asp Ser Arg Asp
 115 120 125
 Leu Gly Ser Met Ala Glu Glu Ala Met Pro Ser Phe Ala Gln Ile Phe
 130 135 140
 Leu Thr Val Pro Gly Lys Ser Gly Glu Asp Leu Asp Arg Val Met Phe
 145 150 155 160
 Phe Ile Arg Lys Arg Cys Glu Arg Glu Leu Gly Thr Thr Asn Gly Arg
 165 170 175
 Asp Thr Val Tyr Phe Pro Ser Leu Ser Ser Arg Thr Ile Ile Tyr Lys
 180 185 190
 Gly Met Leu Thr Thr Leu Gln Leu Glu Gly Phe Phe Glu Asp Leu Gly
 195 200 205
 Asp Ala Arg Leu Glu Ser Ala Ile Ala Ile Val His Ser Arg Phe Ser
 210 215 220
 Thr Asn Thr Phe Pro Ser Trp Pro Leu Ala His Pro Tyr Arg Phe Val
 225 230 235 240
 Ala His Asn Gly Glu Ile Asn Thr Val Arg Gly Asn Glu Asn Trp Met
 245 250 255
 Arg Ala Arg Glu Ala Leu Ile Lys Asn Asp Lys Leu Gly Asn Leu Ser
 260 265 270
 Ser Val Leu Pro Ile Cys Thr Pro Glu Gly Ser Asp Thr Ala Arg Phe
 275 280 285
 Asp Glu Ala Leu Glu Leu Leu His Leu Gly Gly Tyr Ser Leu Pro His
 290 295 300
 Ala Val Ala Met Met Ile Pro Gln Ala Trp Glu His Asn Lys Thr Leu
 305 310 315 320
 Ser Pro Glu Leu Arg Asp Phe Tyr Glu Tyr His Ser Cys Leu Met Glu
 325 330 335
 Pro Trp Asp Gly Pro Ala Ala Leu Ala Phe Thr Asp Gly Arg Phe Val
 340 345 350
 Gly Ala Val Leu Asp Arg Asn Gly Leu Arg Pro Gly Arg Ile Thr Ile
 355 360 365
 Thr Asp Ser Gly Leu Val Val Met Ala Ser Glu Ser Gly Val Leu Asp
 370 375 380
 Leu Arg Glu Glu Ser Val Val Lys Arg Thr Arg Val Gln Pro Gly Arg
 385 390 395 400
 Met Phe Leu Val Asp Thr Ala Glu Gly Arg Ile Val Glu Asp Glu Glu
 405 410 415
 Ile Lys Gln Lys Leu Ser Glu Ala Gln Pro Tyr Gly Glu Trp Ile Arg
 420 425 430

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<400> 75
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gcgcatttttttg cca cgc cct gaa gag cac gct cac cgt gaa ttg gat ttg 111
      Leu Pro Arg Pro Glu Glu His Ala His Arg Glu Leu Asp Leu
      1             5             10
ggt ggt gaa tac aag tgg cgc cgc gaa ggt gaa tac cac ctg ttc aac 159
Gly Gly Glu Tyr Lys Trp Arg Arg Glu Gly Glu Tyr His Leu Phe Asn
  15             20             25             30
cca gaa acc atc ttc aag ctg cag cat gca acg cgt tct ggc agc tac 207
Pro Glu Thr Ile Phe Lys Leu Gln His Ala Thr Arg Ser Gly Ser Tyr
      35             40             45
gag att ttc aag gat tac acc cgc aag gtt gat gat caa tcc act cgc 255
Glu Ile Phe Lys Asp Tyr Thr Arg Lys Val Asp Asp Gln Ser Thr Arg

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50					55					60					
ttg ggt act att cgt gga ctg ttt gag ttc agc acg gac cgc aag cca	303														
Leu Gly Thr Ile Arg Gly Leu Phe Glu Phe Ser Thr Asp Arg Lys Pro															
65	70					75									
att tcg gtg tct gag gtg gag ccg gtc agt gag atc gtg aag cgt ttc	351														
Ile Ser Val Ser Glu Val Glu Pro Val Ser Glu Ile Val Lys Arg Phe															
80	85					90									
tcc act ggt gcg atg tct tat ggc tcg att tct gct gaa gcc cat gag	399														
Ser Thr Gly Ala Met Ser Tyr Gly Ser Ile Ser Ala Glu Ala His Glu															
95	100					105					110				
gtc ttg gcc atc gcc atg aac cga ctg ggc ggt atg tcc aac tcc ggc	447														
Val Leu Ala Ile Ala Met Asn Arg Leu Gly Gly Met Ser Asn Ser Gly															
115	120					125									
gaa ggt ggc gag gac gcc cgc cga ttt gat gtg gaa ccc aac ggt gac	495														
Glu Gly Gly Glu Asp Ala Arg Arg Phe Asp Val Glu Pro Asn Gly Asp															
130	135					140									
tgg aag cgc tct gcc att aag cag gtg gcc tcg gga cgt ttc ggc gtg	543														
Trp Lys Arg Ser Ala Ile Lys Gln Val Ala Ser Gly Arg Phe Gly Val															
145	150					155									
acc agc cac tac ttg aac aac tgc acc gat att cag atc aag atg gca	591														
Thr Ser His Tyr Leu Asn Asn Cys Thr Asp Ile Gln Ile Lys Met Ala															
160	165					170									
cag ggc gca aag ccc ggt gaa ggt ggc cag ctg cca cca aac aag gtg	639														
Gln Gly Ala Lys Pro Gly Glu Gly Gly Gln Leu Pro Pro Asn Lys Val															
175	180					185					190				
tac cca tgg gtt gca gaa gtc cgc atc acc acc cca ggc gtt ggt ctg	687														
Tyr Pro Trp Val Ala Glu Val Arg Ile Thr Thr Pro Gly Val Gly Leu															
195	200					205									
att tcc cct cca cca cac cac gat att tac tcc att gag gat ctg gct	735														
Ile Ser Pro Pro Pro His His Asp Ile Tyr Ser Ile Glu Asp Leu Ala															
210	215					220									
cag ctg atc cac gac ctg aag aac gct aac cca cgc gca cga atc cac	783														
Gln Leu Ile His Asp Leu Lys Asn Ala Asn Pro Arg Ala Arg Ile His															
225	230					235									
gtg aag cta gtg gca gaa caa ggc gtg ggc acc gtt gcc gca ggt gtg	831														
Val Lys Leu Val Ala Glu Gln Gly Val Gly Thr Val Ala Ala Gly Val															
240	245					250									
tcc aaa gca cac gct gat gtg gtg ctt att tcc ggc cac gat ggc gga	879														
Ser Lys Ala His Ala Asp Val Val Leu Ile Ser Gly His Asp Gly Gly															
255	260					265					270				
act ggc gca tct cct ttg acc tcc ctg aag cat gcc ggt ggt cca tgg	927														
Thr Gly Ala Ser Pro Leu Thr Ser Leu Lys His Ala Gly Gly Pro Trp															
275	280					285									
gag ttg ggc ttg gct gaa acc cag caa acg ttg ctg ctc aac ggc ctg	975														
Glu Leu Gly Leu Ala Glu Thr Gln Gln Thr Leu Leu Leu Asn Gly Leu															
290	295					300									

cgc gat cgt att cgc gtg cag tgc gat ggt cag ctg aaa act ggc cga 1023
 Arg Asp Arg Ile Arg Val Gln Cys Asp Gly Gln Leu Lys Thr Gly Arg
 305 310 315

 gac gtg gtt atc gca gct ctt ctc ggt gcc gaa gaa ttc ggt ttt gcc 1071
 Asp Val Val Ile Ala Ala Leu Leu Gly Ala Glu Glu Phe Gly Phe Ala
 320 325 330

 acc gca ccg ctg gtg gtt gaa ggc tgc atc atg atg cgc gtc tgc cac 1119
 Thr Ala Pro Leu Val Val Glu Gly Cys Ile Met Met Arg Val Cys His
 335 340 345 350

 ctg gac acc tgc ccg gtg ggt atc gct acc cag aac ccg gat ttg cgt 1167
 Leu Asp Thr Cys Pro Val Gly Ile Ala Thr Gln Asn Pro Asp Leu Arg
 355 360 365

 tcc aag ttc acc ggc aag gct gaa cac gtg gtc aac ttc ttc acc ttc 1215
 Ser Lys Phe Thr Gly Lys Ala Glu His Val Val Asn Phe Phe Thr Phe
 370 375 380

 atc gcc cag gaa gtc cgt gag tac ttg gca cag ctt ggt ttc cgc tct 1263
 Ile Ala Gln Glu Val Arg Glu Tyr Leu Ala Gln Leu Gly Phe Arg Ser
 385 390 395

 att gat gaa gcc gtc gga caa gcc cag gtg ctg cgc aag cgt tcc gga 1311
 Ile Asp Glu Ala Val Gly Gln Ala Gln Val Leu Arg Lys Arg Ser Gly
 400 405 410

 atc cca gct gat tcc cgc gca gca cac ctg gat ttg agc cca att ttc 1359
 Ile Pro Ala Asp Ser Arg Ala Ala His Leu Asp Leu Ser Pro Ile Phe
 415 420 425 430

 atc 1362
 Ile

<210> 76

<211> 431

<212> PRT

<213> Corynebacterium glutamicum

<400> 76

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 Glu Tyr Lys Trp Arg Arg Glu Gly Glu Tyr His Leu Phe Asn Pro Glu
 20 25 30

 Thr Ile Phe Lys Leu Gln His Ala Thr Arg Ser Gly Ser Tyr Glu Ile
 35 40 45

 Phe Lys Asp Tyr Thr Arg Lys Val Asp Asp Gln Ser Thr Arg Leu Gly
 50 55 60

 Thr Ile Arg Gly Leu Phe Glu Phe Ser Thr Asp Arg Lys Pro Ile Ser
 65 70 75 80

 Val Ser Glu Val Glu Pro Val Ser Glu Ile Val Lys Arg Phe Ser Thr
 85 90 95

Gly Ala Met Ser Tyr Gly Ser Ile Ser Ala Glu Ala His Glu Val Leu
 100 105 110
 Ala Ile Ala Met Asn Arg Leu Gly Gly Met Ser Asn Ser Gly Glu Gly
 115 120 125
 Gly Glu Asp Ala Arg Arg Phe Asp Val Glu Pro Asn Gly Asp Trp Lys
 130 135 140
 Arg Ser Ala Ile Lys Gln Val Ala Ser Gly Arg Phe Gly Val Thr Ser
 145 150 155 160
 His Tyr Leu Asn Asn Cys Thr Asp Ile Gln Ile Lys Met Ala Gln Gly
 165 170 175
 Ala Lys Pro Gly Glu Gly Gly Gln Leu Pro Pro Asn Lys Val Tyr Pro
 180 185 190
 Trp Val Ala Glu Val Arg Ile Thr Thr Pro Gly Val Gly Leu Ile Ser
 195 200 205
 Pro Pro Pro His His Asp Ile Tyr Ser Ile Glu Asp Leu Ala Gln Leu
 210 215 220
 Ile His Asp Leu Lys Asn Ala Asn Pro Arg Ala Arg Ile His Val Lys
 225 230 235 240
 Leu Val Ala Glu Gln Gly Val Gly Thr Val Ala Ala Gly Val Ser Lys
 245 250 255
 Ala His Ala Asp Val Val Leu Ile Ser Gly His Asp Gly Gly Thr Gly
 260 265 270
 Ala Ser Pro Leu Thr Ser Leu Lys His Ala Gly Gly Pro Trp Glu Leu
 275 280 285
 Gly Leu Ala Glu Thr Gln Gln Thr Leu Leu Leu Asn Gly Leu Arg Asp
 290 295 300
 Arg Ile Arg Val Gln Cys Asp Gly Gln Leu Lys Thr Gly Arg Asp Val
 305 310 315 320
 Val Ile Ala Ala Leu Leu Gly Ala Glu Glu Phe Gly Phe Ala Thr Ala
 325 330 335
 Pro Leu Val Val Glu Gly Cys Ile Met Met Arg Val Cys His Leu Asp
 340 345 350
 Thr Cys Pro Val Gly Ile Ala Thr Gln Asn Pro Asp Leu Arg Ser Lys
 355 360 365
 Phe Thr Gly Lys Ala Glu His Val Val Asn Phe Phe Thr Phe Ile Ala
 370 375 380
 Gln Glu Val Arg Glu Tyr Leu Ala Gln Leu Gly Phe Arg Ser Ile Asp
 385 390 395 400
 Glu Ala Val Gly Gln Ala Gln Val Leu Arg Lys Arg Ser Gly Ile Pro
 405 410 415

Ala Asp Ser Arg Ala Ala His Leu Asp Leu Ser Pro Ile Phe Ile
 420 425 430

<210> 77

<211> 866

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(843)

<223> FRXA00367

<400> 77

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His Ser Leu Glu Lys Ala Leu Asp Asn Ala Phe Ile Asp Lys Ala Ser	
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gac acg atc acc cgt gcc gca gcg ggt gtg gaa acc agc att gtt att	96
Asp Thr Ile Thr Arg Ala Ala Ala Gly Val Glu Thr Ser Ile Val Ile	
20 25 30	
gat agc tcc atc agc aac gtc aac cgt tca gtt ggc acg atg ctg ggt	144
Asp Ser Ser Ile Ser Asn Val Asn Arg Ser Val Gly Thr Met Leu Gly	
35 40 45	
tct gca gtc agc cgc gtg gct ggt gcc caa ggt ttg cca gac ggc acc	192
Ser Ala Val Ser Arg Val Ala Gly Ala Gln Gly Leu Pro Asp Gly Thr	
50 55 60	
atc acc ttg aat ctt caa ggc tgc gcc ggt aac tcc ttt ggc gcg ttc	240
Ile Thr Leu Asn Leu Gln Gly Cys Ala Gly Asn Ser Phe Gly Ala Phe	
65 70 75 80	
atc cca cga ggc atc acc atc aac ctc acc ggc gat gcc aat gac ttt	288
Ile Pro Arg Gly Ile Thr Ile Asn Leu Thr Gly Asp Ala Asn Asp Phe	
85 90 95	
gtg ggc aag gga tta tct ggc gga aag att gtg atc aag cct tcc gct	336
Val Gly Lys Gly Leu Ser Gly Gly Lys Ile Val Ile Lys Pro Ser Ala	
100 105 110	
cag gct ccg aag cag ctg aag aac aat cca aat atc att gcc gga aac	384
Gln Ala Pro Lys Gln Leu Lys Asn Asn Pro Asn Ile Ile Ala Gly Asn	
115 120 125	
gtg ctt gga tac ggc gca acc agt ggt gaa ttg ttc att cgt ggc cag	432
Val Leu Gly Tyr Gly Ala Thr Ser Gly Glu Leu Phe Ile Arg Gly Gln	
130 135 140	
gtc ggc gaa cgt ttc tgc gtc cgt aac tct ggc gcc acc gca gtg gtt	480
Val Gly Glu Arg Phe Cys Val Arg Asn Ser Gly Ala Thr Ala Val Val	
145 150 155 160	
gaa ggt atc gga aac cac ggt tgt gag tac atg act ggc ggc cga gtc	528
Glu Gly Ile Gly Asn His Gly Cys Glu Tyr Met Thr Gly Gly Arg Val	
165 170 175	
ctg gtt ttg ggc ccg gtt ggt gag aac ttt ggt gcc ggc atg tct ggt	576
Leu Val Leu Gly Pro Val Gly Glu Asn Phe Gly Ala Gly Met Ser Gly	

180	185	190	
ggc att gca tac ctg gct aat tcc ccg gac cta aac cag aag atc aat			624
Gly Ile Ala Tyr Leu Ala Asn Ser Pro Asp Leu Asn Gln Lys Ile Asn			
195	200	205	
ggc gaa ttg gtg gat gtt gtt cca ctg agc gct gac gat ctg acg tgg			672
Gly Glu Leu Val Asp Val Val Pro Leu Ser Ala Asp Asp Leu Thr Trp			
210	215	220	
gct gat gag ctc att gct cgc cac cgc gaa ctc acc gga tcc gag acc			720
Ala Asp Glu Leu Ile Ala Arg His Arg Glu Leu Thr Gly Ser Glu Thr			
225	230	235	240
aag ctg cgt gca caa gat ttg gtg aaa atc atg ccg cgc gat ttc caa			768
Lys Leu Arg Ala Gln Asp Leu Val Lys Ile Met Pro Arg Asp Phe Gln			
245	250	255	
aaa gta ctc aac atc atc gaa acg gcc cac gct gag ggc caa gac cca			816
Lys Val Leu Asn Ile Ile Glu Thr Ala His Ala Glu Gly Gln Asp Pro			
260	265	270	
gca atc aag atc atg gag gca gtg agc taatggccga cccacaagga			863
Ala Ile Lys Ile Met Glu Ala Val Ser			
275	280		
ttc			866
<210> 78			
<211> 281			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 78			
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20	25	30	
Asp Ser Ser Ile Ser Asn Val Asn Arg Ser Val Gly Thr Met Leu Gly			
35	40	45	
Ser Ala Val Ser Arg Val Ala Gly Ala Gln Gly Leu Pro Asp Gly Thr			
50	55	60	
Ile Thr Leu Asn Leu Gln Gly Cys Ala Gly Asn Ser Phe Gly Ala Phe			
65	70	75	80
Ile Pro Arg Gly Ile Thr Ile Asn Leu Thr Gly Asp Ala Asn Asp Phe			
85	90	95	
Val Gly Lys Gly Leu Ser Gly Gly Lys Ile Val Ile Lys Pro Ser Ala			
100	105	110	
Gln Ala Pro Lys Gln Leu Lys Asn Asn Pro Asn Ile Ile Ala Gly Asn			
115	120	125	
Val Leu Gly Tyr Gly Ala Thr Ser Gly Glu Leu Phe Ile Arg Gly Gln			
130	135	140	

Val Gly Glu Arg Phe Cys Val Arg Asn Ser Gly Ala Thr Ala Val Val
 145 150 155 160

Glu Gly Ile Gly Asn His Gly Cys Glu Tyr Met Thr Gly Gly Arg Val
 165 170 175

Leu Val Leu Gly Pro Val Gly Glu Asn Phe Gly Ala Gly Met Ser Gly
 180 185 190

Gly Ile Ala Tyr Leu Ala Asn Ser Pro Asp Leu Asn Gln Lys Ile Asn
 195 200 205

Gly Glu Leu Val Asp Val Val Pro Leu Ser Ala Asp Asp Leu Thr Trp
 210 215 220

Ala Asp Glu Leu Ile Ala Arg His Arg Glu Leu Thr Gly Ser Glu Thr
 225 230 235 240

Lys Leu Arg Ala Gln Asp Leu Val Lys Ile Met Pro Arg Asp Phe Gln
 245 250 255

Lys Val Leu Asn Ile Ile Glu Thr Ala His Ala Glu Gly Gln Asp Pro
 260 265 270

Ala Ile Lys Ile Met Glu Ala Val Ser
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<210> 79

<211> 1494

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1471)

<223> RXN00076

<400> 79

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 Met Thr Thr Pro Leu
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 Arg Val Ala Val Ile Gly Ala Gly Pro Ala Gly Ile Tyr Ala Ser Asp
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ctc ctc atc cgc aat gaa gag cgc gaa gtg ttc gtt gac ctt ttc gag 211
 Leu Leu Ile Arg Asn Glu Glu Arg Glu Val Phe Val Asp Leu Phe Glu
 25 30 35

caa atg cct gca cgc ttc gga ctc atc cgt tac ggc gtt gct cca gac 259
 Gln Met Pro Ala Pro Phe Gly Leu Ile Arg Tyr Gly Val Ala Pro Asp
 40 45 50

cac cca cgc atc aag ggc atc gtt aag tcc ctg cac aac gtg ttg gac 307
 His Pro Arg Ile Lys Gly Ile Val Lys Ser Leu His Asn Val Leu Asp
 55 60 65

aag cca cgc ctg cgc ctg ctc ggt aac att gaa atc ggc aaa gac atc	355
Lys Pro Arg Leu Arg Leu Leu Gly Asn Ile Glu Ile Gly Lys Asp Ile	
70 75 80 85	
acc gtc gaa gaa ctc cgc gac tac tac gat gca gtc gtg ttc tcc acc	403
Thr Val Glu Glu Leu Arg Asp Tyr Tyr Asp Ala Val Val Phe Ser Thr	
90 95 100	
ggc gca gtt gca gac cgc gac ctc aac atc ccc gga att gaa gca gaa	451
Gly Ala Val Ala Asp Arg Asp Leu Asn Ile Pro Gly Ile Glu Ala Glu	
105 110 115	
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Gly Ser Phe Gly Ala Gly Glu Phe Val Gly Phe Tyr Asp Gly Asn Pro	
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Arg Phe Glu Arg Ser Trp Asp Leu Ser Ala Gln Ser Val Ala Val Ile	
135 140 145	
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Gly Val Gly Asn Val Gly Leu Asp Val Ala Arg Ile Leu Ala Lys Thr	
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Gly Asp Glu Leu Lys Val Thr Glu Ile Ser Asp Asn Val Tyr Asp Ser	
170 175 180	
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Leu Lys Glu Asn Lys Ala Thr Glu Val His Val Phe Gly Arg Arg Gly	
185 190 195	
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Pro Ala Gln Val Lys Phe Thr Pro Gln Glu Leu Lys Glu Leu Asp His	
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Ser Pro Thr Ile Asn Val Val Val Asp Pro Glu Asp Ile Asp Tyr Asp	
215 220 225	
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Gly Ala Ser Glu Glu Ala Arg Arg Ala Ser Lys Ser Gln Asp Leu Val	
230 235 240 245	
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Cys Gln Ile Leu Glu Gln Tyr Ala Ile Arg Glu Pro Lys Asp Ala Pro	
250 255 260	
cac acc ctg cag atc cac ctc ttt gaa aac cca gtt gag gtt ctt caa	931
His Thr Leu Gln Ile His Leu Phe Glu Asn Pro Val Glu Val Leu Gln	
265 270 275	
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Lys Asp Gly Lys Val Val Gly Leu Arg Thr Glu Arg Thr Ser Leu Asp	
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Gly Asn Gly Gly Val Asn Gly Thr Gly Glu Phe Lys Asp Trp Pro Val	
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 Gln Ala Val Tyr Arg Ala Val Gly Tyr Lys Ser Asp Pro Ile Asp Gly
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 Val Pro Phe Asp Glu Asn Lys His Val Ile Pro Asn Asp Gly Gly His
 330 335 340

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 Val Leu Thr Ala Pro Gly Ala Glu Pro Val Pro Gly Leu Tyr Ala Thr
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 Gly Trp Ile Lys Arg Gly Pro Ile Gly Leu Ile Gly Asn Thr Lys Ser
 360 365 370

 gac gcc aag gaa acc acc gac atc ctc atc aag gat gcc gtc gcc ggt 1267
 Asp Ala Lys Glu Thr Thr Asp Ile Leu Ile Lys Asp Ala Val Ala Gly
 375 380 385

 gta ctt gaa gct cca aag cac cag ggc gaa gaa gcc atc atc gag ctt 1315
 Val Leu Glu Ala Pro Lys His Gln Gly Glu Glu Ala Ile Ile Glu Leu
 390 395 400 405

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 410 415 420

 ctc gac gca gca gag cgc gca ctc ggt gaa gcc gaa ggc cgc gag cgc 1411
 Leu Asp Ala Ala Glu Arg Ala Leu Gly Glu Ala Glu Gly Arg Glu Arg
 425 430 435

 aag aag att gtt gat tgg gaa gaa atg gtc cgc cag gcc cgc gaa gct 1459
 Lys Lys Ile Val Asp Trp Glu Glu Met Val Arg Gln Ala Arg Glu Ala
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 Pro Ala Ile Val
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<211> 457

<212> PRT

<213> Corynebacterium glutamicum

<400> 80

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20 25 30

Val Asp Leu Phe Glu Gln Met Pro Ala Pro Phe Gly Leu Ile Arg Tyr
35 40 45

Gly Val Ala Pro Asp His Pro Arg Ile Lys Gly Ile Val Lys Ser Leu
50 55 60

His Asn Val Leu Asp Lys Pro Arg Leu Arg Leu Leu Gly Asn Ile Glu
65 70 75 80

Ile Gly Lys Asp Ile Thr Val Glu Glu Leu Arg Asp Tyr Tyr Asp Ala
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 Val Val Phe Ser Thr Gly Ala Val Ala Asp Arg Asp Leu Asn Ile Pro
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 Gly Ile Glu Ala Glu Gly Ser Phe Gly Ala Gly Glu Phe Val Gly Phe
 115 120 125
 Tyr Asp Gly Asn Pro Arg Phe Glu Arg Ser Trp Asp Leu Ser Ala Gln
 130 135 140
 Ser Val Ala Val Ile Gly Val Gly Asn Val Gly Leu Asp Val Ala Arg
 145 150 155 160
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 165 170 175
 Asn Val Tyr Asp Ser Leu Lys Glu Asn Lys Ala Thr Glu Val His Val
 180 185 190
 Phe Gly Arg Arg Gly Pro Ala Gln Val Lys Phe Thr Pro Gln Glu Leu
 195 200 205
 Lys Glu Leu Asp His Ser Pro Thr Ile Asn Val Val Val Asp Pro Glu
 210 215 220
 Asp Ile Asp Tyr Asp Gly Ala Ser Glu Glu Ala Arg Arg Ala Ser Lys
 225 230 235 240
 Ser Gln Asp Leu Val Cys Gln Ile Leu Glu Gln Tyr Ala Ile Arg Glu
 245 250 255
 Pro Lys Asp Ala Pro His Thr Leu Gln Ile His Leu Phe Glu Asn Pro
 260 265 270
 Val Glu Val Leu Gln Lys Asp Gly Lys Val Val Gly Leu Arg Thr Glu
 275 280 285
 Arg Thr Ser Leu Asp Gly Asn Gly Gly Val Asn Gly Thr Gly Glu Phe
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 Lys Asp Trp Pro Val Gln Ala Val Tyr Arg Ala Val Gly Tyr Lys Ser
 305 310 315 320
 Asp Pro Ile Asp Gly Val Pro Phe Asp Glu Asn Lys His Val Ile Pro
 325 330 335
 Asn Asp Gly Gly His Val Leu Thr Ala Pro Gly Ala Glu Pro Val Pro
 340 345 350
 Gly Leu Tyr Ala Thr Gly Trp Ile Lys Arg Gly Pro Ile Gly Leu Ile
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Met Thr Thr Pro Leu																5
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cgc gta gcc gtc atc gga gct ggc cct gct ggc att tac gca tcc gac																163
Arg Val Ala Val Ile Gly Ala Gly Pro Ala Gly Ile Tyr Ala Ser Asp																20
10 15																
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Leu Leu Ile Arg Asn Glu Glu Arg Glu Val Phe Val Asp Leu Phe Glu																35
25 30																
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Gln Met Pro Ala Pro Phe Gly Leu Ile Arg Tyr Gly Val Ala Pro Asp																50
40 45																
cac cca cgc atc aag ggc atc gtt aag tcc ctg cac aac gtg ttg gac																307
His Pro Arg Ile Lys Gly Ile Val Lys Ser Leu His Asn Val Leu Asp																65
55 60																
aag cca cgc ctg cgc ctg ctc ggt aac att gaa atc ggc aaa gac atc																355
Lys Pro Arg Leu Arg Leu Leu Gly Asn Ile Glu Ile Gly Lys Asp Ile																85
70 75 80																
acc gtc gaa gaa ctc cgc gac tac tac gat gca gtc gtg ttc tcc acc																403
Thr Val Glu Glu Leu Arg Asp Tyr Tyr Asp Ala Val Val Phe Ser Thr																100
90 95																
ggc gca gtt gca gac cgc gac ctc aac atc ccc gga att gaa gca gaa																451
Gly Ala Val Ala Asp Arg Asp Leu Asn Ile Pro Gly Ile Glu Ala Glu																115
105 110																
ggc tcc ttc ggt gcc ggc gag ttc gtt ggc ttc tac gac ggc aac cca																499
Gly Ser Phe Gly Ala Gly Glu Phe Val Gly Phe Tyr Asp Gly Asn Pro																120 125 130

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 Arg Phe Glu Arg Ser Trp Asp Leu Ser Ala Gln Ser Val Ala Val Ile
 135 140 145

ggc gtt ggt aac gtc ggc ctc gac gta gcc cgc atc ctg gct aag aca 595
 Gly Val Gly Asn Val Gly Leu Asp Val Ala Arg Ile Leu Ala Lys Thr
 150 155 160 165

ggc gac gag ctc aaa gtc acc gaa att tcc gac aac gtc tac gac tcc 643
 Gly Asp Glu Leu Lys Val Thr Glu Ile Ser Asp Asn Val Tyr Asp Ser
 170 175 180

ctc aaa gaa aac aag gyc wct gaa gtg cac gtt ttc gga cgt cgg tgg 691
 Leu Lys Glu Asn Lys Xaa Xaa Glu Val His Val Phe Gly Arg Arg Trp
 185 190 195

ccc agc aca ggt caa gtt cac ccc aca gga act maa aga act cgr cca 739
 Pro Ser Thr Gly Gln Val His Pro Thr Gly Thr Xaa Arg Thr Xaa Pro
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<213> Corynebacterium glutamicum

<400> 82

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 20 25 30

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 35 40 45

Gly Val Ala Pro Asp His Pro Arg Ile Lys Gly Ile Val Lys Ser Leu
 50 55 60

His Asn Val Leu Asp Lys Pro Arg Leu Arg Leu Leu Gly Asn Ile Glu
 65 70 75 80

Ile Gly Lys Asp Ile Thr Val Glu Glu Leu Arg Asp Tyr Tyr Asp Ala
 85 90 95

Val Val Phe Ser Thr Gly Ala Val Ala Asp Arg Asp Leu Asn Ile Pro
 100 105 110

Gly Ile Glu Ala Glu Gly Ser Phe Gly Ala Gly Glu Phe Val Gly Phe
 115 120 125

Tyr Asp Gly Asn Pro Arg Phe Glu Arg Ser Trp Asp Leu Ser Ala Gln
 130 135 140

Ser Val Ala Val Ile Gly Val Gly Asn Val Gly Leu Asp Val Ala Arg
 145 150 155 160

Ile Leu Ala Lys Thr Gly Asp Glu Leu Lys Val Thr Glu Ile Ser Asp
 165 170 175
 Asn Val Tyr Asp Ser Leu Lys Glu Asn Lys Xaa Xaa Glu Val His Val
 180 185 190
 Phe Gly Arg Arg Trp Pro Ser Thr Gly Gln Val His Pro Thr Gly Thr
 195 200 205
 Xaa Arg Thr Xaa Pro Leu Pro His His Gln Arg Gly Cys
 210 215 220

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 Met Tyr Pro Asn Leu
 1 5
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 Phe Arg Thr Ala Thr Ala His Glu Glu Gly Glu Tyr Ile Ile Thr Gly
 10 15 20
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 Asp Glu Ser Ala Asp Glu Ile Ala Ala Leu Gly Leu Ala Glu Arg Ala
 25 30 35
 gca ggc tcc acg ctt ggt gaa cgt aaa ttt gct gtc aac acc gtg gaa 259
 Ala Gly Ser Thr Leu Gly Glu Arg Lys Phe Ala Val Asn Thr Val Glu
 40 45 50
 ttc cac ggc aac aac ggc cac gtc acc gga ctc acc ggc aac caa atc 307
 Phe His Gly Asn Asn Gly His Val Thr Gly Leu Thr Gly Asn Gln Ile
 55 60 65
 cga gtt gtc aac ggc aaa cgt gaa cca atc gaa ggc acc gaa ttc ccc 355
 Arg Val Val Asn Gly Lys Arg Glu Pro Ile Glu Gly Thr Glu Phe Pro
 70 75 80 85
 ttc gaa gca gac ctc gtt ctt gtt gca ctt ggc ttc acc ggc gca gaa 403
 Phe Glu Ala Asp Leu Val Leu Val Ala Leu Gly Phe Thr Gly Ala Glu
 90 95 100
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 Gln Gly Gly Leu Ala His Glu Leu Gly Val Gly Phe Asp Asp Arg Gly
 105 110 115
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 Arg Ile Leu Arg Asp Ser Glu Tyr Arg Ser Pro Thr Asn Ser Arg Val

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Tyr Ile Ala Gly Asp Asn Gly Arg Gly Gln Ser Leu Ile Val Trp Ala			
135	140	145	
atc gcc gaa ggc cgc gca tgc gcc gca gct atc gac gcc gat ctc atg			595
Ile Ala Glu Gly Arg Ala Cys Ala Ala Ala Ile Asp Ala Asp Leu Met			
150	155	160	165
ggt gaa act gca ctc cct gta gca gtt gca cca cag gac gtg ccg ctg			643
Gly Glu Thr Ala Leu Pro Val Ala Val Ala Pro Gln Asp Val Pro Leu			
170	175	180	
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Ala Val			

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<211> 183

<212> PRT

<213> Corynebacterium glutamicum

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Leu Ala Glu Arg Ala Ala Gly Ser Thr Leu Gly Glu Arg Lys Phe Ala			
35	40	45	
Val Asn Thr Val Glu Phe His Gly Asn Asn Gly His Val Thr Gly Leu			
50	55	60	
Thr Gly Asn Gln Ile Arg Val Val Asn Gly Lys Arg Glu Pro Ile Glu			
65	70	75	80
Gly Thr Glu Phe Pro Phe Glu Ala Asp Leu Val Leu Val Ala Leu Gly			
85	90	95	
Phe Thr Gly Ala Glu Gln Gly Gly Leu Ala His Glu Leu Gly Val Gly			
100	105	110	
Phe Asp Asp Arg Gly Arg Ile Leu Arg Asp Ser Glu Tyr Arg Ser Pro			
115	120	125	
Thr Asn Ser Arg Val Tyr Ile Ala Gly Asp Asn Gly Arg Gly Gln Ser			
130	135	140	
Leu Ile Val Trp Ala Ile Ala Glu Gly Arg Ala Cys Ala Ala Ala Ile			
145	150	155	160
Asp Ala Asp Leu Met Gly Glu Thr Ala Leu Pro Val Ala Val Ala Pro			
165	170	175	
Gln Asp Val Pro Leu Ala Val			
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 Ala His Glu Leu Gly Val Gly Phe Asp Asp Arg Gly Arg Ile Leu Arg
 20 25 30

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 Asp Ser Glu Tyr Arg Ser Pro Thr Asn Ser Arg Val Tyr Ile Ala Gly
 35 40 45

 gac aac ggc cgt ggc cag tcc ctg atc gtg tgg gca atc gcc gaa ggc 192
 Asp Asn Gly Arg Gly Gln Ser Leu Ile Val Trp Ala Ile Ala Glu Gly
 50 55 60

 cgc gca tgc gcc gca gct atc gac gcc gat ctc atg ggt gaa act gca 240
 Arg Ala Cys Ala Ala Ala Ile Asp Ala Asp Leu Met Gly Glu Thr Ala
 65 70 75 80

 ctc cct gta gca gtt gca cca cag gac gtg ccg ctg gct gtc 282
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 20 25 30

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 35 40 45

 Asp Asn Gly Arg Gly Gln Ser Leu Ile Val Trp Ala Ile Ala Glu Gly
 50 55 60

 Arg Ala Cys Ala Ala Ala Ile Asp Ala Asp Leu Met Gly Glu Thr Ala
 65 70 75 80

 Leu Pro Val Ala Val Ala Pro Gln Asp Val Pro Leu Ala Val

Gly Lys Lys Val Val Ile Ile Gly Gly Gly Asp Thr Gly Thr Asp Cys
 170 175 180
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 Phe Gly Thr Ala Leu Arg Gln Gly Ala Glu Ser Val Thr Gln Phe Asp
 185 190 195
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 <213> Corynebacterium glutamicum

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 35 40 45
 Ala Gln Gln Leu Thr Arg Ala Gly His Ser Val Thr Val Phe Glu Arg
 50 55 60
 Asp Asp Arg Leu Gly Gly Leu Met Arg Tyr Gly Val Pro Glu Tyr Lys
 65 70 75 80
 Met Glu Asn Arg Trp Ile Asp Arg Arg Ile Glu Gln Met Glu Ala Glu
 85 90 95
 Gly Thr Thr Phe Gln Val Gly Thr Ser Pro Arg Ala Ala Glu Leu Ala
 100 105 110
 Leu Phe Asp Ala Ile Leu Leu Ala Thr Gly Thr Pro Val Ala Arg Glu
 115 120 125
 Leu Ser Val Pro Gly His Asp Leu Asn Gly Ile His Ala Ala Met Asp
 130 135 140
 Tyr Leu Thr Ala Gln Asn Arg Ile Asn Glu Gly Asp Gly Glu Val Ser
 145 150 155 160
 Pro Ile Asn Ala Lys Gly Lys Lys Val Val Ile Ile Gly Gly Gly Asp
 165 170 175
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 180 185 190
 Val Thr Gln Phe Asp Ile Arg Pro Arg Ala Pro Phe Gln Arg Ala Asp
 195 200 205
 Ser

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Gly Lys Lys Val Val Ile Ile Gly Gly Gly Asp Thr Gly Thr Asp Cys
170 175 180

ttc ggc acc gca ctg cgc caa gga gca gaa tca gtc acc caa ttt gat 691
 Phe Gly Thr Ala Leu Arg Gln Gly Ala Glu Ser Val Thr Gln Phe Asp
 185 190 195

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 35 40 45

Ala Gln Gln Leu Thr Arg Ala Gly His Ser Val Thr Val Phe Glu Arg
 50 55 60

Asp Asp Arg Leu Gly Gly Leu Met Arg Tyr Gly Val Pro Glu Tyr Lys
 65 70 75 80

Met Glu Asn Arg Trp Ile Asp Arg Arg Ile Glu Gln Met Glu Ala Glu
 85 90 95

Gly Thr Thr Phe Gln Val Gly Thr Ser Pro Arg Ala Ala Glu Leu Ala
 100 105 110

Leu Phe Asp Ala Ile Leu Leu Ala Thr Gly Thr Pro Val Ala Arg Glu
 115 120 125

Leu Ser Val Pro Gly His Asp Leu Asn Gly Ile His Ala Ala Met Asp
 130 135 140

Tyr Leu Thr Ala Gln Asn Arg Ile Asn Glu Gly Asp Gly Glu Val Ser
 145 150 155 160

Pro Ile Asn Ala Lys Gly Lys Lys Val Val Ile Ile Gly Gly Gly Asp
 165 170 175

Thr Gly Thr Asp Cys Phe Gly Thr Ala Leu Arg Gln Gly Ala Glu Ser
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Val Thr Gln Phe Asp Ile Arg Pro Arg Ala Pro Phe Gln Arg Ala Asp
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Gly Phe Ile Lys Tyr Ser Arg Arg Glu Pro Ala His Arg Pro Val Pro
                        10           15           20

ctg cgc ctc atg gac cac tcc gag gtc tac gaa aag gca ccg gca ggt 211
Leu Arg Leu Met Asp His Ser Glu Val Tyr Glu Lys Ala Pro Ala Gly
                        25           30           35

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Gln Ile Glu Glu Gln Ala Ala Arg Cys Met Asp Cys Gly Val Pro Phe
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Cys His Glu Gly Cys Pro Leu Gly Asn Ile Ile Pro Glu Trp Asn Asp
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  20           25           30

Lys Ala Pro Ala Gly Gln Ile Glu Glu Gln Ala Ala Arg Cys Met Asp
  35           40           45

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Cys Gly Val Pro Phe Cys His Glu Gly Cys Pro Leu Gly Asn Ile Ile
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 Pro Glu Trp Asn Asp Leu Val Arg Gln Gly Arg Trp Lys Glu Ala Tyr
 65 70 75 80
 Asp Arg Leu His Ala Thr Asn Asn Phe Pro Glu Phe Thr Gly Arg Leu
 85 90 95
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 Ser Val Thr Ile Lys Asn Val
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 Met Thr Val Asp Glu
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 Gln Val Ser Asn Tyr Tyr Asp Met Leu Leu Lys Arg Asn Ala Gly Glu
 10 15 20
 cct gaa ttt cac cag gca gtg gca gag gtt ttg gaa tct ttg aag atc 211
 Pro Glu Phe His Gln Ala Val Ala Glu Val Leu Glu Ser Leu Lys Ile
 25 30 35
 gtc ctg gaa aag gac cct cat tac gct gat tac ggt ctc atc cag cgc 259
 Val Leu Glu Lys Asp Pro His Tyr Ala Asp Tyr Gly Leu Ile Gln Arg
 40 45 50
 ctg tgc gag cct gag cgt cag ctc atc ttc cgt gtg cct tgg gtt gat 307
 Leu Cys Glu Pro Glu Arg Gln Leu Ile Phe Arg Val Pro Trp Val Asp
 55 60 65
 gac cag ggc cag gtc cac gtc aac cgt ggt ttc cgc gtg cag ttc aac 355
 Asp Gln Gly Gln Val His Val Asn Arg Gly Phe Arg Val Gln Phe Asn
 70 75 80 85
 tct gca ctt gga cca tac aag ggc ggc ctg cgc ttc cac cca tct gta 403
 Ser Ala Leu Gly Pro Tyr Lys Gly Gly Leu Arg Phe His Pro Ser Val
 90 95 100
 aac ctg ggc att gtg aag ttc ctg ggc ttt gag cag atc ttt aaa aac 451
 Asn Leu Gly Ile Val Lys Phe Leu Gly Phe Glu Gln Ile Phe Lys Asn
 105 110 115

tcc cta acc ggc ctg cca atc ggt ggt ggc aag ggt gga tcc gac ttc	499
Ser Leu Thr Gly Leu Pro Ile Gly Gly Gly Lys Gly Gly Ser Asp Phe	
120 125 130	
gac cct aag ggc aag tcc gat ctg gaa atc atg cgt ttc tgc cag tcc	547
Asp Pro Lys Gly Lys Ser Asp Leu Glu Ile Met Arg Phe Cys Gln Ser	
135 140 145	
ttc atg acc gag ctg cac cgc cac atc ggt gag tac cgc gac gtt cct	595
Phe Met Thr Glu Leu His Arg His Ile Gly Glu Tyr Arg Asp Val Pro	
150 155 160 165	
gca ggt aac atc gga gtt ggt ggc cac gag atc ggt tac ctg ttt ggc	643
Ala Gly Asn Ile Gly Val Gly Gly His Glu Ile Gly Tyr Leu Phe Gly	
170 175 180	
cac tac cgt cgc atg gct aac cag cac gag tcc ggc gtt ttg acc ggt	691
His Tyr Arg Arg Met Ala Asn Gln His Glu Ser Gly Val Leu Thr Gly	
185 190 195	
aag ggc ctg acc tgg ggt gga tcc ctg gtc cgc acc gag gca act ggc	739
Lys Gly Leu Thr Trp Gly Gly Ser Leu Val Arg Thr Glu Ala Thr Gly	
200 205 210	
tac ggc tgc gtt tac ttc gtg agt gaa atg atc aag gct aag ggc gag	787
Tyr Gly Cys Val Tyr Phe Val Ser Glu Met Ile Lys Ala Lys Gly Glu	
215 220 225	
agc atc agc ggc cag aag atc atc gtt tcc ggt tcc ggc aac gta gca	835
Ser Ile Ser Gly Gln Lys Ile Ile Val Ser Gly Ser Gly Asn Val Ala	
230 235 240 245	
acc tac gcg att gaa aag gct cag gaa ctc ggc gca acc gtt att ggt	883
Thr Tyr Ala Ile Glu Lys Ala Gln Glu Leu Gly Ala Thr Val Ile Gly	
250 255 260	
ttc tcc gat tcc agc ggt tgg gtt cat acc cct aac ggc gtt gac gtg	931
Phe Ser Asp Ser Ser Gly Trp Val His Thr Pro Asn Gly Val Asp Val	
265 270 275	
gct aag ctc cgc gaa atc aag gaa gtt cgt cgc gca cgc gta tcc gtg	979
Ala Lys Leu Arg Glu Ile Lys Glu Val Arg Arg Ala Arg Val Ser Val	
280 285 290	
tac gcc gac gaa gtt gaa ggc gca acc tac cac acc gac ggt tcc atc	1027
Tyr Ala Asp Glu Val Glu Gly Ala Thr Tyr His Thr Asp Gly Ser Ile	
295 300 305	
tgg gat ctc aag tgc gat atc gct ctt cct tgt gca act cag aac gag	1075
Trp Asp Leu Lys Cys Asp Ile Ala Leu Pro Cys Ala Thr Gln Asn Glu	
310 315 320 325	
ctc aac ggc gag aac gct aag act ctt gca gac aac ggc tgc cgt ttc	1123
Leu Asn Gly Glu Asn Ala Lys Thr Leu Ala Asp Asn Gly Cys Arg Phe	
330 335 340	
gtt gct gaa ggc gcg aac atg cct tcc acc cct gag gct gtt gag gtc	1171
Val Ala Glu Gly Ala Asn Met Pro Ser Thr Pro Glu Ala Val Glu Val	
345 350 355	

ggt ggc gtt gca acc tcc gct ctg gag atg cag cag aac gct tcg cgc 1267
Gly Gly Val Ala Thr Ser Ala Leu Glu Met Gln Gln Asn Ala Ser Arg
375 380 385

gat tcc tgg agc ttc gag tac acc gac gag cgc ctc cag gtg atc atg 1315
Asp Ser Trp Ser Phe Glu Tyr Thr Asp Glu Arg Leu Gln Val Ile Met
390 395 400 405

aag aac atc ttc aag acc tgt gca gag acc gca gca gag tat gga cac 1363
Lys Asn Ile Phe Lys Thr Cys Ala Glu Thr Ala Ala Glu Tyr Gly His
410 415 420

gag aac gat tac gtt gtc ggc gct aac att gct ggc ttc aag aag gta 1411
Glu Asn Asp Tyr Val Val Gly Ala Asn Ile Ala Gly Phe Lys Lys Val
425 430 435

gct gac gcg atg ctg gca cag ggc gtc atc taagaccct gcgctttact 1461
Ala Asp Ala Met Leu Ala Gln Gly Val Ile
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taa	1464
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<210> 94

<211> 447

<212> PRT

<213> Corynebacterium glutamicum

<400> 94

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20 25 30

Glu Ser Leu Lys Ile Val Leu Glu Lys Asp Pro His Tyr Ala Asp Tyr
35 40 45

Gly Leu Ile Gln Arg Leu Cys Glu Pro Glu Arg Gln Leu Ile Phe Arg
50 55 60

Val	Pro	Trp	Val	Asp	Asp	Gln	Gly	Gln	Val	His	Val	Asn	Arg	Gly	Phe
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Arg Val Gln Phe Asn Ser Ala Leu Gly Pro Tyr Lys Gly Gly Leu Arg
85 90 95

Phe His Pro Ser Val Asn Leu Gly Ile Val Lys Phe Leu Gly Phe Glu
100 105 110

Gln Ile Phe Lys Asn Ser Leu Thr Gly Leu Pro Ile Gly Gly Gly Lys
115 120 125

Gly Gly Ser Asp Phe Asp Pro Lys Gly Lys Ser Asp Leu Glu Ile Met
130 135 140

Arg Phe Cys Gln Ser Phe Met Thr Glu Leu His Arg His Ile Gly Glu

145		150		155		160
Tyr Arg Asp Val	Pro Ala Gly Asn Ile	Gly Val Gly Gly His Glu Ile				
	165		170		175	
Gly Tyr Leu Phe	Gly His Tyr Arg Arg	Met Ala Asn Gln His Glu Ser				
	180	185		190		
Gly Val Leu Thr	Gly Lys Gly Leu Thr Trp	Gly Gly Ser Leu Val Arg				
	195	200	205			
Thr Glu Ala Thr	Gly Tyr Gly Cys Val Tyr Phe	Val Ser Glu Met Ile				
	210	215	220			
Lys Ala Lys Gly	Glu Ser Ile Ser Gly Gln Lys	Ile Ile Val Ser Gly				
225	230	235	240			
Ser Gly Asn Val	Ala Thr Tyr Ala Ile	Glu Lys Ala Gln Glu Leu Gly				
	245	250	255			
Ala Thr Val Ile	Gly Phe Ser Asp Ser Ser	Gly Trp Val His Thr Pro				
	260	265	270			
Asn Gly Val Asp	Val Ala Lys Leu Arg Glu Ile	Lys Glu Val Arg Arg				
	275	280	285			
Ala Arg Val Ser	Val Tyr Ala Asp Glu Val	Glu Gly Ala Thr Tyr His				
	290	295	300			
Thr Asp Gly Ser	Ile Trp Asp Leu Lys Cys Asp	Ile Ala Leu Pro Cys				
305	310	315	320			
Ala Thr Gln Asn	Glu Leu Asn Gly Glu Asn	Ala Lys Thr Leu Ala Asp				
	325	330	335			
Asn Gly Cys Arg	Phe Val Ala Glu Gly Ala	Asn Met Pro Ser Thr Pro				
	340	345	350			
Glu Ala Val Glu	Val Phe Arg Glu Arg Asp	Ile Arg Phe Gly Pro Gly				
	355	360	365			
Lys Ala Ala Asn	Ala Gly Gly Val Ala Thr Ser	Ala Leu Glu Met Gln				
	370	375	380			
Gln Asn Ala Ser	Arg Asp Ser Trp Ser Phe	Glu Tyr Thr Asp Glu Arg				
385	390	395	400			
Leu Gln Val Ile	Met Lys Asn Ile Phe Lys	Thr Cys Ala Glu Thr Ala				
	405	410	415			
Ala Glu Tyr Gly	His Glu Asn Asp Tyr Val	Val Gly Ala Asn Ile Ala				
	420	425	430			
Gly Phe Lys Lys	Val Ala Asp Ala Met Leu	Ala Gln Gly Val Ile				
	435	440	445			

<210> 95

<211> 1461

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1438)

<223> RXA00323

<400> 95

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atgcgcagtc gatgtcccat cgctgcgtag attagttttc atg aac agc gaa cag 115
Met Asn Ser Glu Gln
1 5

gaa ttt gta ctc agc gcc att gaa gaa cgc gac att aag ttt gtg cgt 163
Glu Phe Val Leu Ser Ala Ile Glu Glu Arg Asp Ile Lys Phe Val Arg
10 15 20

cta tgg ttc act gac att ctt ggc cac ttg aag tca gtg gtt gtg gct 211
Leu Trp Phe Thr Asp Ile Leu Gly His Leu Lys Ser Val Val Val Ala
25 30 35

cct gca gaa cta gag tct gcg ttg gaa gaa ggc atc gga ttc gat ggc 259
Pro Ala Glu Leu Glu Ser Ala Leu Glu Glu Gly Ile Gly Phe Asp Gly
40 45 50

tca gcc att gag ggc tac gcg cgt atc tcg gaa gcg gac acc att gcc 307
Ser Ala Ile Glu Gly Tyr Ala Arg Ile Ser Glu Ala Asp Thr Ile Ala
55 60 65

cgc cca gat cca tcg aca ttc cag gtc ctc cca cta gaa gcg ggc atc 355
Arg Pro Asp Pro Ser Thr Phe Gln Val Leu Pro Leu Glu Ala Gly Ile
70 75 80 85

tca aaa ctg cag gca gca cgc ctg ttt tgc gat gtc acg atg cca gac 403
Ser Lys Leu Gln Ala Ala Arg Leu Phe Cys Asp Val Thr Met Pro Asp
90 95 100

gga cag cca tct ttt tct gac ccg cgc caa gtg ctg cgc agg cag gtc 451
Gly Gln Pro Ser Phe Ser Asp Pro Arg Gln Val Leu Arg Arg Gln Val
105 110 115

caa cta gct gca gat gaa ggc ttg acc tgc atg atc tca cca gag att 499
Gln Leu Ala Ala Asp Glu Gly Leu Thr Cys Met Ile Ser Pro Glu Ile
120 125 130

gag ttc tat ttg gtg caa agc ctt cgc acc aac gga ctg cca cct gtg 547
Glu Phe Tyr Leu Val Gln Ser Leu Arg Thr Asn Gly Leu Pro Pro Val
135 140 145

ccc act gac aac ggc gga tat ttc gac caa gcc aca ttc aat gag gcg 595
Pro Thr Asp Asn Gly Gly Tyr Phe Asp Gln Ala Thr Phe Asn Glu Ala
150 155 160 165

ccg aat ttc cgt cga aac gcg atg gta gcg ctg gag gaa ctc ggc atc 643
Pro Asn Phe Arg Arg Asn Ala Met Val Ala Leu Glu Glu Leu Gly Ile
170 175 180

cct gtc gag ttc tcc cac cat gaa act gca cct ggc cag caa gaa atc 691
Pro Val Glu Phe Ser His His Glu Thr Ala Pro Gly Gln Gln Glu Ile
185 190 195

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gat tta cgc cat gcg gat gcg ctc acc atg gcc gac aac atc atg acc	739
Asp Leu Arg His Ala Asp Ala Leu Thr Met Ala Asp Asn Ile Met Thr	
200 205 210	
ttc cgc tac atc atg aaa cag gtg gca agg gac caa ggc gtc ggg gca	787
Phe Arg Tyr Ile Met Lys Gln Val Ala Arg Asp Gln Gly Val Gly Ala	
215 220 225	
tca ttt atg ccc aag cca ttc caa gaa cat gca ggc tcc gcc atg cac	835
Ser Phe Met Pro Lys Pro Phe Gln Glu His Ala Gly Ser Ala Met His	
230 235 240 245	
acg cac atg tcc tta ttt gag ggc gat acc aac gcg ttc cac gat cca	883
Thr His Met Ser Leu Phe Glu Gly Asp Thr Asn Ala Phe His Asp Pro	
250 255 260	
gac gat tct tac atg ctg tcc aaa acc gca aaa cag ttc atc gct gga	931
Asp Asp Ser Tyr Met Leu Ser Lys Thr Ala Lys Gln Phe Ile Ala Gly	
265 270 275	
atc ttg cat cac gct cca gaa ttc acc gct gtg acc aac cag tgg gtc	979
Ile Leu His His Ala Pro Glu Phe Thr Ala Val Thr Asn Gln Trp Val	
280 285 290	
aat tcc tac aaa cgc atc gtg tac gga aac gaa gct cca act gcg gca	1027
Asn Ser Tyr Lys Arg Ile Val Tyr Gly Asn Glu Ala Pro Thr Ala Ala	
295 300 305	
acc tgg ggt gta tct aat cgt tct gcg ctg gtt cgt gtt cct acc tac	1075
Thr Trp Gly Val Ser Asn Arg Ser Ala Leu Val Arg Val Pro Thr Tyr	
310 315 320 325	
cgt ttg aat aag gag gag tcg cgc cgg gtg gag gtg cgt ctt cct gat	1123
Arg Leu Asn Lys Glu Glu Ser Arg Arg Val Glu Val Arg Leu Pro Asp	
330 335 340	
acc gct tgt aac cca tat ttg gcg ttt tca gtg atg ctc ggc gct ggt	1171
Thr Ala Cys Asn Pro Tyr Leu Ala Phe Ser Val Met Leu Gly Ala Gly	
345 350 355	
ttg aaa ggc att aaa gaa ggt tat gag ctc gac gag cca gct gag gac	1219
Leu Lys Gly Ile Lys Glu Gly Tyr Glu Leu Asp Glu Pro Ala Glu Asp	
360 365 370	
gat atc tcc aac ttg agc ttc cgg gaa cgt cgc gcc atg ggc tac aac	1267
Asp Ile Ser Asn Leu Ser Phe Arg Glu Arg Arg Ala Met Gly Tyr Asn	
375 380 385	
gat ctg cca agc agc ctt gat cag gca ctg cgc caa atg gaa aag tca	1315
Asp Leu Pro Ser Ser Leu Asp Gln Ala Leu Arg Gln Met Glu Lys Ser	
390 395 400 405	
gag ctt gtt gct gac atc ctc ggt gag cac gtt ttt gag ttt ttc ttg	1363
Glu Leu Val Ala Asp Ile Leu Gly Glu His Val Phe Glu Phe Phe Leu	
410 415 420	
cgc aat aag tgg cgt gaa tgg cgt gac tac caa gag cag atc act ccg	1411
Arg Asn Lys Trp Arg Glu Trp Arg Asp Tyr Gln Glu Gln Ile Thr Pro	
425 430 435	
tgg gag ctc cga aac aat ctt gat tac tagacttttg cactccaatg	1458

Trp Glu Leu Arg Asn Asn Leu Asp Tyr
 440 445

gaa

1461

<210> 96

<211> 446

<212> PRT

<213> Corynebacterium glutamicum

<400> 96

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Ile Lys Phe Val Arg Leu Trp Phe Thr Asp Ile Leu Gly His Leu Lys
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Ser Val Val Val Ala Pro Ala Glu Leu Glu Ser Ala Leu Glu Glu Gly
 35 40 45

Ile Gly Phe Asp Gly Ser Ala Ile Glu Gly Tyr Ala Arg Ile Ser Glu
 50 55 60

Ala Asp Thr Ile Ala Arg Pro Asp Pro Ser Thr Phe Gln Val Leu Pro
 65 70 75 80

Leu Glu Ala Gly Ile Ser Lys Leu Gln Ala Ala Arg Leu Phe Cys Asp
 85 90 95

Val Thr Met Pro Asp Gly Gln Pro Ser Phe Ser Asp Pro Arg Gln Val
 100 105 110

Leu Arg Arg Gln Val Gln Leu Ala Ala Asp Glu Gly Leu Thr Cys Met
 115 120 125

Ile Ser Pro Glu Ile Glu Phe Tyr Leu Val Gln Ser Leu Arg Thr Asn
 130 135 140

Gly Leu Pro Pro Val Pro Thr Asp Asn Gly Gly Tyr Phe Asp Gln Ala
 145 150 155 160

Thr Phe Asn Glu Ala Pro Asn Phe Arg Arg Asn Ala Met Val Ala Leu
 165 170 175

Glu Glu Leu Gly Ile Pro Val Glu Phe Ser His His Glu Thr Ala Pro
 180 185 190

Gly Gln Gln Glu Ile Asp Leu Arg His Ala Asp Ala Leu Thr Met Ala
 195 200 205

Asp Asn Ile Met Thr Phe Arg Tyr Ile Met Lys Gln Val Ala Arg Asp
 210 215 220

Gln Gly Val Gly Ala Ser Phe Met Pro Lys Pro Phe Gln Glu His Ala
 225 230 235 240

Gly Ser Ala Met His Thr His Met Ser Leu Phe Glu Gly Asp Thr Asn
 245 250 255

Ala Phe His Asp Pro Asp Asp Ser Tyr Met Leu Ser Lys Thr Ala Lys

260					265					270					
Gln	Phe	Ile	Ala	Gly	Ile	Leu	His	His	Ala	Pro	Glu	Phe	Thr	Ala	Val
		275					280					285			
Thr	Asn	Gln	Trp	Val	Asn	Ser	Tyr	Lys	Arg	Ile	Val	Tyr	Gly	Asn	Glu
	290					295					300				
Ala	Pro	Thr	Ala	Ala	Thr	Trp	Gly	Val	Ser	Asn	Arg	Ser	Ala	Leu	Val
305					310					315					320
Arg	Val	Pro	Thr	Tyr	Arg	Leu	Asn	Lys	Glu	Glu	Ser	Arg	Arg	Val	Glu
			325						330					335	
Val	Arg	Leu	Pro	Asp	Thr	Ala	Cys	Asn	Pro	Tyr	Leu	Ala	Phe	Ser	Val
			340					345					350		
Met	Leu	Gly	Ala	Gly	Leu	Lys	Gly	Ile	Lys	Glu	Gly	Tyr	Glu	Leu	Asp
	355						360					365			
Glu	Pro	Ala	Glu	Asp	Asp	Ile	Ser	Asn	Leu	Ser	Phe	Arg	Glu	Arg	Arg
	370					375					380				
Ala	Met	Gly	Tyr	Asn	Asp	Leu	Pro	Ser	Ser	Leu	Asp	Gln	Ala	Leu	Arg
385						390					395				400
Gln	Met	Glu	Lys	Ser	Glu	Leu	Val	Ala	Asp	Ile	Leu	Gly	Glu	His	Val
			405						410					415	
Phe	Glu	Phe	Phe	Leu	Arg	Asn	Lys	Trp	Arg	Glu	Trp	Arg	Asp	Tyr	Gln
			420					425					430		
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 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1531)
 <223> RXA00335

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 Val Ala Phe Glu Thr
 1 5

 ccg gaa gaa att gtc aag ttc atc aag gat gaa aac gtc gag ttc gtt 163
 Pro Glu Glu Ile Val Lys Phe Ile Lys Asp Glu Asn Val Glu Phe Val
 10 15 20

 gac gtt cga ttc acc gac ctt ccc ggc acc gag cag cac ttc agc atc 211
 Asp Val Arg Phe Thr Asp Leu Pro Gly Thr Glu Gln His Phe Ser Ile
 25 30 35

cca gct gcc agc ttc gat gca gat aca atc gaa gaa ggt ctc gca ttc	259
Pro Ala Ala Ser Phe Asp Ala Asp Thr Ile Glu Glu Gly Leu Ala Phe	
40 45 50	
gac gga tcc tcg atc cgt ggc ttc acc acg atc gac gaa tct gac atg	307
Asp Gly Ser Ser Ile Arg Gly Phe Thr Thr Ile Asp Glu Ser Asp Met	
55 60 65	
aat ctc ctg cca gac ctc gga acg gcc acc ctt gat cca ttc cgc aag	355
Asn Leu Leu Pro Asp Leu Gly Thr Ala Thr Leu Asp Pro Phe Arg Lys	
70 75 80 85	
gca aag acc ctg aac gtt aag ttc ttc gtt cac gat cct ttc acc cgc	403
Ala Lys Thr Leu Asn Val Lys Phe Phe Val His Asp Pro Phe Thr Arg	
90 95 100	
gag gca ttc tcc cgc gac cca cgc aac gtg gca cgc aag gca gag cag	451
Glu Ala Phe Ser Arg Asp Pro Arg Asn Val Ala Arg Lys Ala Glu Gln	
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Tyr Leu Ala Ser Thr Gly Ile Ala Asp Thr Cys Asn Phe Gly Ala Glu	
120 125 130	
gct gag ttc tac ctc ttc gac tcc gtt cgc tac tcc acc gag atg aac	547
Ala Glu Phe Tyr Leu Phe Asp Ser Val Arg Tyr Ser Thr Glu Met Asn	
135 140 145	
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Ser Gly Phe Tyr Glu Val Asp Thr Glu Glu Gly Trp Trp Asn Arg Gly	
150 155 160 165	
aag gaa acc aac ctc gac ggc acc cca aac ctg ggc gca aag aac cgc	643
Lys Glu Thr Asn Leu Asp Gly Thr Pro Asn Leu Gly Ala Lys Asn Arg	
170 175 180	
gtc aag ggt ggc tac ttc cca gta gca cca tac gac caa acc gtt gac	691
Val Lys Gly Gly Tyr Phe Pro Val Ala Pro Tyr Asp Gln Thr Val Asp	
185 190 195	
gtg cgc gat gac atg gtt cgc aac ctc gca gct tcc ggc ttc gct ctt	739
Val Arg Asp Asp Met Val Arg Asn Leu Ala Ala Ser Gly Phe Ala Leu	
200 205 210	
gag cgt ttc cac cac gaa gtc ggt ggc gga cag cag gaa atc aac tac	787
Glu Arg Phe His His Glu Val Gly Gly Gly Gln Gln Glu Ile Asn Tyr	
215 220 225	
cgc ttc aac acc atg ctc cac gcg gca gat gat atc cag acc ttc aag	835
Arg Phe Asn Thr Met Leu His Ala Ala Asp Asp Ile Gln Thr Phe Lys	
230 235 240 245	
tac atc atc aag aac acc gct cgc ctc cac ggc aag gct gca acc ttc	883
Tyr Ile Ile Lys Asn Thr Ala Arg Leu His Gly Lys Ala Ala Thr Phe	
250 255 260	
atg cct aag cca ctg gct ggc gac aac ggt tcc ggc atg cac gct cac	931
Met Pro Lys Pro Leu Ala Gly Asp Asn Gly Ser Gly Met His Ala His	
265 270 275	
cag tcc ctc tgg aag gac ggc aag cca ctc ttc cac gat gag tcc ggc	979

Gln	Ser	Leu	Trp	Lys	Asp	Gly	Lys	Pro	Leu	Phe	His	Asp	Glu	Ser	Gly		
		280					285					290					
tac	gca	ggc	ctg	tcc	gac	atc	gcc	cgc	tac	tac	atc	ggc	ggc	atc	ctg	1027	
Tyr	Ala	Gly	Leu	Ser	Asp	Ile	Ala	Arg	Tyr	Tyr	Ile	Gly	Gly	Ile	Leu		
	295					300					305						
cac	cac	gca	ggc	gct	gtt	ctg	gcg	ttc	acc	aac	gca	acc	ctg	aac	tcc	1075	
His	His	Ala	Gly	Ala	Val	Leu	Ala	Phe	Thr	Asn	Ala	Thr	Leu	Asn	Ser		
310					315					320					325		
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Tyr	His	Arg	Leu	Val	Pro	Gly	Phe	Glu	Ala	Pro	Ile	Asn	Leu	Val	Tyr		
				330					335					340			
tca	cag	cgc	aac	cgt	tcc	gct	gct	gtc	cgt	atc	cca	atc	acc	gga	tcc	1171	
Ser	Gln	Arg	Asn	Arg	Ser	Ala	Ala	Val	Arg	Ile	Pro	Ile	Thr	Gly	Ser		
			345					350					355				
aac	ccg	aag	gca	aag	cgc	atc	gaa	ttc	cgc	gct	cca	gac	cca	tca	ggc	1219	
Asn	Pro	Lys	Ala	Lys	Arg	Ile	Glu	Phe	Arg	Ala	Pro	Asp	Pro	Ser	Gly		
		360					365					370					
aac	cca	tac	ctg	ggc	ttt	gca	gcg	atg	atg	atg	gcc	ggc	ctc	gac	ggc	1267	
Asn	Pro	Tyr	Leu	Gly	Phe	Ala	Ala	Met	Met	Met	Ala	Gly	Leu	Asp	Gly		
		375				380					385						
atc	aag	aac	cgc	atc	gag	cca	cac	gct	cca	gtg	gac	aag	gac	ctc	tac	1315	
Ile	Lys	Asn	Arg	Ile	Glu	Pro	His	Ala	Pro	Val	Asp	Lys	Asp	Leu	Tyr		
390					395					400					405		
gaa	cta	cca	cca	gag	gaa	gct	gca	tcc	att	cca	cag	gca	cca	acc	tcc	1363	
Glu	Leu	Pro	Pro	Glu	Glu	Ala	Ala	Ser	Ile	Pro	Gln	Ala	Pro	Thr	Ser		
				410					415					420			
ctg	gaa	gca	tcc	ctg	aag	gca	ctg	cag	gaa	gac	acc	gac	ttc	ctc	acc	1411	
Leu	Glu	Ala	Ser	Leu	Lys	Ala	Leu	Gln	Glu	Asp	Thr	Asp	Phe	Leu	Thr		
			425					430					435				
gag	tct	gac	gtc	ttc	acc	gag	gat	ctc	atc	gag	gcg	tac	atc	cag	tac	1459	
Glu	Ser	Asp	Val	Phe	Thr	Glu	Asp	Leu	Ile	Glu	Ala	Tyr	Ile	Gln	Tyr		
		440					445					450					
aag	tac	gac	aac	gag	atc	tcc	cca	gtt	cgc	ctg	cgc	cca	acc	ccg	cag	1507	
Lys	Tyr	Asp	Asn	Glu	Ile	Ser	Pro	Val	Arg	Leu	Arg	Pro	Thr	Pro	Gln		
	455					460					465						
gaa	ttc	gaa	ttg	tac	ttc	gac	tgc	taattcactt	agctagccga	tag						1554	
Glu	Phe	Glu	Leu	Tyr	Phe	Asp	Cys										
470					475												

<210> 98

<211> 477

<212> PRT

<213> Corynebacterium glutamicum

<400> 98

Val	Ala	Phe	Glu	Thr	Pro	Glu	Glu	Ile	Val	Lys	Phe	Ile	Lys	Asp	Glu
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Asn Val Glu Phe Val Asp Val Arg Phe Thr Asp Leu Pro Gly Thr Glu
 20 25 30
 Gln His Phe Ser Ile Pro Ala Ala Ser Phe Asp Ala Asp Thr Ile Glu
 35 40 45
 Glu Gly Leu Ala Phe Asp Gly Ser Ser Ile Arg Gly Phe Thr Thr Ile
 50 55 60
 Asp Glu Ser Asp Met Asn Leu Leu Pro Asp Leu Gly Thr Ala Thr Leu
 65 70 75 80
 Asp Pro Phe Arg Lys Ala Lys Thr Leu Asn Val Lys Phe Phe Val His
 85 90 95
 Asp Pro Phe Thr Arg Glu Ala Phe Ser Arg Asp Pro Arg Asn Val Ala
 100 105 110
 Arg Lys Ala Glu Gln Tyr Leu Ala Ser Thr Gly Ile Ala Asp Thr Cys
 115 120 125
 Asn Phe Gly Ala Glu Ala Glu Phe Tyr Leu Phe Asp Ser Val Arg Tyr
 130 135 140
 Ser Thr Glu Met Asn Ser Gly Phe Tyr Glu Val Asp Thr Glu Glu Gly
 145 150 155 160
 Trp Trp Asn Arg Gly Lys Glu Thr Asn Leu Asp Gly Thr Pro Asn Leu
 165 170 175
 Gly Ala Lys Asn Arg Val Lys Gly Gly Tyr Phe Pro Val Ala Pro Tyr
 180 185 190
 Asp Gln Thr Val Asp Val Arg Asp Asp Met Val Arg Asn Leu Ala Ala
 195 200 205
 Ser Gly Phe Ala Leu Glu Arg Phe His His Glu Val Gly Gly Gly Gln
 210 215 220
 Gln Glu Ile Asn Tyr Arg Phe Asn Thr Met Leu His Ala Ala Asp Asp
 225 230 235 240
 Ile Gln Thr Phe Lys Tyr Ile Ile Lys Asn Thr Ala Arg Leu His Gly
 245 250 255
 Lys Ala Ala Thr Phe Met Pro Lys Pro Leu Ala Gly Asp Asn Gly Ser
 260 265 270
 Gly Met His Ala His Gln Ser Leu Trp Lys Asp Gly Lys Pro Leu Phe
 275 280 285
 His Asp Glu Ser Gly Tyr Ala Gly Leu Ser Asp Ile Ala Arg Tyr Tyr
 290 295 300
 Ile Gly Gly Ile Leu His His Ala Gly Ala Val Leu Ala Phe Thr Asn
 305 310 315 320
 Ala Thr Leu Asn Ser Tyr His Arg Leu Val Pro Gly Phe Glu Ala Pro
 325 330 335
 Ile Asn Leu Val Tyr Ser Gln Arg Asn Arg Ser Ala Ala Val Arg Ile

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Pro	Ile	Thr	Gly	Ser	Asn	Pro	Lys	Ala	Lys	Arg	Ile	Glu	Phe	Arg	Ala	
355					360					365						
Pro	Asp	Pro	Ser	Gly	Asn	Pro	Tyr	Leu	Gly	Phe	Ala	Ala	Met	Met	Met	
370					375					380						
Ala	Gly	Leu	Asp	Gly	Ile	Lys	Asn	Arg	Ile	Glu	Pro	His	Ala	Pro	Val	
385					390					395					400	
Asp	Lys	Asp	Leu	Tyr	Glu	Leu	Pro	Pro	Glu	Glu	Ala	Ala	Ser	Ile	Pro	
405					410					415						
Gln	Ala	Pro	Thr	Ser	Leu	Glu	Ala	Ser	Leu	Lys	Ala	Leu	Gln	Glu	Asp	
420					425					430						
Thr	Asp	Phe	Leu	Thr	Glu	Ser	Asp	Val	Phe	Thr	Glu	Asp	Leu	Ile	Glu	
435					440					445						
Ala	Tyr	Ile	Gln	Tyr	Lys	Tyr	Asp	Asn	Glu	Ile	Ser	Pro	Val	Arg	Leu	
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 Met Ser Gly Pro Leu
 1 5

 aga agt gaa cgt aaa gtc gtt ggc ttt gtc aga gac cca ctg cca aaa 163
 Arg Ser Glu Arg Lys Val Val Gly Phe Val Arg Asp Pro Leu Pro Lys
 10 15 20

 gtt ggt tct tta tcg ctg aaa tct gag cat gcc caa gca gat cta gag 211
 Val Gly Ser Leu Ser Leu Lys Ser Glu His Ala Gln Ala Asp Leu Glu
 25 30 35

 cat ttg ggt tgg cgc aat gtt gag tct ttg gat ttg ttg tgg ggc ttg 259
 His Leu Gly Trp Arg Asn Val Glu Ser Leu Asp Leu Leu Trp Gly Leu
 40 45 50

 tca ggt gca ggc gat ccc gat gtc gcg ctg aac ctt ctt att cgg ctg 307
 Ser Gly Ala Gly Asp Pro Asp Val Ala Leu Asn Leu Leu Ile Arg Leu
 55 60 65

 tat cag gca ctt gaa gca atc ggc gag gat gct cga aac gag ctt gat 355

Tyr	Gln	Ala	Leu	Glu	Ala	Ile	Gly	Glu	Asp	Ala	Arg	Asn	Glu	Leu	Asp	
70					75					80					85	
caa	gag	att	cgc	cag	gat	gaa	aaa	cta	cga	gtc	cgc	ctt	ttt	gca	ttg	403
Gln	Glu	Ile	Arg	Gln	Asp	Glu	Lys	Leu	Arg	Val	Arg	Leu	Phe	Ala	Leu	
				90					95					100		
ttg	ggt	ggt	tcc	tcg	gct	gtc	ggt	gat	cac	ttg	gtc	gcc	aat	cct	ttg	451
Leu	Gly	Gly	Ser	Ser	Ala	Val	Gly	Asp	His	Leu	Val	Ala	Asn	Pro	Leu	
			105					110					115			
cag	tgg	aaa	ctc	tta	aaa	ctt	gat	gcg	cca	tcg	agg	gaa	gag	atg	ttt	499
Gln	Trp	Lys	Leu	Leu	Lys	Leu	Asp	Ala	Pro	Ser	Arg	Glu	Glu	Met	Phe	
		120					125					130				
cag	gcg	ctg	ctg	gaa	tct	gtg	aaa	gct	cag	cct	gct	gtg	ctt	gag	gtt	547
Gln	Ala	Leu	Leu	Glu	Ser	Val	Lys	Ala	Gln	Pro	Ala	Val	Leu	Glu	Val	
		135				140					145					
gag	gat	ttc	agc	gat	gca	cac	aac	att	gcc	cga	gac	gat	ttg	agc	acg	595
Glu	Asp	Phe	Ser	Asp	Ala	His	Asn	Ile	Ala	Arg	Asp	Asp	Leu	Ser	Thr	
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cct	ggt	ttt	tac	acg	gct	agt	gtt	acc	ggg	cct	gaa	gca	gag	cga	gtc	643
Pro	Gly	Phe	Tyr	Thr	Ala	Ser	Val	Thr	Gly	Pro	Glu	Ala	Glu	Arg	Val	
				170					175					180		
ttg	aaa	tgg	act	tat	cgc	acg	ttg	ctg	acc	cgg	att	gct	gcg	cat	gat	691
Leu	Lys	Trp	Thr	Tyr	Arg	Thr	Leu	Leu	Thr	Arg	Ile	Ala	Ala	His	Asp	
			185					190					195			
tta	gcg	ggt	acc	tat	ccc	acc	gac	atg	cgg	aga	aaa	ggt	ggc	gat	cct	739
Leu	Ala	Gly	Thr	Tyr	Pro	Thr	Asp	Met	Arg	Arg	Lys	Gly	Gly	Asp	Pro	
		200					205					210				
gtt	ccg	ttt	agc	aca	gtg	acc	atg	cag	ctc	agc	gac	cta	gct	gat	gct	787
Val	Pro	Phe	Ser	Thr	Val	Thr	Met	Gln	Leu	Ser	Asp	Leu	Ala	Asp	Ala	
		215				220					225					
gct	ttg	act	gct	gct	tta	gct	gtg	gca	att	gcc	aat	gtt	tat	ggt	gaa	835
Ala	Leu	Thr	Ala	Ala	Leu	Ala	Val	Ala	Ile	Ala	Asn	Val	Tyr	Gly	Glu	
					235					240					245	
aag	ccg	gtt	gat	tca	gct	tta	tct	gtc	atc	gcg	atg	ggc	aaa	tgt	ggc	883
Lys	Pro	Val	Asp	Ser	Ala	Leu	Ser	Val	Ile	Ala	Met	Gly	Lys	Cys	Gly	
				250					255					260		
gcg	cag	gaa	ttg	aac	tac	att	tca	gat	gtg	gac	gtg	gtg	ttt	gtt	gca	931
Ala	Gln	Glu	Leu	Asn	Tyr	Ile	Ser	Asp	Val	Asp	Val	Val	Phe	Val	Ala	
			265					270					275			
gag	ccg	gca	aac	tct	aaa	tca	aca	cgc	acc	gca	gca	gag	ctc	att	cgc	979
Glu	Pro	Ala	Asn	Ser	Lys	Ser	Thr	Arg	Thr	Ala	Ala	Glu	Leu	Ile	Arg	
		280					285					290				
atc	ggt	agc	aac	tcg	ttc	ttt	gag	gtg	gat	gca	gca	ctt	cgc	cca	gaa	1027
Ile	Gly	Ser	Asn	Ser	Phe	Phe	Glu	Val	Asp	Ala	Ala	Leu	Arg	Pro	Glu	
		295				300					305					
ggt	aaa	agt	ggc	gct	ctt	gtg	cgc	tct	ttg	gat	tcc	cat	atg	gcg	tat	1075
Gly	Lys	Ser	Gly	Ala	Leu	Val	Arg	Ser	Leu	Asp	Ser	His	Met	Ala	Tyr	

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tac aag cgc tgg gcg gaa acc tgg gag ttt cag gca ctg ctg aaa gct				1123
Tyr Lys Arg Trp Ala Glu Thr Trp Glu Phe Gln Ala Leu Leu Lys Ala	330	335	340	
cgt ccc atg acg ggt gat att aac ctt ggg cag tcc tat gtg gat gct				1171
Arg Pro Met Thr Gly Asp Ile Asn Leu Gly Gln Ser Tyr Val Asp Ala	345	350	355	
ctt tca ccg ttg att tgg acg gct agc cag cgg gaa tca ttt gtc aca				1219
Leu Ser Pro Leu Ile Trp Thr Ala Ser Gln Arg Glu Ser Phe Val Thr	360	365	370	
gat gtc caa gct atg cgc cgt cga gtg ttg gac aat gtt ccg gaa gac				1267
Asp Val Gln Ala Met Arg Arg Arg Val Leu Asp Asn Val Pro Glu Asp	375	380	385	
ttg cgt gat cgt gag ctg aag ctt ggt cgc ggt ggt ttg agg gat gtg				1315
Leu Arg Asp Arg Glu Leu Lys Leu Gly Arg Gly Gly Leu Arg Asp Val	390	395	400	405
gag ttt gct gtc cag ctc ctt cag atg gtg cat ggt cgc att gat gag				1363
Glu Phe Ala Val Gln Leu Leu Gln Met Val His Gly Arg Ile Asp Glu	410	415	420	
acg ttg cgg gtt cgg tca acg gta aat gct ttg cat gtg ttg gtt gat				1411
Thr Leu Arg Val Arg Ser Thr Val Asn Ala Leu His Val Leu Val Asp	425	430	435	
cag gga tat gtg ggt cgt gaa gac ggg cat aat ctc att gag tcg tat				1459
Gln Gly Tyr Val Gly Arg Glu Asp Gly His Asn Leu Ile Glu Ser Tyr	440	445	450	
gag ttt ttg cgt ctg ttg gag cat cgc ctt caa ttg gag cgg atc aag				1507
Glu Phe Leu Arg Leu Leu Glu His Arg Leu Gln Leu Glu Arg Ile Lys	455	460	465	
cgc act cac ttg tta ccg aaa cct gat gac cga atg aat atg cgc tgg				1555
Arg Thr His Leu Leu Pro Lys Pro Asp Asp Arg Met Asn Met Arg Trp	470	475	480	485
ttg gcg cgc gct tct ggg ttt act ggt tcg atg gag caa agt tcg gcc				1603
Leu Ala Arg Ala Ser Gly Phe Thr Gly Ser Met Glu Gln Ser Ser Ala	490	495	500	
aaa gct atg gaa cgg cat ttg cgt aag gtt cgt ttg cag att cag tcg				1651
Lys Ala Met Glu Arg His Leu Arg Lys Val Arg Leu Gln Ile Gln Ser	505	510	515	
ttg cat agt cag ctg ttt tat cgg cca ctg ctg aac tct gtg gtc aac				1699
Leu His Ser Gln Leu Phe Tyr Arg Pro Leu Leu Asn Ser Val Val Asn	520	525	530	
ttg agc gcg gat gcc atc agg ttg tct ccg gat gct gca aag cta caa				1747
Leu Ser Ala Asp Ala Ile Arg Leu Ser Pro Asp Ala Ala Lys Leu Gln	535	540	545	
ttg gcg gca ttg gga tac ctg cat cca tca cgt gct tat gaa cac ctg				1795
Leu Ala Ala Leu Gly Tyr Leu His Pro Ser Arg Ala Tyr Glu His Leu	550	555	560	565

act gct ctt gca tca gga gct agc cgt aaa gcc aag att cag gcg atg	1843
Thr Ala Leu Ala Ser Gly Ala Ser Arg Lys Ala Lys Ile Gln Ala Met	
570 575 580	
ttg ctg ccc acg ttg atg gag tgg ctg tct caa aca gct gaa cca gat	1891
Leu Leu Pro Thr Leu Met Glu Trp Leu Ser Gln Thr Ala Glu Pro Asp	
585 590 595	
gcg gga ttg ctg aat tac cgc aag ctt tct gat gct tcc tat gat cgc	1939
Ala Gly Leu Leu Asn Tyr Arg Lys Leu Ser Asp Ala Ser Tyr Asp Arg	
600 605 610	
agc tgg ttt ttg cgc atg ctg cgt gat gag ggc gta gtg ggg cag cgg	1987
Ser Trp Phe Leu Arg Met Leu Arg Asp Glu Gly Val Val Gly Gln Arg	
615 620 625	
ttg atg cgt att ttg gga aat tct ccc tat att tct gaa ctg att atc	2035
Leu Met Arg Ile Leu Gly Asn Ser Pro Tyr Ile Ser Glu Leu Ile Ile	
630 635 640 645	
tcc act ccg gac ttt atg aaa cag ctg ggt gat gcg gcg tct ggt cct	2083
Ser Thr Pro Asp Phe Met Lys Gln Leu Gly Asp Ala Ala Ser Gly Pro	
650 655 660	
aaa ttg ctt gct act gca ccg act cag gtt gtg aaa gca atc aag gca	2131
Lys Leu Leu Ala Thr Ala Pro Thr Gln Val Val Lys Ala Ile Lys Ala	
665 670 675	
acg gtg tcg cgt cat gag tca cct gat cgg gcg atc cag gct gca cga	2179
Thr Val Ser Arg His Glu Ser Pro Asp Arg Ala Ile Gln Ala Ala Arg	
680 685 690	
tcg ctg agg agg cag gag ctg gca cgc att gcc tct gct gat ttg ctc	2227
Ser Leu Arg Arg Gln Glu Leu Ala Arg Ile Ala Ser Ala Asp Leu Leu	
695 700 705	
aac atg ctc act gtt cag gaa gta tgc caa agc ttg tca cta gtc tgg	2275
Asn Met Leu Thr Val Gln Glu Val Cys Gln Ser Leu Ser Leu Val Trp	
710 715 720 725	
gat gcg gtg ttg gat gct gcc ttg gat gcg gaa atc cgt gct gca ctt	2323
Asp Ala Val Leu Asp Ala Ala Leu Asp Ala Glu Ile Arg Ala Ala Leu	
730 735 740	
aac gat cca cag aaa cca gat cag cct ctg gcc aat att tct gtg atc	2371
Asn Asp Pro Gln Lys Pro Asp Gln Pro Leu Ala Asn Ile Ser Val Ile	
745 750 755	
ggc atg ggc cgt ttg ggt gga gca gaa ctt gga tac ggt tct gat gcc	2419
Gly Met Gly Arg Leu Gly Gly Ala Glu Leu Gly Tyr Gly Ser Asp Ala	
760 765 770	
gat gtg atg ttt gta tgc gag ccg gta gcc ggt gtg gaa gag cat gag	2467
Asp Val Met Phe Val Cys Glu Pro Val Ala Gly Val Glu Glu His Glu	
775 780 785	
gcc gtc aca tgg tct att gct atc tgt gat tcc atg cgg tcg agg ctt	2515
Ala Val Thr Trp Ser Ile Ala Ile Cys Asp Ser Met Arg Ser Arg Leu	
790 795 800 805	

gcg cag cct tcc ggt gat cca cct ttg gag gtg gat ctg ggg ctg cgt	2563
Ala Gln Pro Ser Gly Asp Pro Pro Leu Glu Val Asp Leu Gly Leu Arg	
810 815 820	
cct gaa ggg aga tct ggt gcg att gtg cgc acc gtt gat tcc tat gtg	2611
Pro Glu Gly Arg Ser Gly Ala Ile Val Arg Thr Val Asp Ser Tyr Val	
825 830 835	
aag tac tac gaa aag tgg ggt gaa act tgg gag att cag gcg ctg ctg	2659
Lys Tyr Tyr Glu Lys Trp Gly Glu Thr Trp Glu Ile Gln Ala Leu Leu	
840 845 850	
agg gct gcg tgg gtt gct ggt gat cgt gag ctg ggt att aag ttc ttg	2707
Arg Ala Ala Trp Val Ala Gly Asp Arg Glu Leu Gly Ile Lys Phe Leu	
855 860 865	
gag tcg att gat cgt ttc cgc tac cca gtt gac ggg gca acg cag gcg	2755
Glu Ser Ile Asp Arg Phe Arg Tyr Pro Val Asp Gly Ala Thr Gln Ala	
870 875 880 885	
cag ctt cgt gaa gtt cgt cga att aag gcg agg gtg gat aat gag agg	2803
Gln Leu Arg Glu Val Arg Arg Ile Lys Ala Arg Val Asp Asn Glu Arg	
890 895 900	
ctt ccg cgc ggg gct gat cga aat acc cat acc aag ctg ggt cgg gga	2851
Leu Pro Arg Gly Ala Asp Arg Asn Thr His Thr Lys Leu Gly Arg Gly	
905 910 915	
gcg tta act gac atc gag tgg act gtg cag ttg ttg acc atg atg cat	2899
Ala Leu Thr Asp Ile Glu Trp Thr Val Gln Leu Leu Thr Met Met His	
920 925 930	
gct cat gag att ccg gag ctg cac aat acg tcg acg ttg gaa gtt ctt	2947
Ala His Glu Ile Pro Glu Leu His Asn Thr Ser Thr Leu Glu Val Leu	
935 940 945	
gaa gtg ctg gaa aag cat cag att att aac cct gtg cag gtg cag acg	2995
Glu Val Leu Glu Lys His Gln Ile Ile Asn Pro Val Gln Val Gln Thr	
950 955 960 965	
ctt cgg gaa gcg tgg ctg acg gca acg gct gct agg aat gcg ctt gtg	3043
Leu Arg Glu Ala Trp Leu Thr Ala Thr Ala Ala Arg Asn Ala Leu Val	
970 975 980	
ctg gtc agg ggt aag aga tta gat cag tta cct act cct ggt ccg cac	3091
Leu Val Arg Gly Lys Arg Leu Asp Gln Leu Pro Thr Pro Gly Pro His	
985 990 995	
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Leu Ala Gln Val Ala Gly Ala Ser Gly Trp Asp Pro Asn Glu Tyr Gln	
1000 1005 1010	
gag tat ttg gaa aac tat ctg aaa gtg acc agg aag agt cgt cag gtt	3187
Glu Tyr Leu Glu Asn Tyr Leu Lys Val Thr Arg Lys Ser Arg Gln Val	
1015 1020 1025	
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Val Asp Glu Val Phe Trp Gly Val Asp Ser Met Glu Gln Arg Glu Phe	
1030 1035 1040 1045	
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<213> Corynebacterium glutamicum

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Ala Glu Leu Ile Arg Ile Gly Ser Asn Ser Phe Phe Glu Val Asp Ala
 290 295 300
 Ala Leu Arg Pro Glu Gly Lys Ser Gly Ala Leu Val Arg Ser Leu Asp
 305 310 315 320
 Ser His Met Ala Tyr Tyr Lys Arg Trp Ala Glu Thr Trp Glu Phe Gln
 325 330 335
 Ala Leu Leu Lys Ala Arg Pro Met Thr Gly Asp Ile Asn Leu Gly Gln
 340 345 350
 Ser Tyr Val Asp Ala Leu Ser Pro Leu Ile Trp Thr Ala Ser Gln Arg
 355 360 365
 Glu Ser Phe Val Thr Asp Val Gln Ala Met Arg Arg Arg Val Leu Asp
 370 375 380
 Asn Val Pro Glu Asp Leu Arg Asp Arg Glu Leu Lys Leu Gly Arg Gly
 385 390 395 400
 Gly Leu Arg Asp Val Glu Phe Ala Val Gln Leu Leu Gln Met Val His
 405 410 415
 Gly Arg Ile Asp Glu Thr Leu Arg Val Arg Ser Thr Val Asn Ala Leu
 420 425 430
 His Val Leu Val Asp Gln Gly Tyr Val Gly Arg Glu Asp Gly His Asn
 435 440 445
 Leu Ile Glu Ser Tyr Glu Phe Leu Arg Leu Leu Glu His Arg Leu Gln
 450 455 460
 Leu Glu Arg Ile Lys Arg Thr His Leu Leu Pro Lys Pro Asp Asp Arg
 465 470 475 480
 Met Asn Met Arg Trp Leu Ala Arg Ala Ser Gly Phe Thr Gly Ser Met
 485 490 495
 Glu Gln Ser Ser Ala Lys Ala Met Glu Arg His Leu Arg Lys Val Arg
 500 505 510
 Leu Gln Ile Gln Ser Leu His Ser Gln Leu Phe Tyr Arg Pro Leu Leu
 515 520 525
 Asn Ser Val Val Asn Leu Ser Ala Asp Ala Ile Arg Leu Ser Pro Asp
 530 535 540
 Ala Ala Lys Leu Gln Leu Ala Ala Leu Gly Tyr Leu His Pro Ser Arg
 545 550 555 560
 Ala Tyr Glu His Leu Thr Ala Leu Ala Ser Gly Ala Ser Arg Lys Ala
 565 570 575
 Lys Ile Gln Ala Met Leu Leu Pro Thr Leu Met Glu Trp Leu Ser Gln
 580 585 590
 Thr Ala Glu Pro Asp Ala Gly Leu Leu Asn Tyr Arg Lys Leu Ser Asp
 595 600 605

Ala	Ser	Tyr	Asp	Arg	Ser	Trp	Phe	Leu	Arg	Met	Leu	Arg	Asp	Glu	Gly	610	615	620
Val	Val	Gly	Gln	Arg	Leu	Met	Arg	Ile	Leu	Gly	Asn	Ser	Pro	Tyr	Ile	625	630	635
Ser	Glu	Leu	Ile	Ile	Ser	Thr	Pro	Asp	Phe	Met	Lys	Gln	Leu	Gly	Asp	645	650	655
Ala	Ala	Ser	Gly	Pro	Lys	Leu	Leu	Ala	Thr	Ala	Pro	Thr	Gln	Val	Val	660	665	670
Lys	Ala	Ile	Lys	Ala	Thr	Val	Ser	Arg	His	Glu	Ser	Pro	Asp	Arg	Ala	675	680	685
Ile	Gln	Ala	Ala	Arg	Ser	Leu	Arg	Arg	Gln	Glu	Leu	Ala	Arg	Ile	Ala	690	695	700
Ser	Ala	Asp	Leu	Leu	Asn	Met	Leu	Thr	Val	Gln	Glu	Val	Cys	Gln	Ser	705	710	715
Leu	Ser	Leu	Val	Trp	Asp	Ala	Val	Leu	Asp	Ala	Ala	Leu	Asp	Ala	Glu	725	730	735
Ile	Arg	Ala	Ala	Leu	Asn	Asp	Pro	Gln	Lys	Pro	Asp	Gln	Pro	Leu	Ala	740	745	750
Asn	Ile	Ser	Val	Ile	Gly	Met	Gly	Arg	Leu	Gly	Gly	Ala	Glu	Leu	Gly	755	760	765
Tyr	Gly	Ser	Asp	Ala	Asp	Val	Met	Phe	Val	Cys	Glu	Pro	Val	Ala	Gly	770	775	780
Val	Glu	Glu	His	Glu	Ala	Val	Thr	Trp	Ser	Ile	Ala	Ile	Cys	Asp	Ser	785	790	795
Met	Arg	Ser	Arg	Leu	Ala	Gln	Pro	Ser	Gly	Asp	Pro	Pro	Leu	Glu	Val	805	810	815
Asp	Leu	Gly	Leu	Arg	Pro	Glu	Gly	Arg	Ser	Gly	Ala	Ile	Val	Arg	Thr	820	825	830
Val	Asp	Ser	Tyr	Val	Lys	Tyr	Tyr	Glu	Lys	Trp	Gly	Glu	Thr	Trp	Glu	835	840	845
Ile	Gln	Ala	Leu	Leu	Arg	Ala	Ala	Trp	Val	Ala	Gly	Asp	Arg	Glu	Leu	850	855	860
Gly	Ile	Lys	Phe	Leu	Glu	Ser	Ile	Asp	Arg	Phe	Arg	Tyr	Pro	Val	Asp	865	870	875
Gly	Ala	Thr	Gln	Ala	Gln	Leu	Arg	Glu	Val	Arg	Arg	Ile	Lys	Ala	Arg	885	890	895
Val	Asp	Asn	Glu	Arg	Leu	Pro	Arg	Gly	Ala	Asp	Arg	Asn	Thr	His	Thr	900	905	910
Lys	Leu	Gly	Arg	Gly	Ala	Leu	Thr	Asp	Ile	Glu	Trp	Thr	Val	Gln	Leu	915	920	925
Leu	Thr	Met	Met	His	Ala	His	Glu	Ile	Pro	Glu	Leu	His	Asn	Thr	Ser			

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Thr Leu Glu Val Leu Glu Val Leu Glu Lys His Gln Ile Ile Asn Pro 945 950 955 960		
Val Gln Val Gln Thr Leu Arg Glu Ala Trp Leu Thr Ala Thr Ala Ala 965 970 975		
Arg Asn Ala Leu Val Leu Val Arg Gly Lys Arg Leu Asp Gln Leu Pro 980 985 990		
Thr Pro Gly Pro His Leu Ala Gln Val Ala Gly Ala Ser Gly Trp Asp 995 1000 1005		
Pro Asn Glu Tyr Gln Glu Tyr Leu Glu Asn Tyr Leu Lys Val Thr Arg 1010 1015 1020		
Lys Ser Arg Gln Val Val Asp Glu Val Phe Trp Gly Val Asp Ser Met 1025 1030 1035 1040		
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 <223> RXN03176

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gat gac gac atc gaa ttc acc atg caa agt att tcc aag cca ttt gcc Asp Asp Asp Ile Glu Phe Thr Met Gln Ser Ile Ser Lys Pro Phe Ala 35 40 45	144
tac gca ctc gca ctc caa gaa tgc ggc ttt gat gag gtc tct gca tcc Tyr Ala Leu Ala Leu Gln Glu Cys Gly Phe Asp Glu Val Ser Ala Ser 50 55 60	192
gtg gcc ttg gag ccc tcc ggt gag gcc ttc aac gaa ctt tcc ctc gac Val Ala Leu Glu Pro Ser Gly Glu Ala Phe Asn Glu Leu Ser Leu Asp 65 70 75 80	240
ggc gaa aac cgc ccc atg aac ccc atg atc aac gcc ggc gcg atc gcc Gly Glu Asn Arg Pro Met Asn Pro Met Ile Asn Ala Gly Ala Ile Ala 85 90 95	288
atc aac cag ctg atc aac ggc tcc gat tcc acc gtg gaa gac cgc gtg Ile Asn Gln Leu Ile Asn Gly Ser Asp Ser Thr Val Glu Asp Arg Val	336

100	105	110	
gaa aaa atc cga cac tac ttc tct gaa ctt gct gga cgc gaa ctc acc			384
Glu Lys Ile Arg His Tyr Phe Ser Glu Leu Ala Gly Arg Glu Leu Thr			
115	120	125	
atc gac cgc gtg ctt gcc gaa tcc gaa ctc gcc ggc gcc gac cgc aac			432
Ile Asp Arg Val Leu Ala Glu Ser Glu Leu Ala Gly Ala Asp Arg Asn			
130	135	140	
ctc tcc atc gcc cac atg ctg cgc aat tac ggc gtc atc gaa gac gaa			480
Leu Ser Ile Ala His Met Leu Arg Asn Tyr Gly Val Ile Glu Asp Glu			
145	150	155	160
gcc cac gac gcc gtc ctc agc tac acg ctg caa tgc gcc atc aaa gta			528
Ala His Asp Ala Val Leu Ser Tyr Thr Leu Gln Cys Ala Ile Lys Val			
165	170	175	
acc acg cgc gac ctc gca gtc atg acc gcc acg ctc gcc gcc ggc ggc			576
Thr Thr Arg Asp Leu Ala Val Met Thr Ala Thr Leu Ala Ala Gly Gly			
180	185	190	
aca cac cca att acc ggc aag aag ctt ctc gac gcc cgc gtc tgc cgc			624
Thr His Pro Ile Thr Gly Lys Lys Leu Leu Asp Ala Arg Val Cys Arg			
195	200	205	
ctc acc ctc tcc gtc atg gct tca gca ggc atg tac gac gag gca ggc			672
Leu Thr Leu Ser Val Met Ala Ser Ala Gly Met Tyr Asp Glu Ala Gly			
210	215	220	
cag tgg ctc tcc acc gta ggc atc ccc gcg aaa tca gga gtc gcc ggc			720
Gln Trp Leu Ser Thr Val Gly Ile Pro Ala Lys Ser Gly Val Ala Gly			
225	230	235	240
gga ctc atc ggc att ctg cca ggt cag ctg ggc atc gcc aca ttt tcc			768
Gly Leu Ile Gly Ile Leu Pro Gly Gln Leu Gly Ile Ala Thr Phe Ser			
245	250	255	
cca cgc ctg aac ccc aaa ggc aac agc gtg cgc ggc gta aaa ata ttc			816
Pro Arg Leu Asn Pro Lys Gly Asn Ser Val Arg Gly Val Lys Ile Phe			
260	265	270	
aaa cag ctt tcc gac gac atg ggc ctc cac ctc atg tcc acc gag			861
Lys Gln Leu Ser Asp Asp Met Gly Leu His Leu Met Ser Thr Glu			
275	280	285	

<210> 102

<211> 287

<212> PRT

<213> Corynebacterium glutamicum

<400> 102

Glu	Leu	Ala	Asp	Tyr	Ile	Pro	Glu	Leu	Lys	Ser	Ala	Asp	Pro	Asn	Pro
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Leu	Ala	Val	Ala	Leu	Cys	Thr	Val	Asn	Gly	His	Ile	Tyr	Ser	Ala	Gly
		20						25					30		

Asp	Asp	Asp	Ile	Glu	Phe	Thr	Met	Gln	Ser	Ile	Ser	Lys	Pro	Phe	Ala
		35					40					45			

Tyr Ala Leu Ala Leu Gln Glu Cys Gly Phe Asp Glu Val Ser Ala Ser
 50 55 60
 Val Ala Leu Glu Pro Ser Gly Glu Ala Phe Asn Glu Leu Ser Leu Asp
 65 70 75 80
 Gly Glu Asn Arg Pro Met Asn Pro Met Ile Asn Ala Gly Ala Ile Ala
 85 90 95
 Ile Asn Gln Leu Ile Asn Gly Ser Asp Ser Thr Val Glu Asp Arg Val
 100 105 110
 Glu Lys Ile Arg His Tyr Phe Ser Glu Leu Ala Gly Arg Glu Leu Thr
 115 120 125
 Ile Asp Arg Val Leu Ala Glu Ser Glu Leu Ala Gly Ala Asp Arg Asn
 130 135 140
 Leu Ser Ile Ala His Met Leu Arg Asn Tyr Gly Val Ile Glu Asp Glu
 145 150 155 160
 Ala His Asp Ala Val Leu Ser Tyr Thr Leu Gln Cys Ala Ile Lys Val
 165 170 175
 Thr Thr Arg Asp Leu Ala Val Met Thr Ala Thr Leu Ala Ala Gly Gly
 180 185 190
 Thr His Pro Ile Thr Gly Lys Lys Leu Leu Asp Ala Arg Val Cys Arg
 195 200 205
 Leu Thr Leu Ser Val Met Ala Ser Ala Gly Met Tyr Asp Glu Ala Gly
 210 215 220
 Gln Trp Leu Ser Thr Val Gly Ile Pro Ala Lys Ser Gly Val Ala Gly
 225 230 235 240
 Gly Leu Ile Gly Ile Leu Pro Gly Gln Leu Gly Ile Ala Thr Phe Ser
 245 250 255
 Pro Arg Leu Asn Pro Lys Gly Asn Ser Val Arg Gly Val Lys Ile Phe
 260 265 270
 Lys Gln Leu Ser Asp Asp Met Gly Leu His Leu Met Ser Thr Glu
 275 280 285

<210> 103

<211> 861

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(861)

<223> FRXA02879

<400> 103

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 Glu Leu Ala Asp Tyr Ile Pro Glu Leu Lys Ser Ala Asp Pro Asn Pro
 1 5 10 15

48

ctg gca gta gcc ctg tgc acc gtt aac gga cac atc tac agc gca ggc	96
Leu Ala Val Ala Leu Cys Thr Val Asn Gly His Ile Tyr Ser Ala Gly	
20 25 30	
gat gac gac atc gaa ttc acc atg caa agt att tcc aag cca ttt gcc	144
Asp Asp Asp Ile Glu Phe Thr Met Gln Ser Ile Ser Lys Pro Phe Ala	
35 40 45	
tac gca ctc gca ctc caa gaa tgc ggc ttt gat gag gtc tct gca tcc	192
Tyr Ala Leu Ala Leu Gln Glu Cys Gly Phe Asp Glu Val Ser Ala Ser	
50 55 60	
gtg gcc ttg gag ccc tcc ggt gag gcc ttc aac gaa ctt tcc ctc gac	240
Val Ala Leu Glu Pro Ser Gly Glu Ala Phe Asn Glu Leu Ser Leu Asp	
65 70 75 80	
ggc gaa aac cgc ccc atg aac ccc atg atc aac gcc ggc gcg atc gcc	288
Gly Glu Asn Arg Pro Met Asn Pro Met Ile Asn Ala Gly Ala Ile Ala	
85 90 95	
atc aac cag ctg atc aac ggc tcc gat tcc acc gtg gaa gac cgc gtg	336
Ile Asn Gln Leu Ile Asn Gly Ser Asp Ser Thr Val Glu Asp Arg Val	
100 105 110	
gaa aaa atc cga cac tac ttc tct gaa ctt gct gga cgc gaa ctc acc	384
Glu Lys Ile Arg His Tyr Phe Ser Glu Leu Ala Gly Arg Glu Leu Thr	
115 120 125	
atc gac cgc gtg ctt gcc gaa tcc gaa ctc gcc ggc gcc gac cgc aac	432
Ile Asp Arg Val Leu Ala Glu Ser Glu Leu Ala Gly Ala Asp Arg Asn	
130 135 140	
ctc tcc atc gcc cac atg ctg cgc aat tac ggc gtc atc gaa gac gaa	480
Leu Ser Ile Ala His Met Leu Arg Asn Tyr Gly Val Ile Glu Asp Glu	
145 150 155 160	
gcc cac gac gcc gtc ctc agc tac acg ctg caa tgc gcc atc aaa gta	528
Ala His Asp Ala Val Leu Ser Tyr Thr Leu Gln Cys Ala Ile Lys Val	
165 170 175	
acc acg cgc gac ctc gca gtc atg acc gcc acg ctc gcc gcc ggc ggc	576
Thr Thr Arg Asp Leu Ala Val Met Thr Ala Thr Leu Ala Ala Gly Gly	
180 185 190	
aca cac cca att acc ggc aag aag ctt ctc gac gcc cgc gtc tgc cgc	624
Thr His Pro Ile Thr Gly Lys Lys Leu Leu Asp Ala Arg Val Cys Arg	
195 200 205	
ctc acc ctc tcc gtc atg gct tca gca ggc atg tac gac gag gca ggg	672
Leu Thr Leu Ser Val Met Ala Ser Ala Gly Met Tyr Asp Glu Ala Gly	
210 215 220	
cag tgg ctc tcc acc gta ggc atc ccc gcg aaa tca gga gtc gcc ggc	720
Gln Trp Leu Ser Thr Val Gly Ile Pro Ala Lys Ser Gly Val Ala Gly	
225 230 235 240	
gga ctc atc ggc att ctg cca ggt cag ctg ggc atc gcc aca ttt tcc	768
Gly Leu Ile Gly Ile Leu Pro Gly Gln Leu Gly Ile Ala Thr Phe Ser	
245 250 255	

cca cgc ctg aac ccc aaa ggc aac agc gtg cgc ggc gta aaa ata ttc 816
 Pro Arg Leu Asn Pro Lys Gly Asn Ser Val Arg Gly Val Lys Ile Phe
 260 265 270

aaa cag ctt tcc gac gac atg ggc ctc cac ctc atg tcc acc gag 861
 Lys Gln Leu Ser Asp Asp Met Gly Leu His Leu Met Ser Thr Glu
 275 280 285

<210> 104

<211> 287

<212> PRT

<213> Corynebacterium glutamicum

<400> 104

Glu Leu Ala Asp Tyr Ile Pro Glu Leu Lys Ser Ala Asp Pro Asn Pro
 1 5 10 15

Leu Ala Val Ala Leu Cys Thr Val Asn Gly His Ile Tyr Ser Ala Gly
 20 25 30

Asp Asp Asp Ile Glu Phe Thr Met Gln Ser Ile Ser Lys Pro Phe Ala
 35 40 45

Tyr Ala Leu Ala Leu Gln Glu Cys Gly Phe Asp Glu Val Ser Ala Ser
 50 55 60

Val Ala Leu Glu Pro Ser Gly Glu Ala Phe Asn Glu Leu Ser Leu Asp
 65 70 75 80

Gly Glu Asn Arg Pro Met Asn Pro Met Ile Asn Ala Gly Ala Ile Ala
 85 90 95

Ile Asn Gln Leu Ile Asn Gly Ser Asp Ser Thr Val Glu Asp Arg Val
 100 105 110

Glu Lys Ile Arg His Tyr Phe Ser Glu Leu Ala Gly Arg Glu Leu Thr
 115 120 125

Ile Asp Arg Val Leu Ala Glu Ser Glu Leu Ala Gly Ala Asp Arg Asn
 130 135 140

Leu Ser Ile Ala His Met Leu Arg Asn Tyr Gly Val Ile Glu Asp Glu
 145 150 155 160

Ala His Asp Ala Val Leu Ser Tyr Thr Leu Gln Cys Ala Ile Lys Val
 165 170 175

Thr Thr Arg Asp Leu Ala Val Met Thr Ala Thr Leu Ala Ala Gly Gly
 180 185 190

Thr His Pro Ile Thr Gly Lys Lys Leu Leu Asp Ala Arg Val Cys Arg
 195 200 205

Leu Thr Leu Ser Val Met Ala Ser Ala Gly Met Tyr Asp Glu Ala Gly
 210 215 220

Gln Trp Leu Ser Thr Val Gly Ile Pro Ala Lys Ser Gly Val Ala Gly
 225 230 235 240

Gly Leu Ile Gly Ile Leu Pro Gly Gln Leu Gly Ile Ala Thr Phe Ser

				245						250						255			
Pro	Arg	Leu	Asn	Pro	Lys	Gly	Asn	Ser	Val	Arg	Gly	Val	Lys	Ile	Phe				
			260					265					270						
Lys	Gln	Leu	Ser	Asp	Asp	Met	Gly	Leu	His	Leu	Met	Ser	Thr	Glu					
		275					280					285							

<210> 105

<211> 1155

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1132)

<223> RXA00278

<400> 105

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gtgggtcggc	atccgcccc	gtttgcagga	gtacttataa	atg	cac	gct	ttt	cga	115
				Met	His	Ala	Phe	Arg	
				1				5	

cgc	ccc	cct	cca	ctc	acc	acg	cga	gtc	ggc	gct	gca	ttg	ctg	gcc	gca	163
Arg	Pro	Pro	Pro	Leu	Thr	Thr	Arg	Val	Gly	Ala	Ala	Leu	Leu	Ala	Ala	
				10					15					20		

acg	ctg	ctt	gct	tcc	tgc	act	cca	aca	cct	gtg	gaa	ccg	gca	gaa	acc	211
Thr	Leu	Leu	Ala	Ser	Cys	Thr	Pro	Thr	Pro	Val	Glu	Pro	Ala	Glu	Thr	
			25					30					35			

ttg	act	gct	ttg	gat	ccc	gat	gcc	ggc	cca	cca	ctg	cca	ccg	gat	tct	259
Leu	Thr	Ala	Leu	Asp	Pro	Asp	Ala	Gly	Pro	Pro	Leu	Pro	Pro	Asp	Ser	
			40				45					50				

tcg	att	gaa	gct	ccc	ggc	gaa	aaa	gag	ccc	att	gtg	gaa	gta	ata	gag	307
Ser	Ile	Glu	Ala	Pro	Gly	Glu	Lys	Glu	Pro	Ile	Val	Glu	Val	Ile	Glu	
	55					60					65					

aat	tgg	cca	ggc	tct	tta	cgc	ccg	gat	gat	ctg	acc	cct	gag	gag	cgg	355
Asn	Trp	Pro	Gly	Ser	Leu	Arg	Pro	Asp	Asp	Leu	Thr	Pro	Glu	Glu	Arg	
	70				75					80					85	

gta	cct	ggc	atc	gtc	aac	cgg	ggc	cgc	atc	att	gtg	ggc	gtg	gat	caa	403
Val	Pro	Gly	Ile	Val	Asn	Arg	Gly	Arg	Ile	Ile	Val	Gly	Val	Asp	Gln	
				90					95					100		

tcg	caa	aac	ttg	ctc	agt	ttc	cgt	gat	ccg	gtg	act	ggc	gag	ctg	cgc	451
Ser	Gln	Asn	Leu	Ser	Phe	Arg	Arg	Asp	Pro	Val	Thr	Gly	Glu	Leu	Arg	
		105						110					115			

ggc	ttt	gaa	gtg	gaa	tta	gcg	agg	gaa	att	tcc	cgc	gac	att	ttc	ggc	499
Gly	Phe	Glu	Val	Glu	Leu	Ala	Arg	Glu	Ile	Ser	Arg	Asp	Ile	Phe	Gly	
		120					125					130				

gac	ccc	aat	aag	gtg	gat	ttc	cga	ttc	gtc	ggc	tcg	tcc	gac	cgt	ctg	547
Asp	Pro	Asn	Lys	Val	Asp	Phe	Arg	Phe	Val	Gly	Ser	Ser	Asp	Arg	Leu	
		135				140					145					

cgt tcc ctt gac caa ggt gat gta gat att gtg att cgt tcc gtc acg 595
 Arg Ser Leu Asp Gln Gly Asp Val Asp Ile Val Ile Arg Ser Val Thr
 150 155 160 165

 atc acc gac gaa cgc gcc aaa ttg gtg gaa ttt tcc aca ccg tac ctg 643
 Ile Thr Asp Glu Arg Ala Lys Leu Val Glu Phe Ser Thr Pro Tyr Leu
 170 175 180

 cgc acc caa acc cgc atg ttg acc atg gaa tct tca gga atc acg tcc 691
 Arg Thr Gln Thr Arg Met Leu Thr Met Glu Ser Ser Gly Ile Thr Ser
 185 190 195

 atc gca gat cta ccc ggc cac acc att tgt gtc acc gat ggc tcc act 739
 Ile Ala Asp Leu Pro Gly His Thr Ile Cys Val Thr Asp Gly Ser Thr
 200 205 210

 tca ttg cag cga gcc cgc acc att gcg ccg gag gcc tca atc tta aaa 787
 Ser Leu Gln Arg Ala Arg Thr Ile Ala Pro Glu Ala Ser Ile Leu Lys
 215 220 225

 act cgc aat tgg tcc gat tgt ctc atg gcg ttg cag cag cat cag gct 835
 Thr Arg Asn Trp Ser Asp Cys Leu Met Ala Leu Gln Gln His Gln Ala
 230 235 240 245

 cag gtc att ttg ggc gat gat gtc att ttg tcc ggc atc gca gca cag 883
 Gln Val Ile Leu Gly Asp Asp Val Ile Leu Ser Gly Ile Ala Ala Gln
 250 255 260

 gat ccc tac acc gag att ctt gat acc tcc ctc gat tcc cat tcc tat 931
 Asp Pro Tyr Thr Glu Ile Leu Asp Thr Ser Leu Asp Ser His Ser Tyr
 265 270 275

 gga gtg gca gcg gca tcg acc act gct gaa aca gac tct tcg ggg ttg 979
 Gly Val Ala Ala Ala Ser Thr Thr Ala Glu Thr Asp Ser Ser Gly Leu
 280 285 290

 att cgg cag gta aac tac aca att gaa cgg atc cgc aca gac cgc atg 1027
 Ile Arg Gln Val Asn Tyr Thr Ile Glu Arg Ile Arg Thr Asp Arg Met
 295 300 305

 tgg tgg aca atg ttc gac gat tgg ttc gga cct tat ctc tgg tcc tac 1075
 Trp Trp Thr Met Phe Asp Asp Trp Phe Gly Pro Tyr Leu Trp Ser Tyr
 310 315 320 325

 ggt cca cca cag ctg cag tac atg cca gag gaa gaa ggg aca gaa aac 1123
 Gly Pro Pro Gln Leu Gln Tyr Met Pro Glu Glu Glu Gly Thr Glu Asn
 330 335 340

 gat gaa gga taatgaagat ttcatccag att 1155
 Asp Glu Gly

<210> 106

<211> 344

<212> PRT

<213> Corynebacterium glutamicum

<400> 106

Met His Ala Phe Arg Arg Pro Pro Pro Leu Thr Thr Arg Val Gly Ala

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Ala Leu Leu	Ala Ala Thr Leu Leu	Ala Ser Cys Thr	Pro Thr Pro Val
	20	25	30
Glu Pro Ala	Glu Thr Leu Thr	Ala Leu Asp Pro	Asp Ala Gly Pro Pro
	35	40	45
Leu Pro Pro	Asp Ser Ser	Ile Glu Ala Pro	Gly Glu Lys Glu Pro Ile
	50	55	60
Val Glu Val	Ile Glu Asn Trp	Pro Gly Ser Leu	Arg Pro Asp Asp Leu
	65	70	75
Thr Pro Glu	Glu Arg Val	Pro Gly Ile Val	Asn Arg Gly Arg Ile Ile
	85	90	95
Val Gly Val	Asp Gln Ser	Gln Asn Leu Leu	Ser Phe Arg Asp Pro Val
	100	105	110
Thr Gly Glu	Leu Arg Gly	Phe Glu Val Glu	Leu Ala Arg Glu Ile Ser
	115	120	125
Arg Asp Ile	Phe Gly Asp	Pro Asn Lys Val	Asp Phe Arg Phe Val Gly
	130	135	140
Ser Ser Asp	Arg Leu Arg	Ser Leu Asp	Gln Gly Asp Val Asp Ile Val
	145	150	155
Ile Arg Ser	Val Thr Ile	Thr Asp Glu Arg	Ala Lys Leu Val Glu Phe
	165	170	175
Ser Thr Pro	Tyr Leu Arg	Thr Gln Thr	Arg Met Leu Thr Met Glu Ser
	180	185	190
Ser Gly Ile	Thr Ser Ile	Ala Asp Leu Pro	Gly His Thr Ile Cys Val
	195	200	205
Thr Asp Gly	Ser Thr Ser	Leu Gln Arg	Ala Arg Thr Ile Ala Pro Glu
	210	215	220
Ala Ser Ile	Leu Lys Thr	Arg Asn Trp Ser	Asp Cys Leu Met Ala Leu
	225	230	235
Gln Gln His	Gln Ala Gln	Val Ile Leu Gly	Asp Asp Val Ile Leu Ser
	245	250	255
Gly Ile Ala	Ala Gln Asp	Pro Tyr Thr	Glu Ile Leu Asp Thr Ser Leu
	260	265	270
Asp Ser His	Ser Tyr Gly	Val Ala Ala	Ala Ser Thr Thr Ala Glu Thr
	275	280	285
Asp Ser Ser	Gly Leu Ile	Arg Gln Val	Asn Tyr Thr Ile Glu Arg Ile
	290	295	300
Arg Thr Asp	Arg Met Trp	Trp Thr Met	Phe Asp Asp Trp Phe Gly Pro
	305	310	315
Tyr Leu Trp	Ser Tyr Gly	Pro Pro Gln	Leu Gln Tyr Met Pro Glu Glu
	325	330	335

Glu Gly Thr Glu Asn Asp Glu Gly
340

<210> 107

<211> 1035

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1012)

<223> RXA00727

<400> 107

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ttcgcagaca ccgcctctga aacgggtact gcatagcact ttg cgt ttc ccc aaa 115
                                   Leu Arg Phe Pro Lys
                                   1           5

atc ccc aag cgc gct gta gcg gcg acc gtc ggc atc gtg gca acc tca 163
Ile Pro Lys Arg Ala Val Ala Ala Thr Val Gly Ile Val Ala Thr Ser
              10              15              20

ttc acc ttg gct tct tgt gtc acc aat gag gag cag ggc aac cca gat 211
Phe Thr Leu Ala Ser Cys Val Thr Asn Glu Glu Gln Gly Asn Pro Asp
              25              30              35

ggc tgg gag cag atc gtt cca gat cct gta ccg gag att cag gcg atg 259
Gly Trp Glu Gln Ile Val Pro Asp Pro Val Pro Glu Ile Gln Ala Met
              40              45              50

gtt ccc gaa gct ctg gct cag cgc ggt gtg ctc acc gcc ggt gcc aac 307
Val Pro Glu Ala Leu Ala Gln Arg Gly Val Leu Thr Ala Gly Ala Asn
              55              60              65

cca cct ttc cca ccg ttt gag ttt aaa gat tcc gat ggt cag att atc 355
Pro Pro Phe Pro Pro Phe Glu Phe Lys Asp Ser Asp Gly Gln Ile Ile
              70              75              80              85

ggg gtg gaa atg gac ctc gtg cgt gca atg gcg ggg gtg atg ggc ttg 403
Gly Val Glu Met Asp Leu Val Arg Ala Met Ala Gly Val Met Gly Leu
              90              95              100

gag ttc agc cct cag gag cag gat ttc tcc ctc atc ctt cca tcg gtt 451
Glu Phe Ser Pro Gln Glu Gln Asp Phe Ser Leu Ile Leu Pro Ser Val
              105              110              115

caa gct ggc acc ctt gat atc gga gcc tct ggc ttc act gac aac gag 499
Gln Ala Gly Thr Leu Asp Ile Gly Ala Ser Gly Phe Thr Asp Asn Glu
              120              125              130

gaa cgc cgc gag aac ttt gat ttc atc gat ttc ctc ttc gca ggt gtg 547
Glu Arg Arg Glu Asn Phe Asp Phe Ile Asp Phe Leu Phe Ala Gly Val
              135              140              145

cag tgg gcg cag gca act gat cgt gaa acc cca atc gat ccg gaa aac 595
Gln Trp Ala Gln Ala Thr Asp Arg Glu Thr Pro Ile Asp Pro Glu Asn
              150              155              160              165

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gcc tgt ggt ctc acc gtt gct gta cag cgc aca acc gtg gca gag acc 643
 Ala Cys Gly Leu Thr Val Ala Val Gln Arg Thr Thr Val Ala Glu Thr
 170 175 180

gac gat gtc cgt cct cgc tca gct caa tgt gaa gcc gaa ggc aaa gag 691
 Asp Asp Val Arg Pro Arg Ser Ala Gln Cys Glu Ala Glu Gly Lys Glu
 185 190 195

ccg atc acc att ttg tct tat gaa acc gca gat act gca gct acc gca 739
 Pro Ile Thr Ile Leu Ser Tyr Glu Thr Ala Asp Thr Ala Ala Thr Ala
 200 205 210

ttg atc ctg gga cgc gca gac gca ctt gct gcg gac tcc cct gtt tca 787
 Leu Ile Leu Gly Arg Ala Asp Ala Leu Ala Ala Asp Ser Pro Val Ser
 215 220 225

gct tgg gct gca gag cgc tcc gaa ggc cgc atc gaa gtt gtg ggc gat 835
 Ala Trp Ala Ala Glu Arg Ser Glu Gly Arg Ile Glu Val Val Gly Asp
 230 235 240 245

atg tac ttg gct gcg cca ttt ggt ttc gca ttc ccg ttg gaa tct gac 883
 Met Tyr Leu Ala Ala Pro Phe Gly Phe Ala Phe Pro Leu Glu Ser Asp
 250 255 260

ctc acc cca gca gca gct gcg gcg ttc caa cac ttg att gac acc ggc 931
 Leu Thr Pro Ala Ala Ala Ala Phe Gln His Leu Ile Asp Thr Gly
 265 270 275

gat tac cag cgc atc atg gcg caa tgg ggc att gaa gaa ggc ctt ctt 979
 Asp Tyr Gln Arg Ile Met Ala Gln Trp Gly Ile Glu Glu Gly Leu Leu
 280 285 290

gat gag gcc ctg atc aac gaa cag cca ctc aac tagagccttc cagcaactaa 1032
 Asp Glu Ala Leu Ile Asn Glu Gln Pro Leu Asn
 295 300

aaa 1035

<210> 108

<211> 304

<212> PRT

<213> Corynebacterium glutamicum

<400> 108

Leu Arg Phe Pro Lys Ile Pro Lys Arg Ala Val Ala Ala Thr Val Gly
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Ile Val Ala Thr Ser Phe Thr Leu Ala Ser Cys Val Thr Asn Glu Glu
 20 25 30

Gln Gly Asn Pro Asp Gly Trp Glu Gln Ile Val Pro Asp Pro Val Pro
 35 40 45

Glu Ile Gln Ala Met Val Pro Glu Ala Leu Ala Gln Arg Gly Val Leu
 50 55 60

Thr Ala Gly Ala Asn Pro Pro Phe Pro Pro Phe Glu Phe Lys Asp Ser
 65 70 75 80


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<210> 109
<211> 1962
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101) .. (1939)
<223> RXA02139
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<400> 109
tcaggaggat ttttcaatca tgtgcggcct tcttggcata ttgactgcaa atgggaacgc 60
tgaagcattc gttcctgcac tcgagcgggc cttgccatgc atg cgc cac cgt ggt 115
Met Arg His Arg Gly

	1	5	
cct gac gat gcc ggc act tgg cat gac gcc gat gca gcg ttt gga ttc			163
Pro Asp Asp Ala Gly Thr Trp His Asp Ala Asp Ala Ala Phe Gly Phe			
	10	15	20
aac cgc ctc tcc atc att gat att gca cac tcc cac caa cca ctg cgt			211
Asn Arg Leu Ser Ile Ile Asp Ile Ala His Ser His Gln Pro Leu Arg			
	25	30	35
tgg gga cct gcg gat gaa ccc gac cgc tac gca atg act ttc aac ggt			259
Trp Gly Pro Ala Asp Glu Pro Asp Arg Tyr Ala Met Thr Phe Asn Gly			
	40	45	50
gag atc tac aac tac gtt gag ctg cgt aaa gag ctc tcg gat ttg gga			307
Glu Ile Tyr Asn Tyr Val Glu Leu Arg Lys Glu Leu Ser Asp Leu Gly			
	55	60	65
tat gcc ttt aat act tct ggc gat ggc gag cca att gtt gtc ggt ttc			355
Tyr Ala Phe Asn Thr Ser Gly Asp Gly Glu Pro Ile Val Val Gly Phe			
	70	75	80
cac cac tgg ggc gag tcc gtg gtc gag cat ctc cgc gga atg ttc ggc			403
His His Trp Gly Glu Ser Val Val Glu His Leu Arg Gly Met Phe Gly			
	90	95	100
att gcc att tgg gat aca aag gaa aag tcg ctt ttc ctt gcg cgt gat			451
Ile Ala Ile Trp Asp Thr Lys Glu Lys Ser Leu Phe Leu Ala Arg Asp			
	105	110	115
cag ttc ggc att aag cca ctg ttc tac gca acc acc gag cat ggc acc			499
Gln Phe Gly Ile Lys Pro Leu Phe Tyr Ala Thr Thr Glu His Gly Thr			
	120	125	130
gtg ttc tcc tca gag aag aag acc atc ttg gag atg gcc gag gag atg			547
Val Phe Ser Ser Glu Lys Lys Thr Ile Leu Glu Met Ala Glu Glu Met			
	135	140	145
aat cta gat ctg ggc ctt gat aag cgc acc att gag cac tac gtg gac			595
Asn Leu Asp Leu Gly Leu Asp Lys Arg Thr Ile Glu His Tyr Val Asp			
	150	155	160
ttg cag tac gtg ccc gag cca gat acc ctt cac gcg cag att tcc cgc			643
Leu Gln Tyr Val Pro Glu Pro Asp Thr Leu His Ala Gln Ile Ser Arg			
	170	175	180
ttg gag tca ggc tgc acc gca aca gtt cgt ccg ggc ggc aag ctg gaa			691
Leu Glu Ser Gly Cys Thr Ala Thr Val Arg Pro Gly Gly Lys Leu Glu			
	185	190	195
cag aag cgt tac ttc aag cct cag ttc cca gta cag aag gtc gta aag			739
Gln Lys Arg Tyr Phe Lys Pro Gln Phe Pro Val Gln Lys Val Val Lys			
	200	205	210
ggt aag gag cag gac ctc ttc gat cgc att gcc cag gtg ttg gag gat			787
Gly Lys Glu Gln Asp Leu Phe Asp Arg Ile Ala Gln Val Leu Glu Asp			
	215	220	225
agc gtc gaa aag cat atg cgt gcc gac gtg acc gta ggc tcg ttc ctt			835
Ser Val Glu Lys His Met Arg Ala Asp Val Thr Val Gly Ser Phe Leu			
	230	235	240
			245

ttc ggc ggc att gac tca acc gca att gcg gcg ctt gca aag cgc cac	883
Phe Gly Gly Ile Asp Ser Thr Ala Ile Ala Ala Leu Ala Lys Arg His	
250 255 260	
aac cct gac ctg ctc acc ttc acc acc ggt ttc gag cgt gaa ggc tac	931
Asn Pro Asp Leu Leu Thr Phe Thr Thr Gly Phe Glu Arg Glu Gly Tyr	
265 270 275	
tcg gag gtc gat gtg gct gcg gag tcc gcc gct gcg att ggc gct gag	979
Ser Glu Val Asp Val Ala Ala Glu Ser Ala Ala Ala Ile Gly Ala Glu	
280 285 290	
cac atc gtg aag att gtc tcg cct gag gaa tac gcc aac gcg att cct	1027
His Ile Val Lys Ile Val Ser Pro Glu Glu Tyr Ala Asn Ala Ile Pro	
295 300 305	
aag atc atg tgg tac ttg gat gat cct gta gct gac cca tca ttg gtc	1075
Lys Ile Met Trp Tyr Leu Asp Asp Pro Val Ala Asp Pro Ser Leu Val	
310 315 320 325	
ccg ctg tac ttc gtg gca gcg gaa gca cgt aag cac gtc aag gtt gtg	1123
Pro Leu Tyr Phe Val Ala Ala Glu Ala Arg Lys His Val Lys Val Val	
330 335 340	
ctg tct ggc gag ggc gca gat gag ctg ttc ggt gga tac acc att tac	1171
Leu Ser Gly Glu Gly Ala Asp Glu Leu Phe Gly Gly Tyr Thr Ile Tyr	
345 350 355	
aag gag ccg cta tcg ctt gct cca ttt gag aag atc cct tcc cca cta	1219
Lys Glu Pro Leu Ser Leu Ala Pro Phe Glu Lys Ile Pro Ser Pro Leu	
360 365 370	
cgt aaa ggc ctg gga aag ctc agc aag gtt ctg cca gac ggc atg aag	1267
Arg Lys Gly Leu Gly Lys Leu Ser Lys Val Leu Pro Asp Gly Met Lys	
375 380 385	
ggc aag tcc ctt ctt gag cgt ggc tcc atg acc atg gaa gag cgc tac	1315
Gly Lys Ser Leu Leu Glu Arg Gly Ser Met Thr Met Glu Glu Arg Tyr	
390 395 400 405	
tac ggc aac gct cgc tcc ttc aat ttc gag cag atg caa cgc gtt att	1363
Tyr Gly Asn Ala Arg Ser Phe Asn Phe Glu Gln Met Gln Arg Val Ile	
410 415 420	
cca tgg gca aag cgc gaa tgg gac cac gcg gaa gtc act gcg ccg atc	1411
Pro Trp Ala Lys Arg Glu Trp Asp His Arg Glu Val Thr Ala Pro Ile	
425 430 435	
tac gca cag tcc cgc aac ttt gat cca gta gcc cgc atg caa cac ctg	1459
Tyr Ala Gln Ser Arg Asn Phe Asp Pro Val Ala Arg Met Gln His Leu	
440 445 450	
gat ctg ttc acc tgg atg cgc ggc gac atc ctg gtc aag gct gac aag	1507
Asp Leu Phe Thr Trp Met Arg Gly Asp Ile Leu Val Lys Ala Asp Lys	
455 460 465	
atc aac atg gcg aac tcc ctt gag ctg cga gtt cca ttc ttg gat aag	1555
Ile Asn Met Ala Asn Ser Leu Glu Leu Arg Val Pro Phe Leu Asp Lys	
470 475 480 485	

gaa gtt ttc aag gtt gca gag acc att cct tac gac ctg aag att gcc 1603
 Glu Val Phe Lys Val Ala Glu Thr Ile Pro Tyr Asp Leu Lys Ile Ala
 490 495 500

aac ggt acc acc aag tac gcg ctg cgc agg gca ctc gag cag att gtt 1651
 Asn Gly Thr Thr Lys Tyr Ala Leu Arg Arg Ala Leu Glu Gln Ile Val
 505 510 515

ccg cct cac gtt ttg cac cgc aag aag ctg ggc ttc cct gtt ccc atg 1699
 Pro Pro His Val Leu His Arg Lys Lys Leu Gly Phe Pro Val Pro Met
 520 525 530

cgc cac tgg ctt gcc ggc gat gag ctg ttc ggt tgg gcg cag gac acc 1747
 Arg His Trp Leu Ala Gly Asp Glu Leu Phe Gly Trp Ala Gln Asp Thr
 535 540 545

atc aag gaa tcc ggt act gaa gat atc ttc aac aag cag gct gtg ctg 1795
 Ile Lys Glu Ser Gly Thr Glu Asp Ile Phe Asn Lys Gln Ala Val Leu
 550 555 560 565

gat atg ctg aac gag cac cgc gat ggc gtg tca gat cat tcc cgt cga 1843
 Asp Met Leu Asn Glu His Arg Asp Gly Val Ser Asp His Ser Arg Arg
 570 575 580

ctg tgg act gtt ctg tca ttt atg gtg tgg cac ggc att ttt gtg gaa 1891
 Leu Trp Thr Val Leu Ser Phe Met Val Trp His Gly Ile Phe Val Glu
 585 590 595

aac cgc att gat cca cag att gag gac cgc tcc tac cca gtc gag ctt 1939
 Asn Arg Ile Asp Pro Gln Ile Glu Asp Arg Ser Tyr Pro Val Glu Leu
 600 605 610

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<210> 110

<211> 613

<212> PRT

<213> Corynebacterium glutamicum

<400> 110

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 20 25 30

His Gln Pro Leu Arg Trp Gly Pro Ala Asp Glu Pro Asp Arg Tyr Ala
 35 40 45

Met Thr Phe Asn Gly Glu Ile Tyr Asn Tyr Val Glu Leu Arg Lys Glu
 50 55 60

Leu Ser Asp Leu Gly Tyr Ala Phe Asn Thr Ser Gly Asp Gly Glu Pro
 65 70 75 80

Ile Val Val Gly Phe His His Trp Gly Glu Ser Val Val Glu His Leu
 85 90 95

Arg Gly Met Phe Gly Ile Ala Ile Trp Asp Thr Lys Glu Lys Ser Leu
 100 105 110

Phe	Leu	Ala	Arg	Asp	Gln	Phe	Gly	Ile	Lys	Pro	Leu	Phe	Tyr	Ala	Thr		
	115						120					125					
Thr	Glu	His	Gly	Thr	Val	Phe	Ser	Ser	Glu	Lys	Lys	Thr	Ile	Leu	Glu		
	130					135					140						
Met	Ala	Glu	Glu	Met	Asn	Leu	Asp	Leu	Gly	Leu	Asp	Lys	Arg	Thr	Ile		
145					150					155					160		
Glu	His	Tyr	Val	Asp	Leu	Gln	Tyr	Val	Pro	Glu	Pro	Asp	Thr	Leu	His		
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Ala	Gln	Ile	Ser	Arg	Leu	Glu	Ser	Gly	Cys	Thr	Ala	Thr	Val	Arg	Pro		
			180					185					190				
Gly	Gly	Lys	Leu	Glu	Gln	Lys	Arg	Tyr	Phe	Lys	Pro	Gln	Phe	Pro	Val		
	195						200					205					
Gln	Lys	Val	Val	Lys	Gly	Lys	Glu	Gln	Asp	Leu	Phe	Asp	Arg	Ile	Ala		
	210					215					220						
Gln	Val	Leu	Glu	Asp	Ser	Val	Glu	Lys	His	Met	Arg	Ala	Asp	Val	Thr		
225					230					235				240			
Val	Gly	Ser	Phe	Leu	Phe	Gly	Gly	Ile	Asp	Ser	Thr	Ala	Ile	Ala	Ala		
			245					250						255			
Leu	Ala	Lys	Arg	His	Asn	Pro	Asp	Leu	Leu	Thr	Phe	Thr	Thr	Gly	Phe		
			260					265					270				
Glu	Arg	Glu	Gly	Tyr	Ser	Glu	Val	Asp	Val	Ala	Ala	Glu	Ser	Ala	Ala		
	275						280					285					
Ala	Ile	Gly	Ala	Glu	His	Ile	Val	Lys	Ile	Val	Ser	Pro	Glu	Glu	Tyr		
	290					295					300						
Ala	Asn	Ala	Ile	Pro	Lys	Ile	Met	Trp	Tyr	Leu	Asp	Asp	Pro	Val	Ala		
305					310					315				320			
Asp	Pro	Ser	Leu	Val	Pro	Leu	Tyr	Phe	Val	Ala	Ala	Glu	Ala	Arg	Lys		
			325					330						335			
His	Val	Lys	Val	Val	Leu	Ser	Gly	Glu	Gly	Ala	Asp	Glu	Leu	Phe	Gly		
		340						345					350				
Gly	Tyr	Thr	Ile	Tyr	Lys	Glu	Pro	Leu	Ser	Leu	Ala	Pro	Phe	Glu	Lys		
	355						360					365					
Ile	Pro	Ser	Pro	Leu	Arg	Lys	Gly	Leu	Gly	Lys	Leu	Ser	Lys	Val	Leu		
	370					375					380						
Pro	Asp	Gly	Met	Lys	Gly	Lys	Ser	Leu	Leu	Glu	Arg	Gly	Ser	Met	Thr		
385					390					395				400			
Met	Glu	Glu	Arg	Tyr	Tyr	Gly	Asn	Ala	Arg	Ser	Phe	Asn	Phe	Glu	Gln		
			405					410						415			
Met	Gln	Arg	Val	Ile	Pro	Trp	Ala	Lys	Arg	Glu	Trp	Asp	His	Arg	Glu		
		420						425					430				

Val Thr Ala Pro Ile Tyr Ala Gln Ser Arg Asn Phe Asp Pro Val Ala
 435 440 445

Arg Met Gln His Leu Asp Leu Phe Thr Trp Met Arg Gly Asp Ile Leu
 450 455 460

Val Lys Ala Asp Lys Ile Asn Met Ala Asn Ser Leu Glu Leu Arg Val
 465 470 475 480

Pro Phe Leu Asp Lys Glu Val Phe Lys Val Ala Glu Thr Ile Pro Tyr
 485 490 495

Asp Leu Lys Ile Ala Asn Gly Thr Thr Lys Tyr Ala Leu Arg Arg Ala
 500 505 510

Leu Glu Gln Ile Val Pro Pro His Val Leu His Arg Lys Lys Leu Gly
 515 520 525

Phe Pro Val Pro Met Arg His Trp Leu Ala Gly Asp Glu Leu Phe Gly
 530 535 540

Trp Ala Gln Asp Thr Ile Lys Glu Ser Gly Thr Glu Asp Ile Phe Asn
 545 550 555 560

Lys Gln Ala Val Leu Asp Met Leu Asn Glu His Arg Asp Gly Val Ser
 565 570 575

Asp His Ser Arg Arg Leu Trp Thr Val Leu Ser Phe Met Val Trp His
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Gly Ile Phe Val Glu Asn Arg Ile Asp Pro Gln Ile Glu Asp Arg Ser
 595 600 605

Tyr Pro Val Glu Leu
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<210> 111
 <211> 1284
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1261)
 <223> RXN00116

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 Met Ser Asn Asp Phe
 1 5

gtc gtt tct agg ctt aga ccc ttt ggt gaa acg att ttt gca acc atg 163
 Val Val Ser Arg Leu Arg Pro Phe Gly Glu Thr Ile Phe Ala Thr Met
 10 15 20

acc cag cga gct gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt 211
 Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe
 25 30 35

cct gat gag gat ggt cct cgt cgg atg tta gag atc gcg tcg gag cag	259
Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln	
40 45 50	
att ctc ggg gga aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg	307
Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser	
55 60 65	
ttg agg gca gct gtg gct cgt gat cat ttg gag agg ttt gat ctg gag	355
Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu	
70 75 80 85	
tac aac cct gat tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg	403
Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala	
90 95 100	
att acg gcg act gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc	451
Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile	
105 110 115	
gtt ttg gaa ccg tat tac gat gcg tat gcg gcg gct att gcg ttg gcg	499
Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu Ala	
120 125 130	
ggg gcg acg ccg gtg gcg gtt cct ttg cag gag gtg gag aac tcg tgg	547
Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser Trp	
135 140 145	
gat gtg gat gtc gat aag ttg cat gcg gcg gtg act aag aag acg ccg	595
Asp Val Asp Val Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr Arg	
150 155 160 165	
atg att atc gtt aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct	643
Met Ile Ile Val Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser	
170 175 180	
aag aag gcg ttg aag cag ttg gcg ggt gtt gct cgt gcg tat gac ttg	691
Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala Arg Ala Tyr Asp Leu	
185 190 195	
ttg gtg ttg tca gat gag gtg tat gag cat ctt gtt ttt gat gat cag	739
Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu Val Phe Asp Asp Gln	
200 205 210	
aag cat gtg agt gtc gcg aag ctg ccc ggt atg tgg gat cgc acg gtg	787
Lys His Val Ser Val Ala Lys Leu Pro Gly Met Trp Asp Arg Thr Val	
215 220 225	
acg gtg tcg tcg gcg gcg aaa acg ttc aat gtg act ggt tgg aag acg	835
Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val Thr Gly Trp Lys Thr	
230 235 240 245	
ggg tgg gcg ttg gca ccg gag ccg ttg ttg gag gcg gtg ttg aag gcg	883
Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu Ala Val Leu Lys Ala	
250 255 260	
aag cag ttt atg tct tat gtg ggg gct aca cct ttt cag ccg gct gtg	931
Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro Phe Gln Pro Ala Val	
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$\langle 210 \rangle$ 112

<211> 387

<212> PRT

<213> Corynebacterium glutamicum

 $\langle 400 \rangle$ 112

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20 25 30

Leu Gly Gln Gly Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu
35 40 45

Ile Ala Ser Glu Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly
50 55 60

Arg Gly Asp Ala Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu
65 70 75 80

Arg Phe Asp Leu Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val
85 90 95

Gly Ala Thr Glu Ala Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro
100 105 110

Gly Asp Glu Val Ile Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala
115 120 125

Ala Ile Ala Leu Ala Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu
 130 135 140
 Val Glu Asn Ser Trp Asp Val Asp Val Asp Lys Leu His Ala Ala Val
 145 150 155 160
 Thr Lys Lys Thr Arg Met Ile Ile Val Asn Ser Pro His Asn Pro Thr
 165 170 175
 Gly Ser Val Phe Ser Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala
 180 185 190
 Arg Ala Tyr Asp Leu Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu
 195 200 205
 Val Phe Asp Asp Gln Lys His Val Ser Val Ala Lys Leu Pro Gly Met
 210 215 220
 Trp Asp Arg Thr Val Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val
 225 230 235 240
 Thr Gly Trp Lys Thr Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu
 245 250 255
 Ala Val Leu Lys Ala Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro
 260 265 270
 Phe Gln Pro Ala Val Ala His Ala Ile Glu His Glu Gln Lys Trp Val
 275 280 285
 Ser Lys Met Ser Lys Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr
 290 295 300
 Ala Leu Asp Lys Ala Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr
 305 310 315 320
 Phe Ile Val Ala Asp Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe
 325 330 335
 Glu Leu Ile Glu Lys Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe
 340 345 350
 Val Asp His Pro Lys Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys
 355 360 365
 Lys Lys Glu Glu Thr Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile
 370 375 380
 Lys Lys Leu
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<210> 113

<211> 607

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(607)

<223> FRXA00116

<400> 113

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                                         Met Thr Gln Arg Ala
                                         1           5

gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt cct gat gag gat 163
Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe Pro Asp Glu Asp
                        10                15                20

ggg cct cgt cgg atg tta gag atc gcg tcg gag cag att ctc ggg gga 211
Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln Ile Leu Gly Gly
                        25                30                35

aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg ttg agg gca gct 259
Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser Leu Arg Ala Ala
                        40                45                50

gtg gct cgt gat cat ttg gag agg ttt gat ctg gag tac aac cct gat 307
Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu Tyr Asn Pro Asp
                        55                60                65

tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg att acg gcg act 355
Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala Ile Thr Ala Thr
                        70                75                80                85

gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc gtt ttg gaa ccg 403
Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile Val Leu Glu Pro
                        90                95                100

tat tac gat gcg tat gcg gcg gct att gcg ttg gcg ggg gcg acg cgg 451
Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu Ala Gly Ala Thr Arg
                        105                110                115

gtg gcg gtt cct ttg cag gag gtg gag aac tcg tgg gat gtg gat gtc 499
Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser Trp Asp Val Asp Val
                        120                125                130

gat aag ttg cat gcg gcg gtg act aag aag acg cgg atg att atc gtt 547
Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr Arg Met Ile Ile Val
                        135                140                145

aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct aag aag gcg ttg 595
Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser Lys Lys Ala Leu
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aag cag ttg gcg
Lys Gln Leu Ala
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<210> 114

<211> 169

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 114

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Gln	Ile	Leu 35	Gly	Gly	Asn	Asn	Gln 40	Tyr	Ser	Ala	Gly	Arg 45	Gly	Asp	Ala
Ser	Leu 50	Arg	Ala	Ala	Val	Ala 55	Arg	Asp	His	Leu	Glu 60	Arg	Phe	Asp	Leu
Glu 65	Tyr	Asn	Pro	Asp	Ser 70	Glu	Val	Leu	Ile	Thr 75	Val	Gly	Ala	Thr	Glu 80
Ala	Ile	Thr	Ala	Thr 85	Val	Leu	Gly	Leu	Val 90	Glu	Pro	Gly	Asp	Glu 95	Val
Ile	Val	Leu 100	Glu	Pro	Tyr	Tyr	Asp 105	Ala	Tyr	Ala	Ala	Ala 110	Ile	Ala	Leu
Ala	Gly 115	Ala	Thr	Arg	Val	Ala 120	Val	Pro	Leu	Gln	Glu	Val 125	Glu	Asn	Ser
Trp 130	Asp	Val	Asp	Val	Asp 135	Lys	Leu	His	Ala	Ala	Val 140	Thr	Lys	Lys	Thr
Arg 145	Met	Ile	Ile	Val	Asn 150	Ser	Pro	His	Asn	Pro 155	Thr	Gly	Ser	Val	Phe 160
Ser	Lys	Lys	Ala	Leu 165	Lys	Gln	Leu	Ala							

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<212> DNA
<213> Corynebacterium glutamicum
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<223> RXN00618
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Asp	Arg	Glu	Phe	Arg	Glu	Arg	Ile	Ala	Asp	Trp	His	Ser	Ala	Thr	Tyr	
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gac	gta	gac	acc	aac	cct	gac	aat	gtt	att	gtc	acc	acc	ggg	tct	tca	355
Asp	Val	Asp	Thr	Asn	Pro	Asp	Asn	Val	Ile	Val	Thr	Thr	Gly	Ser	Ser	
	70				75					80					85	
ggg	gga	ttc	gtg	gca	tcg	ttt	atc	gcc	acc	ttg	gat	cac	ggg	gat	tat	403
Gly	Gly	Phe	Val	Ala	Ser	Phe	Ile	Ala	Thr	Leu	Asp	His	Gly	Asp	Tyr	
				90					95					100		
gtg	gca	atg	cct	acc	ccg	ggg	tac	ccg	gca	tat	cgc	aat	att	ctg	gaa	451
Val	Ala	Met	Pro	Thr	Pro	Gly	Tyr	Pro	Ala	Tyr	Arg	Asn	Ile	Leu	Glu	
			105					110					115			
tct	ttg	ggg	gcg	aag	gtt	ctg	aac	ctg	cgc	tgt	act	gca	gag	act	cgt	499
Ser	Leu	Gly	Ala	Lys	Val	Leu	Asn	Leu	Arg	Cys	Thr	Ala	Glu	Thr	Arg	
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ttc	cag	cca	acc	gct	caa	atg	ttg	gag	gaa	ctg	cca	cac	aag	ccg	aag	547
Phe	Gln	Pro	Thr	Ala	Gln	Met	Leu	Glu	Glu	Leu	Pro	His	Lys	Pro	Lys	
	135					140					145					
gct	gtt	att	gtc	acc	agc	cca	gga	aac	cca	acg	ggc	acc	atc	att	gat	595
Ala	Val	Ile	Val	Thr	Ser	Pro	Gly	Asn	Pro	Thr	Gly	Thr	Ile	Ile	Asp	
	150				155					160					165	
ccg	gaa	gag	cta	gag	cgc	atc	gcc	aag	tgg	tgc	gat	gac	aat	gat	gct	643
Pro	Glu	Glu	Leu	Glu	Arg	Ile	Ala	Lys	Trp	Cys	Asp	Asp	Asn	Asp	Ala	
				170					175					180		
gtt	ctt	atc	tct	gat	gag	gac	tac	cac	ggc	atg	agc	ttt	ggg	cgt	ccg	691
Val	Leu	Ile	Ser	Asp	Glu	Asp	Tyr	His	Gly	Met	Ser	Phe	Gly	Arg	Pro	
			185					190					195			
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Leu	Ala	Thr	Ala	His	Gln	Phe	Ser	Lys	Asn	Ala	Ile	Val	Val	Gly	Thr	
		200					205					210				
ttg	tcc	aag	tac	ttc	tcc	atg	acg	ggg	tgg	cgc	gtg	ggg	tgg	atc	atc	787
Leu	Ser	Lys	Tyr	Phe	Ser	Met	Thr	Gly	Trp	Arg	Val	Gly	Trp	Ile	Ile	
	215					220					225					
gtt	cca	gat	gag	ctg	gtc	aca	ccg	att	gaa	aac	ctg	cag	gct	tct	ctt	835
Val	Pro	Asp	Glu	Leu	Val	Thr	Pro	Ile	Glu	Asn	Leu	Gln	Ala	Ser	Leu	
	230				235					240					245	
tcc	ttg	tgt	gct	cct	gcc	atc	ggg	cag	gct	gcg	gga	cgc	gca	gcc	ttc	883
Ser	Leu	Cys	Ala	Pro	Ala	Ile	Gly	Gln	Ala	Ala	Gly	Arg	Ala	Ala	Phe	
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act	ttg	gag	gct	ggg	gcc	gaa	ctt	gat	gcc	cac	gtt	gaa	gcg	tat	cgc	931
Thr	Leu	Glu	Ala	Gly	Ala	Glu	Leu	Asp	Ala	His	Val	Glu	Ala	Tyr	Arg	
			265					270					275			
gag	gcc	cgg	gag	gtg	ttc	gtc	gat	aag	ctc	cct	gaa	atc	ggg	ctt	ggc	979
Glu	Ala	Arg	Glu	Val	Phe	Val	Asp	Lys	Leu	Pro	Glu	Ile	Gly	Leu	Gly	
		280					285					290				
act	ttc	gcc	gac	ccg	gat	ggc	ggc	ctg	tat	ttg	tgg	gtc	gat	gtt	tct	1027

Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val Ser
 295 300 305
 gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat gaa 1075
 Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp Glu
 310 315 320 325
 gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa ggc 1123
 Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu Gly
 330 335 340
 cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc att 1171
 His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr Ile
 345 350 355
 gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac 1217
 Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys
 360 365
 taggttagtt tcg 1230

<210> 116
 <211> 369
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 116
 Met Gln Met Leu Asp Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp
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 Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala
 20 25 30
 Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr
 35 40 45
 Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp
 50 55 60
 His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val
 65 70 75 80
 Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr Leu
 85 90 95
 Asp His Gly Asp Tyr Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr
 100 105 110
 Arg Asn Ile Leu Glu Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys
 115 120 125
 Thr Ala Glu Thr Arg Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu
 130 135 140
 Pro His Lys Pro Lys Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr
 145 150 155 160
 Gly Thr Ile Ile Asp Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys
 165 170 175

Asp Asp Asn Asp Ala Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met
 180 185 190
 Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala
 195 200 205
 Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg
 210 215 220
 Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn
 225 230 235 240
 Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala
 245 250 255
 Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His
 260 265 270
 Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro
 275 280 285
 Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu
 290 295 300
 Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu
 305 310 315 320
 Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe
 325 330 335
 Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser
 340 345 350
 Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys
 355 360 365
 Lys

<210> 117

<211> 657

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(634)

<223> FRXA00618

<400> 117

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caatgatgct gttcttatct ctgatgagga ctaccacggc atg agc ttt ggt cgt 115
 Met Ser Phe Gly Arg
 1 5

ccg ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt 163
 Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly
 10 15 20

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acc ttg tcc aag tac ttc tcc atg acg ggt tgg cgc gtg ggt tgg atc 211
Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile
      25                      30                      35

atc gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct 259
Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser
      40                      45                      50

ctt tcc ttg tgt gct cct gcc atc ggg cag gct gcg gga cgc gca gcc 307
Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala
      55                      60                      65

ttc act ttg gag gct ggg gcc gaa ctt gat gcc cac gtt gaa gcg tat 355
Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr
      70                      75                      80                      85

cgc gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt 403
Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu
      90                      95                      100

ggc act ttc gcc gac ccg gat ggc ggc ctg tat ttg tgg gtc gat gtt 451
Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val
      105                      110                      115

tct gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat 499
Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp
      120                      125                      130

gaa gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa 547
Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu
      135                      140                      145

ggc cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc 595
Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr
      150                      155                      160                      165

att gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac 644
Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys
      170                      175

taggttagtt tcg 657

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<210> 118

<211> 178

<212> PRT

<213> Corynebacterium glutamicum

<400> 118

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Met Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn
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Ala Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp
      20                      25                      30

Arg Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu
      35                      40                      45

Asn Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala
      50                      55                      60

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Ala Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala
 65 70 75 80

His Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu
 85 90 95

Pro Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr
 100 105 110

Leu Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala
 115 120 125

Leu Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp
 130 135 140

Phe Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala
 145 150 155 160

Ser Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile
 165 170 175

Lys Lys

<210> 119
 <211> 385
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(385)
 <223> FRXA00627

<400> 119
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 gaagccaagc actagaagca atgttcagcc gtttcgcgtc atg cag atg ttg gac 115
 Met Gln Met Leu Asp
 1 5

cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163
 Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys
 10 15 20

gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211
 Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala
 25 30 35

gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259
 Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly
 40 45 50

gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307
 Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr
 55 60 65

gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355
 Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser
 70 75 80 85

ggt gga ttc gtg gca tcg ttt atc gcc acc 385
Gly Gly Phe Val Ala Ser Phe Ile Ala Thr
90 95

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<210> 120
<211> 95
<212> PRT
<213> Corynebacterium glutamicum
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<400> 120															
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1				5					10					15	
Thr	Leu	Met	Phe	Cys	Ala	Gly	Gln	Pro	Ser	Thr	Gly	Ala	Pro	Glu	Ala
			20					25					30		
Val	Ile	Glu	Glu	Ala	Glu	Ile	Ala	Leu	Arg	Ser	Gly	Pro	Leu	Gly	Tyr
		35					40					45			
Thr	Glu	Val	Ile	Gly	Asp	Arg	Glu	Phe	Arg	Glu	Arg	Ile	Ala	Asp	Trp
	50					55					60				
His	Ser	Ala	Thr	Tyr	Asp	Val	Asp	Thr	Asn	Pro	Asp	Asn	Val	Ile	Val
65					70					75					80
Thr	Thr	Gly	Ser	Ser	Gly	Gly	Phe	Val	Ala	Ser	Phe	Ile	Ala	Thr	
				85					90					95	

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<210> 121
<211> 1434
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1411)
<223> RXA02550
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<400> 121
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tagctttcaa ctacgcacac aaagtggcaa cattgagcgg  gtg  act  aca  gac  aag  115
                                         Val Thr Thr Asp Lys
                                           1                               5

cgc  aaa  acc  tct  aag  acc  acc  gac  acc  gcc  aac  aag  gct  gtg  ggc  gcg  163
Arg  Lys  Thr  Ser  Lys  Thr  Thr  Asp  Thr  Ala  Asn  Lys  Ala  Val  Gly  Ala
                        10                        15                        20

gat  cag  gca  gcg  cgt  ccc  act  cgg  cga  aca  act  cgc  cgc  atc  ttc  gat  211
Asp  Gln  Ala  Ala  Arg  Pro  Thr  Arg  Arg  Thr  Thr  Arg  Arg  Ile  Phe  Asp
                        25                        30                        35

cag  tcg  gag  aag  atg  aag  gac  gtg  ctg  tac  gag  atc  cgt  ggc  ccg  gtg  259
Gln  Ser  Glu  Lys  Met  Lys  Asp  Val  Leu  Tyr  Glu  Ile  Arg  Gly  Pro  Val
                        40                        45                        50

gcc  gcg  gag  gcg  gaa  cgc  atg  gag  ctt  gat  ggg  cat  aac  atc  tta  aag  307

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Ala	Ala	Glu	Ala	Glu	Arg	Met	Glu	Leu	Asp	Gly	His	Asn	Ile	Leu	Lys		
55						60					65						
ctc	aac	acg	gga	aat	cca	gcc	gtg	ttc	gga	ttc	gat	gcc	ccc	gac	gtg	355	
Leu	Asn	Thr	Gly	Asn	Pro	Ala	Val	Phe	Gly	Phe	Asp	Ala	Pro	Asp	Val		
70					75				80						85		
att	atg	cgt	gac	atg	atc	gcc	aac	ctt	cca	act	tcc	caa	ggg	tat	tcc	403	
Ile	Met	Arg	Asp	Met	Ile	Ala	Asn	Leu	Pro	Thr	Ser	Gln	Gly	Tyr	Ser		
				90				95						100			
acc	tcc	aaa	ggc	att	att	ccg	gcc	cgg	cga	gca	gtg	gtc	acc	cgc	tac	451	
Thr	Ser	Lys	Gly	Ile	Ile	Pro	Ala	Arg	Arg	Ala	Val	Val	Thr	Arg	Tyr		
			105				110						115				
gaa	gtt	gtg	ccc	gga	ttc	ccc	cac	ttc	gat	gtt	gat	gat	gtg	ttc	tta	499	
Glu	Val	Val	Pro	Gly	Phe	Pro	His	Phe	Asp	Val	Asp	Asp	Val	Phe	Leu		
			120				125					130					
ggc	aac	ggt	gtc	tca	gaa	cta	atc	acc	atg	acc	acc	caa	gca	ctc	ctc	547	
Gly	Asn	Gly	Val	Ser	Glu	Leu	Ile	Thr	Met	Thr	Thr	Gln	Ala	Leu	Leu		
			135				140					145					
aac	gac	ggc	gat	gaa	gtt	ctt	atc	ccc	gca	ccg	gac	tac	cca	ctg	tgg	595	
Asn	Asp	Gly	Asp	Glu	Val	Leu	Ile	Pro	Ala	Pro	Asp	Tyr	Pro	Leu	Trp		
150					155				160						165		
act	gcc	gca	acc	tcc	ctg	gct	ggt	ggt	aag	cct	gtg	cac	tac	ctc	tgt	643	
Thr	Ala	Ala	Thr	Ser	Leu	Ala	Gly	Gly	Lys	Pro	Val	His	Tyr	Leu	Cys		
				170					175					180			
gat	gag	gaa	gat	gac	tgg	aac	cca	tcc	atc	gaa	gac	atc	aag	tcc	aaa	691	
Asp	Glu	Glu	Asp	Asp	Trp	Asn	Pro	Ser	Ile	Glu	Asp	Ile	Lys	Ser	Lys		
			185					190					195				
atc	tca	gag	aaa	acc	aaa	gct	att	gtg	gtg	atc	aac	ccc	aac	aac	ccc	739	
Ile	Ser	Glu	Lys	Thr	Lys	Ala	Ile	Val	Val	Ile	Asn	Pro	Asn	Asn	Pro		
			200				205					210					
acg	gga	gct	gtc	tac	ccg	cgc	cgg	gtg	ttg	gaa	caa	atc	gtc	gag	att	787	
Thr	Gly	Ala	Val	Tyr	Pro	Arg	Arg	Val	Leu	Glu	Gln	Ile	Val	Glu	Ile		
			215				220					225					
gca	cgc	gag	cat	gac	ctg	ctg	att	ttg	gcc	gat	gaa	atc	tac	gac	cgc	835	
Ala	Arg	Glu	His	Asp	Leu	Leu	Ile	Leu	Ala	Asp	Glu	Ile	Tyr	Asp	Arg		
230					235					240					245		
att	ctc	tac	gat	gat	gcc	gag	cac	atc	agc	ctg	gca	acc	ctt	gca	cca	883	
Ile	Leu	Tyr	Asp	Asp	Ala	Glu	His	Ile	Ser	Leu	Ala	Thr	Leu	Ala	Pro		
				250					255					260			
gat	ctc	ctt	tgc	atc	aca	tac	aac	ggt	cta	tcc	aag	gca	tac	cgc	gtc	931	
Asp	Leu	Leu	Cys	Ile	Thr	Tyr	Asn	Gly	Leu	Ser	Lys	Ala	Tyr	Arg	Val		
			265					270					275				
gca	gga	tac	cga	gct	ggc	tgg	atg	gta	ttg	act	gga	cca	aag	caa	tac	979	
Ala	Gly	Tyr	Arg	Ala	Gly	Trp	Met	Val	Leu	Thr	Gly	Pro	Lys	Gln	Tyr		
			280				285					290					
gca	cgt	gga	ttt	att	gag	ggc	ctc	gaa	ctc	ctc	gca	ggc	act	cga	ctc	1027	
Ala	Arg	Gly	Phe	Ile	Glu	Gly	Leu	Glu	Leu	Leu	Ala	Gly	Thr	Arg	Leu		

295	300	305	
tgc cca aat gtc cca gct cag cac gct att cag gta gct ctg ggt gga			1075
Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln Val Ala Leu Gly Gly			
310	315	320	325
cgc cag tcc atc tac gac ctc act ggc gaa cac ggc cga ctc ctg gaa			1123
Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His Gly Arg Leu Leu Glu			
	330	335	340
cag cgc aac atg gca tgg acg aaa ctc aac gaa atc cca ggt gtc agc			1171
Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu Ile Pro Gly Val Ser			
	345	350	355
tgt gtg aaa cca atg gga gct cta tac gcg ttc ccc aag ctc gac ccc			1219
Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe Pro Lys Leu Asp Pro			
	360	365	370
aac gtg tac gaa atc cac gac gac acc caa ctc atg ctg gat ctt ctc			1267
Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu Met Leu Asp Leu Leu			
	375	380	385
cgt gcc gag aaa atc ctc atg gtt cag ggc act ggc ttc aac tgg cca			1315
Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr Gly Phe Asn Trp Pro			
390	395	400	405
cat cac gat cac ttc cga gtg gtc acc ctg cca tgg gca tcc cag ttg			1363
His His Asp His Phe Arg Val Val Thr Leu Pro Trp Ala Ser Gln Leu			
	410	415	420
gaa aac gca att gag cgc ctg ggt aac ttc ctg tcc act tac aag cag			1411
Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu Ser Thr Tyr Lys Gln			
	425	430	435
tagtagttgt taggattcac cac			1434

<210> 122

<211> 437

<212> PRT

<213> Corynebacterium glutamicum

<400> 122

Val Thr Thr Asp Lys Arg Lys Thr Ser Lys Thr Thr Asp Thr Ala Asn
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Lys Ala Val Gly Ala Asp Gln Ala Ala Arg Pro Thr Arg Arg Thr Thr
20 25 30

Arg Arg Ile Phe Asp Gln Ser Glu Lys Met Lys Asp Val Leu Tyr Glu
35 40 45

Ile Arg Gly Pro Val Ala Ala Glu Ala Glu Arg Met Glu Leu Asp Gly
50 55 60

His Asn Ile Leu Lys Leu Asn Thr Gly Asn Pro Ala Val Phe Gly Phe
65 70 75 80

Asp Ala Pro Asp Val Ile Met Arg Asp Met Ile Ala Asn Leu Pro Thr
85 90 95

Ser Gln Gly Tyr Ser Thr Ser Lys Gly Ile Ile Pro Ala Arg Arg Ala
 100 105 110
 Val Val Thr Arg Tyr Glu Val Val Pro Gly Phe Pro His Phe Asp Val
 115 120 125
 Asp Asp Val Phe Leu Gly Asn Gly Val Ser Glu Leu Ile Thr Met Thr
 130 135 140
 Thr Gln Ala Leu Leu Asn Asp Gly Asp Glu Val Leu Ile Pro Ala Pro
 145 150 155 160
 Asp Tyr Pro Leu Trp Thr Ala Ala Thr Ser Leu Ala Gly Gly Lys Pro
 165 170 175
 Val His Tyr Leu Cys Asp Glu Glu Asp Asp Trp Asn Pro Ser Ile Glu
 180 185 190
 Asp Ile Lys Ser Lys Ile Ser Glu Lys Thr Lys Ala Ile Val Val Ile
 195 200 205
 Asn Pro Asn Asn Pro Thr Gly Ala Val Tyr Pro Arg Arg Val Leu Glu
 210 215 220
 Gln Ile Val Glu Ile Ala Arg Glu His Asp Leu Leu Ile Leu Ala Asp
 225 230 235 240
 Glu Ile Tyr Asp Arg Ile Leu Tyr Asp Asp Ala Glu His Ile Ser Leu
 245 250 255
 Ala Thr Leu Ala Pro Asp Leu Leu Cys Ile Thr Tyr Asn Gly Leu Ser
 260 265 270
 Lys Ala Tyr Arg Val Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr
 275 280 285
 Gly Pro Lys Gln Tyr Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu
 290 295 300
 Ala Gly Thr Arg Leu Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln
 305 310 315 320
 Val Ala Leu Gly Gly Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His
 325 330 335
 Gly Arg Leu Leu Glu Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu
 340 345 350
 Ile Pro Gly Val Ser Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe
 355 360 365
 Pro Lys Leu Asp Pro Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu
 370 375 380
 Met Leu Asp Leu Leu Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr
 385 390 395 400
 Gly Phe Asn Trp Pro His His Asp His Phe Arg Val Val Thr Leu Pro
 405 410 415
 Trp Ala Ser Gln Leu Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu

420

425

430

Ser Thr Tyr Lys Gln
435

<210> 123

<211> 1701

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1678)

<223> RXA02193

<400> 123

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agcaccattg tgatttcctt caacttgtga gaggcagtag atg tct aag acg agc 115
Met Ser Lys Thr Ser
1 5

aac aag tct tca gca gac tca aag aat gac gca aaa gcc gaa gac att 163
Asn Lys Ser Ser Ala Asp Ser Lys Asn Asp Ala Lys Ala Glu Asp Ile
10 15 20

gtg aac ggc gag aac caa atc gcc acg aat gag tcg cag tct tca gac 211
Val Asn Gly Glu Asn Gln Ile Ala Thr Asn Glu Ser Gln Ser Ser Asp
25 30 35

agc gct gca gtt tcg gaa cgt gtc gtc gaa cca aaa acc acg gtt cag 259
Ser Ala Ala Val Ser Glu Arg Val Val Glu Pro Lys Thr Thr Val Gln
40 45 50

aaa aag ttc cga atc gaa tcg gat ctg ctt ggt gaa ctt cag atc cca 307
Lys Lys Phe Arg Ile Glu Ser Asp Leu Leu Gly Glu Leu Gln Ile Pro
55 60 65

tcc cac gca tat tac ggg gtg cac acc ctt cgt gcg gtg gac aac ttc 355
Ser His Ala Tyr Tyr Gly Val His Thr Leu Arg Ala Val Asp Asn Phe
70 75 80 85

caa atc tca cga acc acc atc aac cac gtc cca gat ttc att cgc ggc 403
Gln Ile Ser Arg Thr Thr Ile Asn His Val Pro Asp Phe Ile Arg Gly
90 95 100

atg gtc cag gtg aaa aag gcc gca gct tta gca aac cgc cga ctg cac 451
Met Val Gln Val Lys Lys Ala Ala Ala Leu Ala Asn Arg Arg Leu His
105 110 115

aca ctt cca gca caa aaa gca gaa gca att gtc tgg gct tgt gat cag 499
Thr Leu Pro Ala Gln Lys Ala Glu Ala Ile Val Trp Ala Cys Asp Gln
120 125 130

atc ctc att gag gaa cgc tgt atg gat cag ttc ccc atc gat gtg ttc 547
Ile Leu Ile Glu Glu Arg Cys Met Asp Gln Phe Pro Ile Asp Val Phe
135 140 145

cag ggt ggc gca ggt acc tca ctg aac atg aac acc aac gag gtt gtt 595
Gln Gly Gly Ala Gly Thr Ser Leu Asn Met Asn Thr Asn Glu Val Val

150	155	160	165	
gcc aac ctt gca ctt gag ttc tta ggc cat gaa aag ggc gag tac cac Ala Asn Leu Ala Leu Glu Phe Leu Gly His Glu Lys Gly Glu Tyr His	170	175	180	643
atc ctg cac ccc atg gat gat gtg aac atg tcc cag tcc acc aac gat Ile Leu His Pro Met Asp Asp Val Asn Met Ser Gln Ser Thr Asn Asp	185	190	195	691
tcc tac cca act ggt ttc cgc ctg ggc att tac gct gga ctg cag acc Ser Tyr Pro Thr Gly Phe Arg Leu Gly Ile Tyr Ala Gly Leu Gln Thr	200	205	210	739
ctc atc gct gaa att gat gag ctt cag gtt gcg ttc cgc cac aag ggc Leu Ile Ala Glu Ile Asp Glu Leu Gln Val Ala Phe Arg His Lys Gly	215	220	225	787
aat gag ttt gtc gac atc atc aag atg ggc cgc acc cag ttg cag gat Asn Glu Phe Val Asp Ile Ile Lys Met Gly Arg Thr Gln Leu Gln Asp	230	235	240	835
gct gtt ccc atg agc ttg ggc gaa gag ttc cga gca ttc gcg cac aac Ala Val Pro Met Ser Leu Gly Glu Glu Phe Arg Ala Phe Ala His Asn	250	255	260	883
ctc gca gaa gag cag acc gtg ctg cgt gaa gct gcc aac cgt ctc ctc Leu Ala Glu Glu Gln Thr Val Leu Arg Glu Ala Ala Asn Arg Leu Leu	265	270	275	931
gag gtc aat ctt ggt gca acc gca atc ggt act ggt gtg aac act cca Glu Val Asn Leu Gly Ala Thr Ala Ile Gly Thr Gly Val Asn Thr Pro	280	285	290	979
gca ggc tac cgc cac cag gtt gtc gct gct ctg tct gag gtc acc gga Ala Gly Tyr Arg His Gln Val Val Ala Ala Leu Ser Glu Val Thr Gly	295	300	305	1027
ctg gaa cta aag tcc gca cgt gat ctc atc gag gct acc tct gac acc Leu Glu Leu Lys Ser Ala Arg Asp Leu Ile Glu Ala Thr Ser Asp Thr	310	315	320	1075
ggt gca tat gtt cat gcg cac tcc gca atc aag cgt gca gcc atg aaa Gly Ala Tyr Val His Ala His Ser Ala Ile Lys Arg Ala Ala Met Lys	330	335	340	1123
ctg tcc aag atc tgt aac gat cta cgt ctg ctg tct tct ggt cct cgt Leu Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly Pro Arg	345	350	355	1171
gct ggc ttg aac gaa atc aac ctg cca cca cgc cag gct ggt tcc tcc Ala Gly Leu Asn Glu Ile Asn Leu Pro Pro Arg Gln Ala Gly Ser Ser	360	365	370	1219
atc atg cca gcc aag gtc aac cca gtg atc cca gaa gtg gtc aac cag Ile Met Pro Ala Lys Val Asn Pro Val Ile Pro Glu Val Val Asn Gln	375	380	385	1267
gtc tgc ttc aag gtc ttc ggt aac gat ctc acc gtc acc atg gct gcg Val Cys Phe Lys Val Phe Gly Asn Asp Leu Thr Val Thr Met Ala Ala	390	395	400	1315
			405	

gaa gct ggc cag ttg cag ctc aac gtc atg gag cca gtc att ggc gaa 1363
 Glu Ala Gly Gln Leu Gln Leu Asn Val Met Glu Pro Val Ile Gly Glu
 410 415 420

tcc ctc ttc cag tca ctg cgc atc ctg ggc aat gca gcc aag act ttg 1411
 Ser Leu Phe Gln Ser Leu Arg Ile Leu Gly Asn Ala Ala Lys Thr Leu
 425 430 435

cgt gag aag tgc gtc gta gga atc acc gcc aac gct gat gtt tgc cgt 1459
 Arg Glu Lys Cys Val Val Gly Ile Thr Ala Asn Ala Asp Val Cys Arg
 440 445 450

gct tac gtt gat aac tcc atc ggg att atc act tac ctg aac cca ttc 1507
 Ala Tyr Val Asp Asn Ser Ile Gly Ile Ile Thr Tyr Leu Asn Pro Phe
 455 460 465

ctg ggc cac gac att gga gat cag atc ggt aag gaa gca gcc gaa act 1555
 Leu Gly His Asp Ile Gly Asp Gln Ile Gly Lys Glu Ala Ala Glu Thr
 470 475 480 485

ggt cga cca gtg cgt gaa ctc atc ctg gaa aag aag ctc atg gat gaa 1603
 Gly Arg Pro Val Arg Glu Leu Ile Leu Glu Lys Lys Leu Met Asp Glu
 490 495 500

aag acg ctc gag gca gtc ctg tcc aag gag aac ctc atg cac cca atg 1651
 Lys Thr Leu Glu Ala Val Leu Ser Lys Glu Asn Leu Met His Pro Met
 505 510 515

ttc cgc gga agg ctc tac ttg gag aac taatccaaga tctcgtctga 1698
 Phe Arg Gly Arg Leu Tyr Leu Glu Asn
 520 525

tac 1701

<210> 124

<211> 526

<212> PRT

<213> Corynebacterium glutamicum

<400> 124

Met Ser Lys Thr Ser Asn Lys Ser Ser Ala Asp Ser Lys Asn Asp Ala
 1 5 10 15

Lys Ala Glu Asp Ile Val Asn Gly Glu Asn Gln Ile Ala Thr Asn Glu
 20 25 30

Ser Gln Ser Ser Asp Ser Ala Ala Val Ser Glu Arg Val Val Glu Pro
 35 40 45

Lys Thr Thr Val Gln Lys Lys Phe Arg Ile Glu Ser Asp Leu Leu Gly
 50 55 60

Glu Leu Gln Ile Pro Ser His Ala Tyr Tyr Gly Val His Thr Leu Arg
 65 70 75 80

Ala Val Asp Asn Phe Gln Ile Ser Arg Thr Thr Ile Asn His Val Pro
 85 90 95

Asp Phe Ile Arg Gly Met Val Gln Val Lys Lys Ala Ala Ala Leu Ala

100					105					110					
Asn	Arg	Arg	Leu	His	Thr	Leu	Pro	Ala	Gln	Lys	Ala	Glu	Ala	Ile	Val
		115					120					125			
Trp	Ala	Cys	Asp	Gln	Ile	Leu	Ile	Glu	Glu	Arg	Cys	Met	Asp	Gln	Phe
	130					135					140				
Pro	Ile	Asp	Val	Phe	Gln	Gly	Gly	Ala	Gly	Thr	Ser	Leu	Asn	Met	Asn
145					150					155					160
Thr	Asn	Glu	Val	Val	Ala	Asn	Leu	Ala	Leu	Glu	Phe	Leu	Gly	His	Glu
				165					170					175	
Lys	Gly	Glu	Tyr	His	Ile	Leu	His	Pro	Met	Asp	Asp	Val	Asn	Met	Ser
			180					185					190		
Gln	Ser	Thr	Asn	Asp	Ser	Tyr	Pro	Thr	Gly	Phe	Arg	Leu	Gly	Ile	Tyr
		195					200					205			
Ala	Gly	Leu	Gln	Thr	Leu	Ile	Ala	Glu	Ile	Asp	Glu	Leu	Gln	Val	Ala
	210					215					220				
Phe	Arg	His	Lys	Gly	Asn	Glu	Phe	Val	Asp	Ile	Ile	Lys	Met	Gly	Arg
225					230					235					240
Thr	Gln	Leu	Gln	Asp	Ala	Val	Pro	Met	Ser	Leu	Gly	Glu	Glu	Phe	Arg
				245					250					255	
Ala	Phe	Ala	His	Asn	Leu	Ala	Glu	Glu	Gln	Thr	Val	Leu	Arg	Glu	Ala
			260					265					270		
Ala	Asn	Arg	Leu	Leu	Glu	Val	Asn	Leu	Gly	Ala	Thr	Ala	Ile	Gly	Thr
		275					280					285			
Gly	Val	Asn	Thr	Pro	Ala	Gly	Tyr	Arg	His	Gln	Val	Val	Ala	Ala	Leu
	290					295					300				
Ser	Glu	Val	Thr	Gly	Leu	Glu	Leu	Lys	Ser	Ala	Arg	Asp	Leu	Ile	Glu
305					310					315					320
Ala	Thr	Ser	Asp	Thr	Gly	Ala	Tyr	Val	His	Ala	His	Ser	Ala	Ile	Lys
				325					330					335	
Arg	Ala	Ala	Met	Lys	Leu	Ser	Lys	Ile	Cys	Asn	Asp	Leu	Arg	Leu	Leu
			340					345					350		
Ser	Ser	Gly	Pro	Arg	Ala	Gly	Leu	Asn	Glu	Ile	Asn	Leu	Pro	Pro	Arg
		355					360					365			
Gln	Ala	Gly	Ser	Ser	Ile	Met	Pro	Ala	Lys	Val	Asn	Pro	Val	Ile	Pro
	370					375					380				
Glu	Val	Val	Asn	Gln	Val	Cys	Phe	Lys	Val	Phe	Gly	Asn	Asp	Leu	Thr
385					390					395					400
Val	Thr	Met	Ala	Ala	Glu	Ala	Gly	Gln	Leu	Gln	Leu	Asn	Val	Met	Glu
				405					410					415	
Pro	Val	Ile	Gly	Glu	Ser	Leu	Phe	Gln	Ser	Leu	Arg	Ile	Leu	Gly	Asn
			420					425					430		

Ala Ala Lys Thr Leu Arg Glu Lys Cys Val Val Gly Ile Thr Ala Asn
 435 440 445

Ala Asp Val Cys Arg Ala Tyr Val Asp Asn Ser Ile Gly Ile Ile Thr
 450 455 460

Tyr Leu Asn Pro Phe Leu Gly His Asp Ile Gly Asp Gln Ile Gly Lys
 465 470 475 480

Glu Ala Ala Glu Thr Gly Arg Pro Val Arg Glu Leu Ile Leu Glu Lys
 485 490 495

Lys Leu Met Asp Glu Lys Thr Leu Glu Ala Val Leu Ser Lys Glu Asn
 500 505 510

Leu Met His Pro Met Phe Arg Gly Arg Leu Tyr Leu Glu Asn
 515 520 525

<210> 125

<211> 1098

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1075)

<223> RXA02432

<400> 125

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gtgcacataa caactgcagc tagttgatac gctagagcgc atg tcg aag cag cac 115
 Met Ser Lys Gln His
 1 5

tcc aca cca tta aac aat gat gaa gaa cac act tcc gct cct caa aag 163
 Ser Thr Pro Leu Asn Asn Asp Glu Glu His Thr Ser Ala Pro Gln Lys
 10 15 20

gtt gcg gta atc acc acg ggc gga acc atc gcc tgt act tcc gac gca 211
 Val Ala Val Ile Thr Thr Gly Gly Thr Ile Ala Cys Thr Ser Asp Ala
 25 30 35

aat ggg cat ctg ctt ccc acc gtc agc ggt gca gac ctg ctt gcg cca 259
 Asn Gly His Leu Leu Pro Thr Val Ser Gly Ala Asp Leu Leu Ala Pro
 40 45 50

atc gca cca cgg ttc aat gga gcg cag atc gct ttc gaa atc cac gaa 307
 Ile Ala Pro Arg Phe Asn Gly Ala Gln Ile Ala Phe Glu Ile His Glu
 55 60 65

atc aac cgc ctt gat tcc tcc tcc atg acg ttt gag gat ctc gat tcc 355
 Ile Asn Arg Leu Asp Ser Ser Ser Met Thr Phe Glu Asp Leu Asp Ser
 70 75 80 85

atc atc gcc acg gtt cat aag gtg ttg gag gat ccg gat gtt gtt ggc 403
 Ile Ile Ala Thr Val His Lys Val Leu Glu Asp Pro Asp Val Val Gly
 90 95 100

gta gta gtt acc cac ggc acc gat tcc atg gaa gag tcc gcc atc gcc	451
Val Val Val Thr His Gly Thr Asp Ser Met Glu Glu Ser Ala Ile Ala	
105 110 115	
gta gac acc ttc ctt gat gat ccc cgc cca gtc att ttc acc ggc gcc	499
Val Asp Thr Phe Leu Asp Asp Pro Arg Pro Val Ile Phe Thr Gly Ala	
120 125 130	
caa aaa ccc ttc gat cat ccc gaa gcc gac ggc cca aac aac ctt ttc	547
Gln Lys Pro Phe Asp His Pro Glu Ala Asp Gly Pro Asn Asn Leu Phe	
135 140 145	
gaa gcc tgc ctc atc gca tcc gac ccc tcc gct cgc gga att ggt gca	595
Glu Ala Cys Leu Ile Ala Ser Asp Pro Ser Ala Arg Gly Ile Gly Ala	
150 155 160 165	
ctc att gtc ttc ggt cac gcc gtc atc cct gct cgc ggc tgc gtt aaa	643
Leu Ile Val Phe Gly His Ala Val Ile Pro Ala Arg Gly Cys Val Lys	
170 175 180	
tgg cac acc tct gat gag ctg gcg ttt gca acc aac ggc cct gaa gaa	691
Trp His Thr Ser Asp Glu Leu Ala Phe Ala Thr Asn Gly Pro Glu Glu	
185 190 195	
cca gag cgc ccc gat gcg ctg ccc gta gct aaa ttg gcg gat gtc tct	739
Pro Glu Arg Pro Asp Ala Leu Pro Val Ala Lys Leu Ala Asp Val Ser	
200 205 210	
gtc gaa atc atc ccc gca tac cct ggt gcc acc ggc gca atg gtg gaa	787
Val Glu Ile Ile Pro Ala Tyr Pro Gly Ala Thr Gly Ala Met Val Glu	
215 220 225	
gct gcc atc gct gcc ggt gct caa gga ctt gta gtg gaa gca atg gga	835
Ala Ala Ile Ala Ala Gly Ala Gln Gly Leu Val Val Glu Ala Met Gly	
230 235 240 245	
tca ggc aat gtt ggt tcc cgc atg ggt gat gcc cta ggt aaa gca ctt	883
Ser Gly Asn Val Gly Ser Arg Met Gly Asp Ala Leu Gly Lys Ala Leu	
250 255 260	
gac gct gga att ccc gtg gtg atg agc act agg gtt cct cgt ggt gaa	931
Asp Ala Gly Ile Pro Val Val Met Ser Thr Arg Val Pro Arg Gly Glu	
265 270 275	
gta tcc gga gtg tat ggc ggt gca ggt gga ggt gcg act ttg gct gcg	979
Val Ser Gly Val Tyr Gly Gly Ala Gly Gly Gly Ala Thr Leu Ala Ala	
280 285 290	
aag ggc gct gtg gga tct cgc tac ttc aga gct ggt cag gca cgt att	1027
Lys Gly Ala Val Gly Ser Arg Tyr Phe Arg Ala Gly Gln Ala Arg Ile	
295 300 305	
ttg ctc gcg att gcc att gcg acg ggc gca cat ccg gtg acg ctt tac	1075
Leu Leu Ala Ile Ala Ile Ala Thr Gly Ala His Pro Val Thr Leu Tyr	
310 315 320 325	
taatttcgcc cttggtcttg cat	1098

<210> 126

<211> 325

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 126

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Met Ser Lys Gln His Ser Thr Pro Leu Asn Asn Asp Glu Glu His Thr
  1                      5                      10                      15

Ser Ala Pro Gln Lys Val Ala Val Ile Thr Thr Gly Gly Thr Ile Ala
          20                      25                      30

Cys Thr Ser Asp Ala Asn Gly His Leu Leu Pro Thr Val Ser Gly Ala
          35                      40                      45

Asp Leu Leu Ala Pro Ile Ala Pro Arg Phe Asn Gly Ala Gln Ile Ala
  50                      55                      60

Phe Glu Ile His Glu Ile Asn Arg Leu Asp Ser Ser Ser Met Thr Phe
  65                      70                      75                      80

Glu Asp Leu Asp Ser Ile Ile Ala Thr Val His Lys Val Leu Glu Asp
          85                      90                      95

Pro Asp Val Val Gly Val Val Val Thr His Gly Thr Asp Ser Met Glu
          100                      105                      110

Glu Ser Ala Ile Ala Val Asp Thr Phe Leu Asp Asp Pro Arg Pro Val
          115                      120                      125

Ile Phe Thr Gly Ala Gln Lys Pro Phe Asp His Pro Glu Ala Asp Gly
          130                      135                      140

Pro Asn Asn Leu Phe Glu Ala Cys Leu Ile Ala Ser Asp Pro Ser Ala
          145                      150                      155                      160

Arg Gly Ile Gly Ala Leu Ile Val Phe Gly His Ala Val Ile Pro Ala
          165                      170                      175

Arg Gly Cys Val Lys Trp His Thr Ser Asp Glu Leu Ala Phe Ala Thr
          180                      185                      190

Asn Gly Pro Glu Glu Pro Glu Arg Pro Asp Ala Leu Pro Val Ala Lys
          195                      200                      205

Leu Ala Asp Val Ser Val Glu Ile Ile Pro Ala Tyr Pro Gly Ala Thr
          210                      215                      220

Gly Ala Met Val Glu Ala Ala Ile Ala Ala Gly Ala Gln Gly Leu Val
          225                      230                      235                      240

Val Glu Ala Met Gly Ser Gly Asn Val Gly Ser Arg Met Gly Asp Ala
          245                      250                      255

Leu Gly Lys Ala Leu Asp Ala Gly Ile Pro Val Val Met Ser Thr Arg
          260                      265                      270

Val Pro Arg Gly Glu Val Ser Gly Val Tyr Gly Gly Ala Gly Gly Gly
          275                      280                      285

Ala Thr Leu Ala Ala Lys Gly Ala Val Gly Ser Arg Tyr Phe Arg Ala
          290                      295                      300

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Gly Gln Ala Arg Ile Leu Leu Ala Ile Ala Ile Ala Thr Gly Ala His
305 310 315 320

Pro Val Thr Leu Tyr
325

<210> 127

<211> 775

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(775)

<223> RXN03003

<400> 127

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caatgatcgc tgcgctgccg cctcaggcat aatctaacgc atg acc tct cgc acc 115
Met Thr Ser Arg Thr
1 5

ccg ctt gtt tct gtt ctt cct gat ttt ccg tgg gat tcg ctc gct tcc 163
Pro Leu Val Ser Val Leu Pro Asp Phe Pro Trp Asp Ser Leu Ala Ser
10 15 20

gca aaa gcc aaa gct gcg tct cac ccg gat ggg atc gtg aat ctt tct 211
Ala Lys Ala Lys Ala Ala Ser His Pro Asp Gly Ile Val Asn Leu Ser
25 30 35

gtt ggc act ccg gtt gat ccg gtc gcg ccc agc att cag atc gcg ttg 259
Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser Ile Gln Ile Ala Leu
40 45 50

gca gaa gca gcg ggg ttt tcg ggt tac cct caa acc atc ggc acc ccg 307
Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln Thr Ile Gly Thr Pro
55 60 65

gaa ctc cgc gca gcc atc agg ggc gcg ctt gag cgg cgc tac aac atg 355
Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu Arg Arg Tyr Asn Met
70 75 80 85

aca aag ctt gtc gac gcc tcc ctc ctc ccc gtc gtg ggt acc aag gag 403
Thr Lys Leu Val Asp Ala Ser Leu Leu Pro Val Val Gly Thr Lys Glu
90 95 100

gca att gcc ctt ctt cca ttc gcg ttg ggt att tcc ggc acc gtt gtc 451
Ala Ile Ala Leu Leu Pro Phe Ala Leu Gly Ile Ser Gly Thr Val Val
105 110 115

atc cca gag att gcg tac cca acc tac gaa gtc gct gtc gtg gcc gca 499
Ile Pro Glu Ile Ala Tyr Pro Thr Tyr Glu Val Ala Val Val Ala Ala
120 125 130

gga tgc acc gtg ttg cgt tct gat tcg ctg ttt aag ctc ggc ccg cag 547
Gly Cys Thr Val Leu Arg Ser Asp Ser Leu Phe Lys Leu Gly Pro Gln
135 140 145

atc ccg tcg atg atg ttt atc aac tca cca tcc aac ccc aca ggc aag 595

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Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser Asn Pro Thr Gly Lys
150                      155                      160                      165

ggt ctg ggc atc cca cac ttg cgc aag gtt gtg aag tgg gcg cag gaa 643
Val Leu Gly Ile Pro His Leu Arg Lys Val Val Lys Trp Ala Gln Glu
                      170                      175                      180

aac aac gtg atc ctc gca gct gat gaa tgc tac ttg ggt ctt ggc tgg 691
Asn Asn Val Ile Leu Ala Ala Asp Glu Cys Tyr Leu Gly Leu Gly Trp
                      185                      190                      195

gac gat gaa aac cca ccg atc tca att ttg gat cca cgt gtc tgc gat 739
Asp Asp Glu Asn Pro Pro Ile Ser Ile Leu Asp Pro Arg Val Cys Asp
                      200                      205                      210

ggc gac cac acc aac ttg atc gcc att cac tcg ctg 775
Gly Asp His Thr Asn Leu Ile Ala Ile His Ser Leu
                      215                      220                      225

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<210> 128

<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 128

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Met Thr Ser Arg Thr Pro Leu Val Ser Val Leu Pro Asp Phe Pro Trp
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Asp Ser Leu Ala Ser Ala Lys Ala Lys Ala Ala Ser His Pro Asp Gly
                      20                      25                      30

Ile Val Asn Leu Ser Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser
                      35                      40                      45

Ile Gln Ile Ala Leu Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln
                      50                      55                      60

Thr Ile Gly Thr Pro Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu
                      65                      70                      75                      80

Arg Arg Tyr Asn Met Thr Lys Leu Val Asp Ala Ser Leu Leu Pro Val
                      85                      90                      95

Val Gly Thr Lys Glu Ala Ile Ala Leu Leu Pro Phe Ala Leu Gly Ile
                      100                      105                      110

Ser Gly Thr Val Val Ile Pro Glu Ile Ala Tyr Pro Thr Tyr Glu Val
                      115                      120                      125

Ala Val Val Ala Ala Gly Cys Thr Val Leu Arg Ser Asp Ser Leu Phe
                      130                      135                      140

Lys Leu Gly Pro Gln Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser
145                      150                      155                      160

Asn Pro Thr Gly Lys Val Leu Gly Ile Pro His Leu Arg Lys Val Val
                      165                      170                      175

Lys Trp Ala Gln Glu Asn Asn Val Ile Leu Ala Ala Asp Glu Cys Tyr
                      180                      185                      190

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Leu Gly Leu Gly Trp Asp Asp Glu Asn Pro Pro Ile Ser Ile Leu Asp
 195 200 205

Pro Arg Val Cys Asp Gly Asp His Thr Asn Leu Ile Ala Ile His Ser
 210 215 220

Leu
 225

<210> 129

<211> 1206

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1183)

<223> RXN00508

<400> 129

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atcgtatttc tgtccgcggt tgggtggcaca atagttcaac atg aac ttg ctg acc 115
 Met Asn Leu Leu Thr
 1 5

acc aaa att gac ctg gat gcc atc gcc cat aac acg agg gtg ctt aaa 163
 Thr Lys Ile Asp Leu Asp Ala Ile Ala His Asn Thr Arg Val Leu Lys
 10 15 20

caa atg gcg ggt ccg gcg aag ctg atg gcg gtg gtg aag gcg aat gca 211
 Gln Met Ala Gly Pro Ala Lys Leu Met Ala Val Val Lys Ala Asn Ala
 25 30 35

tat aac cat ggc gta gag aag gtc gct ccg gtt att gct gct cat ggt 259
 Tyr Asn His Gly Val Glu Lys Val Ala Pro Val Ile Ala Ala His Gly
 40 45 50

gcg gat gcg ttt ggt gtg gca act ctt gcg gag gct atg cag ttg cgt 307
 Ala Asp Ala Phe Gly Val Ala Thr Leu Ala Glu Ala Met Gln Leu Arg
 55 60 65

gat atc ggc atc agc caa gag gtt ttg tgt tgg att tgg aca ccg gag 355
 Asp Ile Gly Ile Ser Gln Glu Val Leu Cys Trp Ile Trp Thr Pro Glu
 70 75 80 85

cag gat ttc cgc gcc gcc att gat cgc aat att gat ttg gct gtt att 403
 Gln Asp Phe Arg Ala Ala Ile Asp Arg Asn Ile Asp Leu Ala Val Ile
 90 95 100

tct ccc gcg cat gcc aaa gcc ttg atc gaa act gat gcg gag cat att 451
 Ser Pro Ala His Ala Lys Ala Leu Ile Glu Thr Asp Ala Glu His Ile
 105 110 115

cgg gtg tcc atc aag att gat tct ggg ttg cat cgt tcg ggt gtg gat 499
 Arg Val Ser Ile Lys Ile Asp Ser Gly Leu His Arg Ser Gly Val Asp
 120 125 130

gag cag gag tgg gag ggc gtg ttc agc gcg ttg gct gct gcc ccg cac 547

Glu	Gln	Glu	Trp	Glu	Gly	Val	Phe	Ser	Ala	Leu	Ala	Ala	Ala	Pro	His		
135						140					145						
att	gag	gtc	acg	ggc	atg	ttc	acg	cac	ttg	gcg	tgc	gcg	gat	gag	cca	595	
Ile	Glu	Val	Thr	Gly	Met	Phe	Thr	His	Leu	Ala	Cys	Ala	Asp	Glu	Pro		
150					155					160					165		
gag	aat	ccg	gaa	act	gat	cgc	caa	att	att	gct	ttt	cga	cgc	gcc	ctt	643	
Glu	Asn	Pro	Glu	Thr	Asp	Arg	Gln	Ile	Ile	Ala	Phe	Arg	Arg	Ala	Leu		
				170					175						180		
gcg	ctc	gcc	cgc	aag	cac	ggg	ctt	gag	tgc	ccg	gtc	aac	cac	gta	tgc	691	
Ala	Leu	Ala	Arg	Lys	His	Gly	Leu	Glu	Cys	Pro	Val	Asn	His	Val	Cys		
			185					190					195				
aac	tca	cct	gca	ttc	ttg	act	cga	tct	gat	tta	cac	atg	gag	atg	gtc	739	
Asn	Ser	Pro	Ala	Phe	Leu	Thr	Arg	Ser	Asp	Leu	His	Met	Glu	Met	Val		
		200					205					210					
cga	ccg	ggt	ttg	gcc	ttt	tat	ggg	ttg	gaa	ccc	gtg	gcg	gga	ctg	gag	787	
Arg	Pro	Gly	Leu	Ala	Phe	Tyr	Gly	Leu	Glu	Pro	Val	Ala	Gly	Leu	Glu		
	215					220					225						
cat	ggt	ttg	aag	ccg	gcg	atg	acg	tgg	gag	gcg	aag	gtg	agc	gtc	gta	835	
His	Gly	Leu	Lys	Pro	Ala	Met	Thr	Trp	Glu	Ala	Lys	Val	Ser	Val	Val		
230					235				240					245			
aag	caa	att	gaa	gct	gga	caa	ggc	act	tcc	tat	ggc	ctg	acc	tgg	cgc	883	
Lys	Gln	Ile	Glu	Ala	Gly	Gln	Gly	Thr	Ser	Tyr	Gly	Leu	Thr	Trp	Arg		
			250					255						260			
gct	gag	gat	cgc	ggc	ttt	gtg	gct	gtg	gtg	cct	gcg	ggc	tat	gcc	gat	931	
Ala	Glu	Asp	Arg	Gly	Phe	Val	Ala	Val	Val	Pro	Ala	Gly	Tyr	Ala	Asp		
			265				270						275				
ggc	atg	ccg	cgg	cat	gcc	cag	ggg	aaa	ttc	tcc	gtc	acg	att	gat	ggc	979	
Gly	Met	Pro	Arg	His	Ala	Gln	Gly	Lys	Phe	Ser	Val	Thr	Ile	Asp	Gly		
	280						285					290					
ctg	gac	tat	ccg	cag	gtt	ggg	cgc	gta	tgc	atg	gat	cag	ttc	gtt	att	1027	
Leu	Asp	Tyr	Pro	Gln	Val	Gly	Arg	Val	Cys	Met	Asp	Gln	Phe	Val	Ile		
	295					300					305						
tct	ttg	ggc	gac	aat	cca	cac	ggc	gtg	gaa	gct	ggg	gcg	aag	gcc	gtg	1075	
Ser	Leu	Gly	Asp	Asn	Pro	His	Gly	Val	Glu	Ala	Gly	Ala	Lys	Ala	Val		
310					315					320					325		
ata	ttc	ggt	gag	aat	ggg	cat	gac	gca	act	gat	ttt	gcg	gag	cgt	tta	1123	
Ile	Phe	Gly	Glu	Asn	Gly	His	Asp	Ala	Thr	Asp	Phe	Ala	Glu	Arg	Leu		
				330				335						340			
gac	acc	att	aac	tat	gag	gta	gtg	tgc	cga	cca	acc	ggc	cga	act	gtc	1171	
Asp	Thr	Ile	Asn	Tyr	Glu	Val	Val	Cys	Arg	Pro	Thr	Gly	Arg	Thr	Val		
			345					350					355				
cgc	gca	tat	gtt	taagtgaata	cggttaagga	gca										1206	
Arg	Ala	Tyr	Val														
			360														

<210> 130

<211> 361

<212> PRT

<213> Corynebacterium glutamicum

<400> 130

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Met Asn Leu Leu Thr Thr Lys Ile Asp Leu Asp Ala Ile Ala His Asn
  1              5              10              15

Thr Arg Val Leu Lys Gln Met Ala Gly Pro Ala Lys Leu Met Ala Val
      20              25              30

Val Lys Ala Asn Ala Tyr Asn His Gly Val Glu Lys Val Ala Pro Val
      35              40              45

Ile Ala Ala His Gly Ala Asp Ala Phe Gly Val Ala Thr Leu Ala Glu
      50              55              60

Ala Met Gln Leu Arg Asp Ile Gly Ile Ser Gln Glu Val Leu Cys Trp
      65              70              75              80

Ile Trp Thr Pro Glu Gln Asp Phe Arg Ala Ala Ile Asp Arg Asn Ile
      85              90              95

Asp Leu Ala Val Ile Ser Pro Ala His Ala Lys Ala Leu Ile Glu Thr
      100              105              110

Asp Ala Glu His Ile Arg Val Ser Ile Lys Ile Asp Ser Gly Leu His
      115              120              125

Arg Ser Gly Val Asp Glu Gln Glu Trp Glu Gly Val Phe Ser Ala Leu
      130              135              140

Ala Ala Ala Pro His Ile Glu Val Thr Gly Met Phe Thr His Leu Ala
      145              150              155              160

Cys Ala Asp Glu Pro Glu Asn Pro Glu Thr Asp Arg Gln Ile Ile Ala
      165              170              175

Phe Arg Arg Ala Leu Ala Leu Ala Arg Lys His Gly Leu Glu Cys Pro
      180              185              190

Val Asn His Val Cys Asn Ser Pro Ala Phe Leu Thr Arg Ser Asp Leu
      195              200              205

His Met Glu Met Val Arg Pro Gly Leu Ala Phe Tyr Gly Leu Glu Pro
      210              215              220

Val Ala Gly Leu Glu His Gly Leu Lys Pro Ala Met Thr Trp Glu Ala
      225              230              235              240

Lys Val Ser Val Val Lys Gln Ile Glu Ala Gly Gln Gly Thr Ser Tyr
      245              250              255

Gly Leu Thr Trp Arg Ala Glu Asp Arg Gly Phe Val Ala Val Val Pro
      260              265              270

Ala Gly Tyr Ala Asp Gly Met Pro Arg His Ala Gln Gly Lys Phe Ser
      275              280              285

Val Thr Ile Asp Gly Leu Asp Tyr Pro Gln Val Gly Arg Val Cys Met
      290              295              300

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Asp Gln Phe Val Ile Ser Leu Gly Asp Asn Pro His Gly Val Glu Ala
 305 310 315 320

Gly Ala Lys Ala Val Ile Phe Gly Glu Asn Gly His Asp Ala Thr Asp
 325 330 335

Phe Ala Glu Arg Leu Asp Thr Ile Asn Tyr Glu Val Val Cys Arg Pro
 340 345 350

Thr Gly Arg Thr Val Arg Ala Tyr Val
 355 360

<210> 131

<211> 1152

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1129)

<223> RXN00636

<400> 131

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tcgatctggc ccgttcgaac ataaggaata ttctactcc atg atg att gat aca 115
 Met Met Ile Asp Thr
 1 5

cct gct gtt ctc att gac cgc gag cgc tta act gcc aac att tcc agg 163
 Pro Ala Val Leu Ile Asp Arg Glu Arg Leu Thr Ala Asn Ile Ser Arg
 10 15 20

atg gca gct cac gcc ggt gcc cat gag att gcc ctg cgt ccg cat gtg 211
 Met Ala Ala His Ala Gly Ala His Glu Ile Ala Leu Arg Pro His Val
 25 30 35

aaa acg cac aaa atc att gaa att gcg cag atg cag gtc gac gcc ggt 259
 Lys Thr His Lys Ile Ile Glu Ile Ala Gln Met Gln Val Asp Ala Gly
 40 45 50

gcc cga ggg atc acc tgc gca acc att ggc gag gcg gaa att ttt gcc 307
 Ala Arg Gly Ile Thr Cys Ala Thr Ile Gly Glu Ala Glu Ile Phe Ala
 55 60 65

ggc gca ggt ttt acg gac atc ttt att gca tat ccg ctg tat cta acc 355
 Gly Ala Gly Phe Thr Asp Ile Phe Ile Ala Tyr Pro Leu Tyr Leu Thr
 70 75 80 85

gat cat gca gtg caa cgc ctg aac gcg atc ccc gga gaa att tcc att 403
 Asp His Ala Val Gln Arg Leu Asn Ala Ile Pro Gly Glu Ile Ser Ile
 90 95 100

ggc gtg gat tcg gta gag atg gca cag gcg acg gcg ggt ttg cgg gaa 451
 Gly Val Asp Ser Val Glu Met Ala Gln Ala Thr Ala Gly Leu Arg Glu
 105 110 115

gat atc aag gct ctg att gaa gtg gat tcg gga cat cgt aga agt gga 499
 Asp Ile Lys Ala Leu Ile Glu Val Asp Ser Gly His Arg Arg Ser Gly

120	125	130	
gtc acg gcg act gct tca gaa ttg agt cag atc cgc gag gcg ctg ggc Val Thr Ala Thr Ala Ser Glu Leu Ser Gln Ile Arg Glu Ala Leu Gly 135 140 145			547
agc agg tat gca gga gtg ttt act ttt cct ggg cat tct tat ggc ccg Ser Arg Tyr Ala Gly Val Phe Thr Phe Pro Gly His Ser Tyr Gly Pro 150 155 160 165			595
gga aat ggt gag cag gca gca gct gat gag ctt cag gct cta aac aac Gly Asn Gly Glu Gln Ala Ala Ala Asp Glu Leu Gln Ala Leu Asn Asn 170 175 180			643
agc gtc cag cga ctt gct ggc ggc ctg act tct ggc ggt tcc tcg ccg Ser Val Gln Arg Leu Ala Gly Gly Leu Thr Ser Gly Gly Ser Ser Pro 185 190 195			691
tct gcg cag ttt aca gac gca atc gat gag atg cga cca ggc gtg tat Ser Ala Gln Phe Thr Asp Ala Ile Asp Glu Met Arg Pro Gly Val Tyr 200 205 210			739
gtg ttt aac gat tcc cag cag atc acc tcg gga gca tgc act gag aag Val Phe Asn Asp Ser Gln Gln Ile Thr Ser Gly Ala Cys Thr Glu Lys 215 220 225			787
cag gtg gca atg acg gtg ctg tct act gtg gtc agc cga aat gtg tca Gln Val Ala Met Thr Val Leu Ser Thr Val Val Ser Arg Asn Val Ser 230 235 240 245			835
gat cgt cgg atc att ttg gat gcg gga tcc aaa atc ctc agc act gat Asp Arg Arg Ile Ile Leu Asp Ala Gly Ser Lys Ile Leu Ser Thr Asp 250 255 260			883
aaa cca gca tgg att gat ggc aat ggt ttt gtt ctg ggg aat cct gaa Lys Pro Ala Trp Ile Asp Gly Asn Gly Phe Val Leu Gly Asn Pro Glu 265 270 275			931
gcc cga atc tct gct ttg tcg gag cat cac gca acc att ttc tgg cca Ala Arg Ile Ser Ala Leu Ser Glu His His Ala Thr Ile Phe Trp Pro 280 285 290			979
gat aaa gtg cta ctt cca gta atc ggg gag cag ctc aac atc gtg ccc Asp Lys Val Leu Leu Pro Val Ile Gly Glu Gln Leu Asn Ile Val Pro 295 300 305			1027
aac cat gcc tgc aac gtg att aat ttg gtg gat gag gtc tac gtt cgg Asn His Ala Cys Asn Val Ile Asn Leu Val Asp Glu Val Tyr Val Arg 310 315 320 325			1075
gaa gcc gat ggc act ttc cgt acc tgg aag gta gtt gcc cgc ggc aga Glu Ala Asp Gly Thr Phe Arg Thr Trp Lys Val Val Ala Arg Gly Arg 330 335 340			1123
aac aat tagggaaacc tcttgacctt cac Asn Asn			1152

<210> 132

<211> 343

<212> PRT

<213> Corynebacterium glutamicum

<400> 132

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Met Met Ile Asp Thr Pro Ala Val Leu Ile Asp Arg Glu Arg Leu Thr
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Ala Asn Ile Ser Arg Met Ala Ala His Ala Gly Ala His Glu Ile Ala
      20             25             30

Leu Arg Pro His Val Lys Thr His Lys Ile Ile Glu Ile Ala Gln Met
      35             40             45

Gln Val Asp Ala Gly Ala Arg Gly Ile Thr Cys Ala Thr Ile Gly Glu
      50             55             60

Ala Glu Ile Phe Ala Gly Ala Gly Phe Thr Asp Ile Phe Ile Ala Tyr
      65             70             75             80

Pro Leu Tyr Leu Thr Asp His Ala Val Gln Arg Leu Asn Ala Ile Pro
      85             90             95

Gly Glu Ile Ser Ile Gly Val Asp Ser Val Glu Met Ala Gln Ala Thr
      100             105             110

Ala Gly Leu Arg Glu Asp Ile Lys Ala Leu Ile Glu Val Asp Ser Gly
      115             120             125

His Arg Arg Ser Gly Val Thr Ala Thr Ala Ser Glu Leu Ser Gln Ile
      130             135             140

Arg Glu Ala Leu Gly Ser Arg Tyr Ala Gly Val Phe Thr Phe Pro Gly
      145             150             155             160

His Ser Tyr Gly Pro Gly Asn Gly Glu Gln Ala Ala Ala Asp Glu Leu
      165             170             175

Gln Ala Leu Asn Asn Ser Val Gln Arg Leu Ala Gly Gly Leu Thr Ser
      180             185             190

Gly Gly Ser Ser Pro Ser Ala Gln Phe Thr Asp Ala Ile Asp Glu Met
      195             200             205

Arg Pro Gly Val Tyr Val Phe Asn Asp Ser Gln Gln Ile Thr Ser Gly
      210             215             220

Ala Cys Thr Glu Lys Gln Val Ala Met Thr Val Leu Ser Thr Val Val
      225             230             235             240

Ser Arg Asn Val Ser Asp Arg Arg Ile Ile Leu Asp Ala Gly Ser Lys
      245             250             255

Ile Leu Ser Thr Asp Lys Pro Ala Trp Ile Asp Gly Asn Gly Phe Val
      260             265             270

Leu Gly Asn Pro Glu Ala Arg Ile Ser Ala Leu Ser Glu His His Ala
      275             280             285

Thr Ile Phe Trp Pro Asp Lys Val Leu Leu Pro Val Ile Gly Glu Gln
      290             295             300

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Leu Asn Ile Val Pro Asn His Ala Cys Asn Val Ile Asn Leu Val Asp
305 310 315 320

Glu Val Tyr Val Arg Glu Ala Asp Gly Thr Phe Arg Thr Trp Lys Val
325 330 335

Val Ala Arg Gly Arg Asn Asn
340

<210> 133

<211> 879

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(856)

<223> RXA02536

<400> 133

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gcgtattgcc ttgcttcaga tctcgacgaa ttccgataag atg gac aac ttc gcc 115
Met Asp Asn Phe Ala
1 5

ctg ctg cgt gat gct gct gaa aaa gct gcg gaa cag ggg gct cgg gtg 163
Leu Leu Arg Asp Ala Ala Glu Lys Ala Ala Glu Gln Gly Ala Arg Val
10 15 20

ttg gtg ttt ccg gag gcg act tcg caa agc ttt ggt acg gga agg ctt 211
Leu Val Phe Pro Glu Ala Thr Ser Gln Ser Phe Gly Thr Gly Arg Leu
25 30 35

gat act cag gcg gag gag ctc gat ggc gaa ttc tcc acc gcg gta cga 259
Asp Thr Gln Ala Glu Glu Leu Asp Gly Glu Phe Ser Thr Ala Val Arg
40 45 50

aaa tta gcc gat gag ctg gac gtt gtc atc gtt gcg ggc atg ttc acc 307
Lys Leu Ala Asp Glu Leu Asp Val Val Ile Val Ala Gly Met Phe Thr
55 60 65

cct gct gac acc gtg cag cgc ggt gaa aaa acg atc tcg cgc gtc aac 355
Pro Ala Asp Thr Val Gln Arg Gly Glu Lys Thr Ile Ser Arg Val Asn
70 75 80 85

aac acc gtg ctg att agt ggc gct gga ttg cat cag gga tac aac aaa 403
Asn Thr Val Leu Ile Ser Gly Ala Gly Leu His Gln Gly Tyr Asn Lys
90 95 100

att cac aca tat gac gcg ttc ggt tat agg gaa tcc gac act gtg aaa 451
Ile His Thr Tyr Asp Ala Phe Gly Tyr Arg Glu Ser Asp Thr Val Lys
105 110 115

ccg ggc gat gag ctg gtt gta ttc gag gtc gac gat att aaa ttt ggt 499
Pro Gly Asp Glu Leu Val Val Phe Glu Val Asp Asp Ile Lys Phe Gly
120 125 130

gtg gcg aca tgc tac gat att cga ttc cca gaa cag ttc aaa gac ctc 547
Val Ala Thr Cys Tyr Asp Ile Arg Phe Pro Glu Gln Phe Lys Asp Leu

135	140	145	
gcc cgc aac ggt gca cag ata att gtg gtt ccc acg tcg tgg caa gac			595
Ala Arg Asn Gly Ala Gln Ile Ile Val Val Pro Thr Ser Trp Gln Asp			
150	155	160	165
ggt cct gga aaa tta gaa caa tgg gaa gtc ctc cct cgc gcg cgt gca			643
Gly Pro Gly Lys Leu Glu Gln Trp Glu Val Leu Pro Arg Ala Arg Ala			
	170	175	180
ctg gat tcc acc tgc tgg atc gta gcg tgt ggg caa gcg cga ctt cca			691
Leu Asp Ser Thr Cys Trp Ile Val Ala Cys Gly Gln Ala Arg Leu Pro			
	185	190	195
gaa gaa tta cgc gat gaa cga aaa ggc cct acg ggg att ggt cat tcc			739
Glu Glu Leu Arg Asp Glu Arg Lys Gly Pro Thr Gly Ile Gly His Ser			
	200	205	210
atg gtg aca aac cca cac ggt gaa gta att gct agc gcg ggt tat gag			787
Met Val Thr Asn Pro His Gly Glu Val Ile Ala Ser Ala Gly Tyr Glu			
	215	220	225
cca gaa atg ttg atc gcg gat att gat gtc agc ggt ttg gcc aaa att			835
Pro Glu Met Leu Ile Ala Asp Ile Asp Val Ser Gly Leu Ala Lys Ile			
	230	235	240
cgg gag gca ttg cct gtt ctt taaccactgt ctaaggaatc act			879
Arg Glu Ala Leu Pro Val Leu			
	250		

<210> 134

<211> 252

<212> PRT

<213> Corynebacterium glutamicum

<400> 134

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Gln Gly Ala Arg Val Leu Val Phe Pro Glu Ala Thr Ser Gln Ser Phe	
20	30
Gly Thr Gly Arg Leu Asp Thr Gln Ala Glu Glu Leu Asp Gly Glu Phe	
35	45
Ser Thr Ala Val Arg Lys Leu Ala Asp Glu Leu Asp Val Val Ile Val	
50	60
Ala Gly Met Phe Thr Pro Ala Asp Thr Val Gln Arg Gly Glu Lys Thr	
65	80
Ile Ser Arg Val Asn Asn Thr Val Leu Ile Ser Gly Ala Gly Leu His	
85	95
Gln Gly Tyr Asn Lys Ile His Thr Tyr Asp Ala Phe Gly Tyr Arg Glu	
100	110
Ser Asp Thr Val Lys Pro Gly Asp Glu Leu Val Val Phe Glu Val Asp	
115	125

Asp Ile Lys Phe Gly Val Ala Thr Cys Tyr Asp Ile Arg Phe Pro Glu
 130 135 140
 Gln Phe Lys Asp Leu Ala Arg Asn Gly Ala Gln Ile Ile Val Val Pro
 145 150 155 160
 Thr Ser Trp Gln Asp Gly Pro Gly Lys Leu Glu Gln Trp Glu Val Leu
 165 170 175
 Pro Arg Ala Arg Ala Leu Asp Ser Thr Cys Trp Ile Val Ala Cys Gly
 180 185 190
 Gln Ala Arg Leu Pro Glu Glu Leu Arg Asp Glu Arg Lys Gly Pro Thr
 195 200 205
 Gly Ile Gly His Ser Met Val Thr Asn Pro His Gly Glu Val Ile Ala
 210 215 220
 Ser Ala Gly Tyr Glu Pro Glu Met Leu Ile Ala Asp Ile Asp Val Ser
 225 230 235 240
 Gly Leu Ala Lys Ile Arg Glu Ala Leu Pro Val Leu
 245 250

<210> 135
 <211> 1635
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1612)
 <223> RXS00870

<400> 135
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 caacaattca cttcgcagag catttaagga atttacacac atg tct gaa cca caa 115
 Met Ser Glu Pro Gln
 1 5
 acc atc tcg cac tgg att gac ggc gcg att tcc cca tcc act tcc ggc 163
 Thr Ile Ser His Trp Ile Asp Gly Ala Ile Ser Pro Ser Thr Ser Gly
 10 15 20
 aag acc gct cct gtc tac aat cct gca act ggc cag gtc acc gcc aat 211
 Lys Thr Ala Pro Val Tyr Asn Pro Ala Thr Gly Gln Val Thr Ala Asn
 25 30 35
 gtt gcg ctg gct agc cag gaa gag atc gat gcc acc atc gct tct gcc 259
 Val Ala Leu Ala Ser Gln Glu Glu Ile Asp Ala Thr Ile Ala Ser Ala
 40 45 50
 acc aag gct gct aag acg tgg ggc aac ctg tct atc gct aag cgc caa 307
 Thr Lys Ala Ala Lys Thr Trp Gly Asn Leu Ser Ile Ala Lys Arg Gln
 55 60 65
 gct gtg ctt ttc aac ttc cgt gag ctg ctg aat gct cgc aag ggt gag 355
 Ala Val Leu Phe Asn Phe Arg Glu Leu Leu Asn Ala Arg Lys Gly Glu
 70 75 80 85

ctg gcg gag atc atc act gca gag cac ggc aag gtc ttg tcc gat gcc	403
Leu Ala Glu Ile Ile Thr Ala Glu His Gly Lys Val Leu Ser Asp Ala	
90 95 100	
atg ggt gaa atc ctg cgc ggc cag gaa gtc gtg gag ctt gct acc ggt	451
Met Gly Glu Ile Leu Arg Gly Gln Glu Val Val Glu Leu Ala Thr Gly	
105 110 115	
ttc cca cac ctg ctt aaa ggt gcg ttc aac gag aac gtc tcc acc ggc	499
Phe Pro His Leu Leu Lys Gly Ala Phe Asn Glu Asn Val Ser Thr Gly	
120 125 130	
att gat gtg tat tcc ttg aag cag cca ctg ggt gtt gtc ggt atc atc	547
Ile Asp Val Tyr Ser Leu Lys Gln Pro Leu Gly Val Val Gly Ile Ile	
135 140 145	
agc ccg ttc aac ttc cct gcg atg gtg ccg atg tgg ttt ttc cca atc	595
Ser Pro Phe Asn Phe Pro Ala Met Val Pro Met Trp Phe Phe Pro Ile	
150 155 160 165	
gca atc gct gca ggc aac gca gtt att ttg aag cct tca gag aag gat	643
Ala Ile Ala Ala Gly Asn Ala Val Ile Leu Lys Pro Ser Glu Lys Asp	
170 175 180	
cct tcg gca gcg ctg tgg atg gct cag atc tgg aag gaa gct ggt ctt	691
Pro Ser Ala Ala Leu Trp Met Ala Gln Ile Trp Lys Glu Ala Gly Leu	
185 190 195	
cca gac ggc gta ttc aac gtg ctc cag ggc gac aag ctg gct gtt gat	739
Pro Asp Gly Val Phe Asn Val Leu Gln Gly Asp Lys Leu Ala Val Asp	
200 205 210	
ggt ttg ctg aac agc cct gat gtc tct gcg att tcc ttc gtg ggt tcc	787
Gly Leu Leu Asn Ser Pro Asp Val Ser Ala Ile Ser Phe Val Gly Ser	
215 220 225	
acc cca atc gca aag tac atc tac gag act tcc gcg aag aac ggc aag	835
Thr Pro Ile Ala Lys Tyr Ile Tyr Glu Thr Ser Ala Lys Asn Gly Lys	
230 235 240 245	
cgc gtc cag gcg ttg ggc ggc gcg aag aac cac atg ctg gtg ctg cca	883
Arg Val Gln Ala Leu Gly Gly Ala Lys Asn His Met Leu Val Leu Pro	
250 255 260	
gat gct gat ctg gat ctg gtt gcc gat cag gca atc aac gca ggt tac	931
Asp Ala Asp Leu Asp Leu Val Ala Asp Gln Ala Ile Asn Ala Gly Tyr	
265 270 275	
ggc gct gcc ggt gag cgt tgc atg gct gtt tct gtg gtc ttg gct att	979
Gly Ala Ala Gly Glu Arg Cys Met Ala Val Ser Val Val Leu Ala Ile	
280 285 290	
gaa tct gtt gcc gac gag ctc att gag aag atc aag gag cgc atc gac	1027
Glu Ser Val Ala Asp Glu Leu Ile Glu Lys Ile Lys Glu Arg Ile Asp	
295 300 305	
acc ctg cgc atc ggc aac ggt gcc ggc gac gag cag ggc gag ccg cac	1075
Thr Leu Arg Ile Gly Asn Gly Ala Gly Asp Glu Gln Gly Glu Pro His	
310 315 320 325	

ctg ggc cca cta atc acc gac gtc cac cgc gac aag gtc gct tct tat 1123
 Leu Gly Pro Leu Ile Thr Asp Val His Arg Asp Lys Val Ala Ser Tyr
 330 335 340

gtc gac atc gct gag gcc gac ggc gcc aag atc atc gtg gac ggg cgt 1171
 Val Asp Ile Ala Glu Ala Asp Gly Ala Lys Ile Ile Val Asp Gly Arg
 345 350 355

aac tgc gcc gta gac ggg cac gag gag ggc ttc ttc ttc ggc cct acg 1219
 Asn Cys Ala Val Asp Gly His Glu Glu Gly Phe Phe Phe Gly Pro Thr
 360 365 370

ctt atc gac gac atc cca ctc acg ttc cgc gcc tac acc gaa gaa atc 1267
 Leu Ile Asp Asp Ile Pro Leu Thr Phe Arg Ala Tyr Thr Glu Glu Ile
 375 380 385

ttc ggc ccg gtc ctc tct gtc gtt cgt gtc gca tcc ttc gac gag gca 1315
 Phe Gly Pro Val Leu Ser Val Val Arg Val Ala Ser Phe Asp Glu Ala
 390 395 400 405

att gag ctg atc aac tcc ggt gaa ttc ggc aac gga acc gca atc ttc 1363
 Ile Glu Leu Ile Asn Ser Gly Glu Phe Gly Asn Gly Thr Ala Ile Phe
 410 415 420

acc aac gat ggt gga gcg gca cgc cgc ttc cag cat gag atc gaa gtg 1411
 Thr Asn Asp Gly Gly Ala Ala Arg Phe Gln His Glu Ile Glu Val
 425 430 435

ggc atg atc ggc atc aac gta cca atc cca gtg cct gtt gcg tac cac 1459
 Gly Met Ile Gly Ile Asn Val Pro Ile Pro Val Pro Val Ala Tyr His
 440 445 450

tcc ttc ggt ggt tgg aag aac tcc ctc ttc ggt gac gcc aag gca tat 1507
 Ser Phe Gly Gly Trp Lys Asn Ser Leu Phe Gly Asp Ala Lys Ala Tyr
 455 460 465

ggc act caa ggt ttt gat ttc ttc acc agg gaa aag gcg atc acc agc 1555
 Gly Thr Gln Gly Phe Asp Phe Phe Thr Arg Glu Lys Ala Ile Thr Ser
 470 475 480 485

cgt tgg ctc gac cca gca acc cac ggt ggc att aac ctc ggt ttc cca 1603
 Arg Trp Leu Asp Pro Ala Thr His Gly Gly Ile Asn Leu Gly Phe Pro
 490 495 500

cag aac gat taattgaagg agagcacagg act 1635
 Gln Asn Asp

<210> 136

<211> 504

<212> PRT

<213> Corynebacterium glutamicum

<400> 136

Met Ser Glu Pro Gln Thr Ile Ser His Trp Ile Asp Gly Ala Ile Ser
 1 5 10 15

Pro Ser Thr Ser Gly Lys Thr Ala Pro Val Tyr Asn Pro Ala Thr Gly
 20 25 30

Gln Val Thr Ala Asn Val Ala Leu Ala Ser Gln Glu Glu Ile Asp Ala
 35 40 45
 Thr Ile Ala Ser Ala Thr Lys Ala Ala Lys Thr Trp Gly Asn Leu Ser
 50 55 60
 Ile Ala Lys Arg Gln Ala Val Leu Phe Asn Phe Arg Glu Leu Leu Asn
 65 70 75 80
 Ala Arg Lys Gly Glu Leu Ala Glu Ile Ile Thr Ala Glu His Gly Lys
 85 90 95
 Val Leu Ser Asp Ala Met Gly Glu Ile Leu Arg Gly Gln Glu Val Val
 100 105 110
 Glu Leu Ala Thr Gly Phe Pro His Leu Leu Lys Gly Ala Phe Asn Glu
 115 120 125
 Asn Val Ser Thr Gly Ile Asp Val Tyr Ser Leu Lys Gln Pro Leu Gly
 130 135 140
 Val Val Gly Ile Ile Ser Pro Phe Asn Phe Pro Ala Met Val Pro Met
 145 150 155 160
 Trp Phe Phe Pro Ile Ala Ile Ala Ala Gly Asn Ala Val Ile Leu Lys
 165 170 175
 Pro Ser Glu Lys Asp Pro Ser Ala Ala Leu Trp Met Ala Gln Ile Trp
 180 185 190
 Lys Glu Ala Gly Leu Pro Asp Gly Val Phe Asn Val Leu Gln Gly Asp
 195 200 205
 Lys Leu Ala Val Asp Gly Leu Leu Asn Ser Pro Asp Val Ser Ala Ile
 210 215 220
 Ser Phe Val Gly Ser Thr Pro Ile Ala Lys Tyr Ile Tyr Glu Thr Ser
 225 230 235 240
 Ala Lys Asn Gly Lys Arg Val Gln Ala Leu Gly Gly Ala Lys Asn His
 245 250 255
 Met Leu Val Leu Pro Asp Ala Asp Leu Asp Leu Val Ala Asp Gln Ala
 260 265 270
 Ile Asn Ala Gly Tyr Gly Ala Ala Gly Glu Arg Cys Met Ala Val Ser
 275 280 285
 Val Val Leu Ala Ile Glu Ser Val Ala Asp Glu Leu Ile Glu Lys Ile
 290 295 300
 Lys Glu Arg Ile Asp Thr Leu Arg Ile Gly Asn Gly Ala Gly Asp Glu
 305 310 315 320
 Gln Gly Glu Pro His Leu Gly Pro Leu Ile Thr Asp Val His Arg Asp
 325 330 335
 Lys Val Ala Ser Tyr Val Asp Ile Ala Glu Ala Asp Gly Ala Lys Ile
 340 345 350
 Ile Val Asp Gly Arg Asn Cys Ala Val Asp Gly His Glu Glu Gly Phe

355					360					365					
Phe	Phe	Gly	Pro	Thr	Leu	Ile	Asp	Asp	Ile	Pro	Leu	Thr	Phe	Arg	Ala
	370					375					380				
Tyr	Thr	Glu	Glu	Ile	Phe	Gly	Pro	Val	Leu	Ser	Val	Val	Arg	Val	Ala
385					390					395					400
Ser	Phe	Asp	Glu	Ala	Ile	Glu	Leu	Ile	Asn	Ser	Gly	Glu	Phe	Gly	Asn
				405					410					415	
Gly	Thr	Ala	Ile	Phe	Thr	Asn	Asp	Gly	Gly	Ala	Ala	Arg	Arg	Phe	Gln
			420					425					430		
His	Glu	Ile	Glu	Val	Gly	Met	Ile	Gly	Ile	Asn	Val	Pro	Ile	Pro	Val
		435					440					445			
Pro	Val	Ala	Tyr	His	Ser	Phe	Gly	Gly	Trp	Lys	Asn	Ser	Leu	Phe	Gly
	450					455					460				
Asp	Ala	Lys	Ala	Tyr	Gly	Thr	Gln	Gly	Phe	Asp	Phe	Phe	Thr	Arg	Glu
465					470					475					480
Lys	Ala	Ile	Thr	Ser	Arg	Trp	Leu	Asp	Pro	Ala	Thr	His	Gly	Gly	Ile
				485					490					495	
Asn	Leu	Gly	Phe	Pro	Gln	Asn	Asp								
			500												

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<210> 137
<211> 531
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(508)  
<223> RXS02299
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<400> 137																	
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taaaacttgc aggacaaccc ccataaggac accacaggac																	
											atg	ctg	cgc	acc	atc		115
											Met	Leu	Arg	Thr	Ile		
											1				5		
ctc gga agt aag att cac cga gcc act gtc act caa gct gat cta gat																	163
Leu	Gly	Ser	Lys	Ile	His	Arg	Ala	Thr	Val	Thr	Gln	Ala	Asp	Leu	Asp		
				10					15					20			
tat gtt ggc tct gta acc atc gac gcc gac ctg gtt cac gcc gcc gga																	211
Tyr	Val	Gly	Ser	Val	Thr	Ile	Asp	Ala	Asp	Leu	Val	His	Ala	Ala	Gly		
			25				30						35				
ttg atc gaa ggc gaa aaa gtt gcc atc gta gac atc acc aac ggc gct																	259
Leu	Ile	Glu	Gly	Glu	Lys	Val	Ala	Ile	Val	Asp	Ile	Thr	Asn	Gly	Ala		
		40					45					50					
cgt ctg gaa act tat gtc att gtg ggc gac gcc gga acg ggc aat att																	307
Arg	Leu	Glu	Thr	Tyr	Val	Ile	Val	Gly	Asp	Ala	Gly	Thr	Gly	Asn	Ile		

55	60	65	
tgc atc aat ggt gcc gct gca cac ctt att aat cct ggc gat ctt gtg			355
Cys Ile Asn Gly Ala Ala Ala His Leu Ile Asn Pro Gly Asp Leu Val			
70	75	80	85
atc atc atg agc tac ctt cag gca act gat gcg gaa gcc aag gcg tat			403
Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala Glu Ala Lys Ala Tyr			
	90	95	100
gag cca aag att gtg cac gtg gac gcc gac aac cgc atc gtt gcg ctc			451
Glu Pro Lys Ile Val His Val Asp Ala Asp Asn Arg Ile Val Ala Leu			
	105	110	115
ggc aac gat ctt gcg gaa gca cta cct gga tcc ggg ctt ttg acg tcg			499
Gly Asn Asp Leu Ala Glu Ala Leu Pro Gly Ser Gly Leu Leu Thr Ser			
	120	125	130
aga agc att tagcggtttta gctcgccaat att			531
Arg Ser Ile			
135			

<210> 138

<211> 136

<212> PRT

<213> Corynebacterium glutamicum

<400> 138

Met Leu Arg Thr Ile Leu Gly Ser Lys Ile His Arg Ala Thr Val Thr			
1	5	10	15
Gln Ala Asp Leu Asp Tyr Val Gly Ser Val Thr Ile Asp Ala Asp Leu			
	20	25	30
Val His Ala Ala Gly Leu Ile Glu Gly Glu Lys Val Ala Ile Val Asp			
	35	40	45
Ile Thr Asn Gly Ala Arg Leu Glu Thr Tyr Val Ile Val Gly Asp Ala			
	50	55	60
Gly Thr Gly Asn Ile Cys Ile Asn Gly Ala Ala Ala His Leu Ile Asn			
	65	70	75
Pro Gly Asp Leu Val Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala			
	85	90	95
Glu Ala Lys Ala Tyr Glu Pro Lys Ile Val His Val Asp Ala Asp Asn			
	100	105	110
Arg Ile Val Ala Leu Gly Asn Asp Leu Ala Glu Ala Leu Pro Gly Ser			
	115	120	125
Gly Leu Leu Thr Ser Arg Ser Ile			
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<210> 139

<211> 1053

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1030)

<223> RXA01561

<400> 139

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taataatggt catttttcac gagttctaga aaacacaggc atg ctc acc ctc aac 115
                                         Met Leu Thr Leu Asn
                                         1                               5

gat gtc atc acc gcc caa caa cga acc gcc cct cat gtt cga cga acg 163
Asp Val Ile Thr Ala Gln Gln Arg Thr Ala Pro His Val Arg Arg Thr
                               10                               15                               20

cca ctt ttc gaa gca gac ccc atc gac ggc aca caa atc tgg atc aaa 211
Pro Leu Phe Glu Ala Asp Pro Ile Asp Gly Thr Gln Ile Trp Ile Lys
                               25                               30                               35

gca gag ttc ctc caa aag tgc ggc gtg ttc aaa acg cgt gga gca ttc 259
Ala Glu Phe Leu Gln Lys Cys Gly Val Phe Lys Thr Arg Gly Ala Phe
                               40                               45                               50

aac cgc cag ctc gca gct tcg gaa aac gga cta ctc gac cca acg gtt 307
Asn Arg Gln Leu Ala Ala Ser Glu Asn Gly Leu Leu Asp Pro Thr Val
                               55                               60                               65

ggc atc gtc gcg gca tca ggc gga aac gca gga ctc gca aat gct ttt 355
Gly Ile Val Ala Ala Ser Gly Gly Asn Ala Gly Leu Ala Asn Ala Phe
                               70                               75                               80                               85

gcc gca gca tcc tta agc gtt ccc gcc acg gta ttg gtg ccc gaa act 403
Ala Ala Ala Ser Leu Ser Val Pro Ala Thr Val Leu Val Pro Glu Thr
                               90                               95                               100

gcc cca caa gta aaa gtt gat cgc ctc aag caa tac ggt gca acc gtg 451
Ala Pro Gln Val Lys Val Asp Arg Leu Lys Gln Tyr Gly Ala Thr Val
                               105                               110                               115

caa caa atc gga tct gaa tat gcg gaa gca ttt gag gca gct caa acc 499
Gln Gln Ile Gly Ser Glu Tyr Ala Glu Ala Phe Glu Ala Ala Gln Thr
                               120                               125                               130

ttt gag tcg gaa act ggt gct ctg ttt tgc cac gcc tac gac cag ccc 547
Phe Glu Ser Glu Thr Gly Ala Leu Phe Cys His Ala Tyr Asp Gln Pro
                               135                               140                               145

gac atc gca gct gga gca ggc gtc att ggg cta gaa att gtc gaa gat 595
Asp Ile Ala Ala Gly Ala Gly Val Ile Gly Leu Glu Ile Val Glu Asp
                               150                               155                               160                               165

ctt ccc gac gtt gac acc atc gtg gtt gct gtc ggt ggc ggt gga ctc 643
Leu Pro Asp Val Asp Thr Ile Val Val Ala Val Gly Gly Gly Gly Leu
                               170                               175                               180

tat gca gga atc gca gcc gtc gta gca gcc cac gac atc aaa gtg gtg 691
Tyr Ala Gly Ile Ala Ala Val Val Ala Ala His Asp Ile Lys Val Val
                               185                               190                               195

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Ala Val Glu Pro Ser Lys Ile Pro Thr Leu His Asn Ser Leu Ile Ala
      200                      205                      210

ggc caa cca gtc gat gtg aac gtt tct ggt atc gcg gca gat tct ttg 787
Gly Gln Pro Val Asp Val Asn Val Ser Gly Ile Ala Ala Asp Ser Leu
      215                      220                      225

ggg gct cgc caa att gga cga gaa gcc ttt gac atc gca act gcc cat 835
Gly Ala Arg Gln Ile Gly Arg Glu Ala Phe Asp Ile Ala Thr Ala His
      230                      235                      240                      245

ccc cca ata ggc gtc cta gtg gac gat gaa gca atc atc gca gct cga 883
Pro Pro Ile Gly Val Leu Val Asp Asp Glu Ala Ile Ile Ala Ala Arg
      250                      255                      260

cgc cac ctc tgg gac aac tac cgc atc cct gcc gag cat ggc gct gcc 931
Arg His Leu Trp Asp Asn Tyr Arg Ile Pro Ala Glu His Gly Ala Ala
      265                      270                      275

gca gca ctc gcc tct ctt acc agt gga gca tac aaa cct gca gca gat 979
Ala Ala Leu Ala Ser Leu Thr Ser Gly Ala Tyr Lys Pro Ala Ala Asp
      280                      285                      290

gaa aaa gtg gca gtc att gtg tgc gga gcg aac act gac ctc aca aca 1027
Glu Lys Val Ala Val Ile Val Cys Gly Ala Asn Thr Asp Leu Thr Thr
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ctg tgatgtgatt tcaaacgatc aca 1053
Leu
310

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<210> 140
<211> 310
<212> PRT
<213> Corynebacterium glutamicum

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Gln Ile Trp Ile Lys Ala Glu Phe Leu Gln Lys Cys Gly Val Phe Lys
      35                      40                      45

Thr Arg Gly Ala Phe Asn Arg Gln Leu Ala Ala Ser Glu Asn Gly Leu
      50                      55                      60

Leu Asp Pro Thr Val Gly Ile Val Ala Ala Ser Gly Gly Asn Ala Gly
      65                      70                      75                      80

Leu Ala Asn Ala Phe Ala Ala Ala Ser Leu Ser Val Pro Ala Thr Val
      85                      90                      95

Leu Val Pro Glu Thr Ala Pro Gln Val Lys Val Asp Arg Leu Lys Gln
      100                      105                      110

Tyr Gly Ala Thr Val Gln Gln Ile Gly Ser Glu Tyr Ala Glu Ala Phe

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115					120					125						
Glu	Ala	Ala	Gln	Thr	Phe	Glu	Ser	Glu	Thr	Gly	Ala	Leu	Phe	Cys	His	
130					135					140						
Ala	Tyr	Asp	Gln	Pro	Asp	Ile	Ala	Ala	Gly	Ala	Gly	Val	Ile	Gly	Leu	
145					150					155					160	
Glu	Ile	Val	Glu	Asp	Leu	Pro	Asp	Val	Asp	Thr	Ile	Val	Val	Ala	Val	
165					170					175						
Gly	Gly	Gly	Gly	Leu	Tyr	Ala	Gly	Ile	Ala	Ala	Val	Val	Ala	Ala	His	
180					185					190						
Asp	Ile	Lys	Val	Val	Ala	Val	Glu	Pro	Ser	Lys	Ile	Pro	Thr	Leu	His	
195					200					205						
Asn	Ser	Leu	Ile	Ala	Gly	Gln	Pro	Val	Asp	Val	Asn	Val	Ser	Gly	Ile	
210					215					220						
Ala	Ala	Asp	Ser	Leu	Gly	Ala	Arg	Gln	Ile	Gly	Arg	Glu	Ala	Phe	Asp	
225					230					235					240	
Ile	Ala	Thr	Ala	His	Pro	Pro	Ile	Gly	Val	Leu	Val	Asp	Asp	Glu	Ala	
245					250					255						
Ile	Ile	Ala	Ala	Arg	Arg	His	Leu	Trp	Asp	Asn	Tyr	Arg	Ile	Pro	Ala	
260					265					270						
Glu	His	Gly	Ala	Ala	Ala	Ala	Leu	Ala	Ser	Leu	Thr	Ser	Gly	Ala	Tyr	
275					280					285						
Lys	Pro	Ala	Ala	Asp	Glu	Lys	Val	Ala	Val	Ile	Val	Cys	Gly	Ala	Asn	
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Thr	Asp	Leu	Thr	Thr	Leu											
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<211> 1470

<212> DNA

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<220>

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<222> (101)..(1447)

<223> RXA01850

<400> 141

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				Met	Ala	Ile	Ser	Val	
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gtt	gat	cta	ttt	agc	atc	ggg	atc	gga	cca	tca	tcc	tca	cat	acc	gtc	163
Val	Asp	Leu	Phe	Ser	Ile	Gly	Ile	Gly	Pro	Ser	Ser	Ser	His	Thr	Val	
				10				15						20		

ggc	ccc	atg	aga	gcc	gcc	ctc	acg	tat	atc	tct	gaa	ttt	ccc	agc	tcg	211
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Gly	Pro	Met	Arg	Ala	Ala	Leu	Thr	Tyr	Ile	Ser	Glu	Phe	Pro	Ser	Ser		
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cat	gtc	gat	atc	acg	ttg	cac	gga	tcc	ctt	gcc	gcc	acc	ggg	aaa	ggc	259	
His	Val	Asp	Ile	Thr	Leu	His	Gly	Ser	Leu	Ala	Ala	Thr	Gly	Lys	Gly		
		40					45					50					
cac	tgc	act	gac	cgg	gcg	gta	tta	ctg	ggg	ctg	gtg	gga	tgg	gaa	cca	307	
His	Cys	Thr	Asp	Arg	Ala	Val	Leu	Leu	Gly	Leu	Val	Gly	Trp	Glu	Pro		
		55				60					65						
acg	ata	gtt	ccc	att	gat	gct	gca	ccc	tca	ccc	ggc	gcg	ccg	att	cct	355	
Thr	Ile	Val	Pro	Ile	Asp	Ala	Ala	Pro	Ser	Pro	Gly	Ala	Pro	Ile	Pro		
		70			75				80						85		
gcg	aaa	ggg	tct	gtg	aac	ggg	cca	aag	gga	acg	gtg	tcg	tat	tcc	ctg	403	
Ala	Lys	Gly	Ser	Val	Asn	Gly	Pro	Lys	Gly	Thr	Val	Ser	Tyr	Ser	Leu		
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Thr	Phe	Asp	Pro	His	Pro	Leu	Pro	Glu	His	Pro	Asn	Ala	Val	Thr	Phe		
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aaa	gga	tca	acc	aca	agg	act	tat	ttg	tcg	gtg	ggg	ggg	ggg	ttc	att	499	
Lys	Gly	Ser	Thr	Thr	Arg	Thr	Tyr	Leu	Ser	Val	Gly	Gly	Gly	Phe	Ile		
			120					125				130					
atg	acg	ttg	gag	gat	ttc	cgg	aag	ctg	gac	gat	atc	gga	tca	ggg	gtg	547	
Met	Thr	Leu	Glu	Asp	Phe	Arg	Lys	Leu	Asp	Asp	Ile	Gly	Ser	Gly	Val		
		135				140					145						
tca	acc	att	cat	cca	gag	gca	gag	gtg	cct	tgt	cct	ttt	cag	aag	agt	595	
Ser	Thr	Ile	His	Pro	Glu	Ala	Glu	Val	Pro	Cys	Pro	Phe	Gln	Lys	Ser		
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tcc	caa	tta	ctc	gca	tat	ggg	cgc	gat	ttt	gcg	gag	gtc	atg	aag	gat	643	
Ser	Gln	Leu	Leu	Ala	Tyr	Gly	Arg	Asp	Phe	Ala	Glu	Val	Met	Lys	Asp		
				170					175					180			
aat	gag	cgc	tta	atc	cac	ggg	gat	ctt	ggc	aca	gtg	gat	gcc	cat	ttg	691	
Asn	Glu	Arg	Leu	Ile	His	Gly	Asp	Leu	Gly	Thr	Val	Asp	Ala	His	Leu		
			185					190					195				
gat	cga	gtg	tgg	cag	att	atg	cag	gag	tgc	gtg	gca	caa	ggc	atc	gca	739	
Asp	Arg	Val	Trp	Gln	Ile	Met	Gln	Glu	Cys	Val	Ala	Gln	Gly	Ile	Ala		
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acg	ccg	ggg	att	tta	ccg	ggg	ggg	ttg	aat	gtg	caa	cgt	cgg	gcg	ccg	787	
Thr	Pro	Gly	Ile	Leu	Pro	Gly	Gly	Leu	Asn	Val	Gln	Arg	Arg	Ala	Pro		
		215				220					225						
cag	gta	cac	gcg	ctg	att	agc	aac	ggg	gat	acg	tgt	gag	ctg	ggg	gct	835	
Gln	Val	His	Ala	Leu	Ile	Ser	Asn	Gly	Asp	Thr	Cys	Glu	Leu	Gly	Ala		
				235						240					245		
gat	ctt	gat	gct	gtg	gag	tgg	gtg	aat	ctg	tac	gcc	ttg	gcg	gtg	aat	883	
Asp	Leu	Asp	Ala	Val	Glu	Trp	Val	Asn	Leu	Tyr	Ala	Leu	Ala	Val	Asn		
				250				255						260			
gaa	gaa	aac	gcc	gct	ggg	ggg	cgt	gtg	gtt	act	gct	ccg	act	aat	ggg	931	
Glu	Glu	Asn	Ala	Ala	Gly	Gly	Arg	Val	Val	Thr	Ala	Pro	Thr	Asn	Gly		

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gct gcg ggg att att ccg gcg gtg atg cac tat gcg cgg gat ttt ttg			979
Ala Ala Gly Ile Ile Pro Ala Val Met His Tyr Ala Arg Asp Phe Leu			
280	285	290	
aca ggt ttt ggg gcg gag cag gcg cgg acg ttt ttg tat acc gcg ggt			1027
Thr Gly Phe Gly Ala Glu Gln Ala Arg Thr Phe Leu Tyr Thr Ala Gly			
295	300	305	
gcg gtg ggc atc atc att aag gaa aat gcc tcg atc tct ggc gcg gag			1075
Ala Val Gly Ile Ile Ile Lys Glu Asn Ala Ser Ile Ser Gly Ala Glu			
310	315	320	325
gtg ggg tgt cag ggt gag gtt ggt tca gcg tcc gcg atg gcg gct gcc			1123
Val Gly Cys Gln Gly Glu Val Gly Ser Ala Ser Ala Met Ala Ala Ala			
	330	335	340
ggg ttg tgt gca gtc tta ggt ggt tct ccg caa cag gtg gaa aac gcc			1171
Gly Leu Cys Ala Val Leu Gly Gly Ser Pro Gln Gln Val Glu Asn Ala			
	345	350	355
gcg gag att gcg ttg gag cac aat ttg gga ttg acg tgc gat ccg gtg			1219
Ala Glu Ile Ala Leu Glu His Asn Leu Gly Leu Thr Cys Asp Pro Val			
	360	365	370
ggc ggg tta gtg cag att ccg tgt att gaa cgc aac gct att gct gcc			1267
Gly Gly Leu Val Gln Ile Pro Cys Ile Glu Arg Asn Ala Ile Ala Ala			
	375	380	385
atg aag tcc atc aat gcg gca agg ctt gcc ccg att ggt gat ggc aac			1315
Met Lys Ser Ile Asn Ala Ala Arg Leu Ala Arg Ile Gly Asp Gly Asn			
	390	395	400
aat cgc gtg agt ttg gat gat gtg gtg gtc acg atg gct gcc acc ggc			1363
Asn Arg Val Ser Leu Asp Asp Val Val Val Thr Met Ala Ala Thr Gly			
	410	415	420
cgg gac atg ctg acc aaa tat aag gaa acg tcc ctt ggt ggt ttg gca			1411
Arg Asp Met Leu Thr Lys Tyr Lys Glu Thr Ser Leu Gly Gly Leu Ala			
	425	430	435
acc acc ttg ggc ttc ccg gtg tcg atg acg gag tgt tagcgggtacg			1457
Thr Thr Leu Gly Phe Pro Val Ser Met Thr Glu Cys			
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gctttaacac ggc			1470

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<211> 449

<212> PRT

<213> Corynebacterium glutamicum

<400> 142

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Ser	Ser	His	Thr	Val	Gly	Pro	Met	Arg	Ala	Ala	Leu	Thr	Tyr	Ile	Ser
		20					25					30			

Glu Phe Pro Ser Ser His Val Asp Ile Thr Leu His Gly Ser Leu Ala
 35 40 45
 Ala Thr Gly Lys Gly His Cys Thr Asp Arg Ala Val Leu Leu Gly Leu
 50 55 60
 Val Gly Trp Glu Pro Thr Ile Val Pro Ile Asp Ala Ala Pro Ser Pro
 65 70 75 80
 Gly Ala Pro Ile Pro Ala Lys Gly Ser Val Asn Gly Pro Lys Gly Thr
 85 90 95
 Val Ser Tyr Ser Leu Thr Phe Asp Pro His Pro Leu Pro Glu His Pro
 100 105 110
 Asn Ala Val Thr Phe Lys Gly Ser Thr Thr Arg Thr Tyr Leu Ser Val
 115 120 125
 Gly Gly Gly Phe Ile Met Thr Leu Glu Asp Phe Arg Lys Leu Asp Asp
 130 135 140
 Ile Gly Ser Gly Val Ser Thr Ile His Pro Glu Ala Glu Val Pro Cys
 145 150 155 160
 Pro Phe Gln Lys Ser Ser Gln Leu Leu Ala Tyr Gly Arg Asp Phe Ala
 165 170 175
 Glu Val Met Lys Asp Asn Glu Arg Leu Ile His Gly Asp Leu Gly Thr
 180 185 190
 Val Asp Ala His Leu Asp Arg Val Trp Gln Ile Met Gln Glu Cys Val
 195 200 205
 Ala Gln Gly Ile Ala Thr Pro Gly Ile Leu Pro Gly Gly Leu Asn Val
 210 215 220
 Gln Arg Arg Ala Pro Gln Val His Ala Leu Ile Ser Asn Gly Asp Thr
 225 230 235 240
 Cys Glu Leu Gly Ala Asp Leu Asp Ala Val Glu Trp Val Asn Leu Tyr
 245 250 255
 Ala Leu Ala Val Asn Glu Glu Asn Ala Ala Gly Gly Arg Val Val Thr
 260 265 270
 Ala Pro Thr Asn Gly Ala Ala Gly Ile Ile Pro Ala Val Met His Tyr
 275 280 285
 Ala Arg Asp Phe Leu Thr Gly Phe Gly Ala Glu Gln Ala Arg Thr Phe
 290 295 300
 Leu Tyr Thr Ala Gly Ala Val Gly Ile Ile Ile Lys Glu Asn Ala Ser
 305 310 315 320
 Ile Ser Gly Ala Glu Val Gly Cys Gln Gly Glu Val Gly Ser Ala Ser
 325 330 335
 Ala Met Ala Ala Ala Gly Leu Cys Ala Val Leu Gly Gly Ser Pro Gln
 340 345 350
 Gln Val Glu Asn Ala Ala Glu Ile Ala Leu Glu His Asn Leu Gly Leu

355	360	365
Thr Cys Asp Pro Val Gly Gly Leu Val Gln Ile Pro Cys Ile Glu Arg		
370	375	380
Asn Ala Ile Ala Ala Met Lys Ser Ile Asn Ala Ala Arg Leu Ala Arg		
385	390	395
Ile Gly Asp Gly Asn Asn Arg Val Ser Leu Asp Asp Val Val Val Thr		
	405	410
Met Ala Ala Thr Gly Arg Asp Met Leu Thr Lys Tyr Lys Glu Thr Ser		
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Leu Gly Gly Leu Ala Thr Thr Leu Gly Phe Pro Val Ser Met Thr Glu		
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		445

Cys

<210> 143
 <211> 1425
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1402)
 <223> RXA00580

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 Met Thr Asp Ala His
 1 5
 caa gcg gac gat gtc cgt tac cag cca ctg aac gag ctt gat cct gag 163
 Gln Ala Asp Asp Val Arg Tyr Gln Pro Leu Asn Glu Leu Asp Pro Glu
 10 15 20
 gtg gct gct gcc atc gct ggg gaa ctt gcc cgt caa cgc gat aca tta 211
 Val Ala Ala Ala Ile Ala Gly Glu Leu Ala Arg Gln Arg Asp Thr Leu
 25 30 35
 gag atg atc gcg tct gag aac ttc gtt ccc cgt tct gtt ttg cag gcg 259
 Glu Met Ile Ala Ser Glu Asn Phe Val Pro Arg Ser Val Leu Gln Ala
 40 45 50
 cag ggt tct gtt ctt acc aat aag tat gcc gag ggt tac cct ggc cgc 307
 Gln Gly Ser Val Leu Thr Asn Lys Tyr Ala Glu Gly Tyr Pro Gly Arg
 55 60 65
 cgt tac tac ggt ggt tgc gaa caa gtt gac atc att gag gat ctt gca 355
 Arg Tyr Tyr Gly Gly Cys Glu Gln Val Asp Ile Ile Glu Asp Leu Ala
 70 75 80 85
 cgt gat cgt gcg aag gct ctc ttc ggt gca gag ttc gcc aat gtt cag 403
 Arg Asp Arg Ala Lys Ala Leu Phe Gly Ala Glu Phe Ala Asn Val Gln
 90 95 100

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Pro	His	Ser	Gly	Ala	Gln	Ala	Asn	Ala	Ala	Val	Leu	Met	Thr	Leu	Ala	
			105					110					115			
gag	cca	ggc	gac	aag	atc	atg	ggt	ctg	tct	ttg	gct	cat	ggt	ggt	cac	499
Glu	Pro	Gly	Asp	Lys	Ile	Met	Gly	Leu	Ser	Leu	Ala	His	Gly	Gly	His	
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ttg	acc	cac	gga	atg	aag	ttg	aac	ttc	tcc	gga	aag	ctg	tac	gag	gtt	547
Leu	Thr	His	Gly	Met	Lys	Leu	Asn	Phe	Ser	Gly	Lys	Leu	Tyr	Glu	Val	
	135					140					145					
gtt	gcg	tac	ggt	gtt	gat	cct	gag	acc	atg	cgt	gtt	gat	atg	gat	cag	595
Val	Ala	Tyr	Gly	Val	Asp	Pro	Glu	Thr	Met	Arg	Val	Asp	Met	Asp	Gln	
150					155					160					165	
gtt	cgt	gag	att	gct	ctg	aag	gag	cag	cca	aag	gta	att	atc	gct	ggc	643
Val	Arg	Glu	Ile	Ala	Leu	Lys	Glu	Gln	Pro	Lys	Val	Ile	Ile	Ala	Gly	
				170					175						180	
tgg	tct	gca	tac	cct	cgc	cac	ctt	gat	ttc	gag	gct	ttc	cag	tct	att	691
Trp	Ser	Ala	Tyr	Pro	Arg	His	Leu	Asp	Phe	Glu	Ala	Phe	Gln	Ser	Ile	
			185					190					195			
gct	gcg	gaa	gtt	ggc	gcg	aag	ctg	tgg	gtc	gat	atg	gct	cac	ttc	gct	739
Ala	Ala	Glu	Val	Gly	Ala	Lys	Leu	Trp	Val	Asp	Met	Ala	His	Phe	Ala	
		200					205					210				
ggt	ctt	gtt	gct	gct	ggt	ttg	cac	cca	agc	cca	gtt	cct	tac	tct	gat	787
Gly	Leu	Val	Ala	Ala	Gly	Leu	His	Pro	Ser	Pro	Val	Pro	Tyr	Ser	Asp	
	215					220					225					
gtt	gtt	tct	tcc	act	gtc	cac	aag	act	ttg	ggt	gga	cct	cgt	tcc	ggc	835
Val	Val	Ser	Ser	Thr	Val	His	Lys	Thr	Leu	Gly	Gly	Pro	Arg	Ser	Gly	
230					235					240					245	
atc	att	ctg	gct	aag	cag	gag	tac	gcg	aag	aag	ctg	aac	tct	tcc	gta	883
Ile	Ile	Leu	Ala	Lys	Gln	Glu	Tyr	Ala	Lys	Lys	Leu	Asn	Ser	Ser	Val	
				250					255					260		
ttc	cca	ggt	cag	cag	ggt	ggt	cct	ttg	atg	cac	gca	gtt	gct	gcg	aag	931
Phe	Pro	Gly	Gln	Gln	Gly	Gly	Pro	Leu	Met	His	Ala	Val	Ala	Ala	Lys	
			265				270						275			
gct	act	tct	ttg	aag	att	gct	ggc	act	gag	cag	ttc	cgt	gac	cgt	cag	979
Ala	Thr	Ser	Leu	Lys	Ile	Ala	Gly	Thr	Glu	Gln	Phe	Arg	Asp	Arg	Gln	
		280				285						290				
gct	cgc	acg	ttg	gag	ggt	gct	cgc	att	ctt	gct	gag	cgt	ctg	act	gct	1027
Ala	Arg	Thr	Leu	Glu	Gly	Ala	Arg	Ile	Leu	Ala	Glu	Arg	Leu	Thr	Ala	
	295					300					305					
tct	gat	gcg	aag	gcc	gct	ggc	gtg	gat	gtc	ttg	acc	ggt	ggc	act	gat	1075
Ser	Asp	Ala	Lys	Ala	Ala	Gly	Val	Asp	Val	Leu	Thr	Gly	Gly	Thr	Asp	
310					315					320					325	
gtg	cac	ttg	gtt	ttg	gct	gat	ctg	cgt	aac	tcc	cag	atg	gat	ggc	cag	1123
Val	His	Leu	Val	Leu	Ala	Asp	Leu	Arg	Asn	Ser	Gln	Met	Asp	Gly	Gln	
				330					335					340		

cag gcg gaa gat ctg ctg cac gag gtt ggt atc act gtg aac cgt aac 1171
 Gln Ala Glu Asp Leu Leu His Glu Val Gly Ile Thr Val Asn Arg Asn
 345 350 355
 gcg gtt cct ttc gat cct cgt cca cca atg gtt act tct ggt ctg cgt 1219
 Ala Val Pro Phe Asp Pro Arg Pro Pro Met Val Thr Ser Gly Leu Arg
 360 365 370
 att ggt act cct gcg ctg gct acc cgt ggt ttc gat att cct gca ttc 1267
 Ile Gly Thr Pro Ala Leu Ala Thr Arg Gly Phe Asp Ile Pro Ala Phe
 375 380 385
 act gag gtt gca gac atc att ggt act gct ttg gct aat ggt aag tcc 1315
 Thr Glu Val Ala Asp Ile Ile Gly Thr Ala Leu Ala Asn Gly Lys Ser
 390 395 400 405
 gca gac att gag tct ctg cgt ggc cgt gta gca aag ctt gct gca gat 1363
 Ala Asp Ile Glu Ser Leu Arg Gly Arg Val Ala Lys Leu Ala Ala Asp
 410 415 420
 tac cca ctg tat gag ggc ttg gaa gac tgg acc atc gtc taagtttttc 1412
 Tyr Pro Leu Tyr Glu Gly Leu Glu Asp Trp Thr Ile Val
 425 430
 tttgagtttt cat 1425

<210> 144

<211> 434

<212> PRT

<213> Corynebacterium glutamicum

<400> 144

Met Thr Asp Ala His Gln Ala Asp Asp Val Arg Tyr Gln Pro Leu Asn
 1 5 10 15
 Glu Leu Asp Pro Glu Val Ala Ala Ala Ile Ala Gly Glu Leu Ala Arg
 20 25 30
 Gln Arg Asp Thr Leu Glu Met Ile Ala Ser Glu Asn Phe Val Pro Arg
 35 40 45
 Ser Val Leu Gln Ala Gln Gly Ser Val Leu Thr Asn Lys Tyr Ala Glu
 50 55 60
 Gly Tyr Pro Gly Arg Arg Tyr Tyr Gly Gly Cys Glu Gln Val Asp Ile
 65 70 75 80
 Ile Glu Asp Leu Ala Arg Asp Arg Ala Lys Ala Leu Phe Gly Ala Glu
 85 90 95
 Phe Ala Asn Val Gln Pro His Ser Gly Ala Gln Ala Asn Ala Ala Val
 100 105 110
 Leu Met Thr Leu Ala Glu Pro Gly Asp Lys Ile Met Gly Leu Ser Leu
 115 120 125
 Ala His Gly Gly His Leu Thr His Gly Met Lys Leu Asn Phe Ser Gly
 130 135 140
 Lys Leu Tyr Glu Val Val Ala Tyr Gly Val Asp Pro Glu Thr Met Arg

145		150		155		160
Val Asp Met Asp Gln Val Arg Glu Ile Ala Leu Lys Glu Gln Pro Lys						
	165			170		175
Val Ile Ile Ala Gly Trp Ser Ala Tyr Pro Arg His Leu Asp Phe Glu						
	180			185		190
Ala Phe Gln Ser Ile Ala Ala Glu Val Gly Ala Lys Leu Trp Val Asp						
	195			200		205
Met Ala His Phe Ala Gly Leu Val Ala Ala Gly Leu His Pro Ser Pro						
	210			215		220
Val Pro Tyr Ser Asp Val Val Ser Ser Thr Val His Lys Thr Leu Gly						
	225			230		235
Gly Pro Arg Ser Gly Ile Ile Leu Ala Lys Gln Glu Tyr Ala Lys Lys						
	245			250		255
Leu Asn Ser Ser Val Phe Pro Gly Gln Gln Gly Gly Pro Leu Met His						
	260			265		270
Ala Val Ala Ala Lys Ala Thr Ser Leu Lys Ile Ala Gly Thr Glu Gln						
	275			280		285
Phe Arg Asp Arg Gln Ala Arg Thr Leu Glu Gly Ala Arg Ile Leu Ala						
	290			295		300
Glu Arg Leu Thr Ala Ser Asp Ala Lys Ala Ala Gly Val Asp Val Leu						
	305			310		315
Thr Gly Gly Thr Asp Val His Leu Val Leu Ala Asp Leu Arg Asn Ser						
	325			330		335
Gln Met Asp Gly Gln Gln Ala Glu Asp Leu Leu His Glu Val Gly Ile						
	340			345		350
Thr Val Asn Arg Asn Ala Val Pro Phe Asp Pro Arg Pro Pro Met Val						
	355			360		365
Thr Ser Gly Leu Arg Ile Gly Thr Pro Ala Leu Ala Thr Arg Gly Phe						
	370			375		380
Asp Ile Pro Ala Phe Thr Glu Val Ala Asp Ile Ile Gly Thr Ala Leu						
	385			390		395
Ala Asn Gly Lys Ser Ala Asp Ile Glu Ser Leu Arg Gly Arg Val Ala						
	405			410		415
Lys Leu Ala Ala Asp Tyr Pro Leu Tyr Glu Gly Leu Glu Asp Trp Thr						
	420			425		430
Ile Val						

<210> 145

<211> 401

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(378)

<223> RXA01821

<400> 145

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cga aac agc caa ggc aaa tgg tgc cca agt acg cga tca cca aaa aat 48
Arg Asn Ser Gln Gly Lys Trp Cys Pro Ser Thr Arg Ser Pro Lys Asn
  1             5             10             15

acc agc atc gaa gac aac ggc gat cac gta gtc atc caa gca ggc gaa 96
Thr Ser Ile Glu Asp Asn Gly Asp His Val Val Ile Gln Ala Gly Glu
      20             25             30

gaa acc aca atc gtg gac cgc gtt atc gtc acc acc ggc agc tgg aca 144
Glu Thr Thr Ile Val Asp Arg Val Ile Val Thr Thr Gly Ser Trp Thr
      35             40             45

agc gag ctc gtg ccc tcc atc gcg cca ctg ctt gaa gtg cga cgc cta 192
Ser Glu Leu Val Pro Ser Ile Ala Pro Leu Leu Glu Val Arg Arg Leu
      50             55             60

gtg ctc acc tgg ttc ctg ccc aac aat cca gtg gac ttc caa ccg gaa 240
Val Leu Thr Trp Phe Leu Pro Asn Asn Pro Val Asp Phe Gln Pro Glu
      65             70             75             80

aac ctg cca tgc ttc atc cgt gac cgt gat ggc ttc cac gta ttt gga 288
Asn Leu Pro Cys Phe Ile Arg Asp Arg Asp Gly Phe His Val Phe Gly
      85             90             95

gca cca tgc gtc gat ggg tac agc atc aaa att gcc gga ttg gat gag 336
Ala Pro Cys Val Asp Gly Tyr Ser Ile Lys Ile Ala Gly Leu Asp Glu
      100             105             110

tgg ggc gtt cca tta agc ctc gat cca ccg atg tgc cct cgg 378
Trp Gly Val Pro Leu Ser Leu Asp Pro Pro Met Cys Pro Arg
      115             120             125

tgatgtcctg atccccggttc cgg 401

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<210> 146

<211> 126

<212> PRT

<213> Corynebacterium glutamicum

<400> 146

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Arg Asn Ser Gln Gly Lys Trp Cys Pro Ser Thr Arg Ser Pro Lys Asn
  1             5             10             15

Thr Ser Ile Glu Asp Asn Gly Asp His Val Val Ile Gln Ala Gly Glu
      20             25             30

Glu Thr Thr Ile Val Asp Arg Val Ile Val Thr Thr Gly Ser Trp Thr
      35             40             45

Ser Glu Leu Val Pro Ser Ile Ala Pro Leu Leu Glu Val Arg Arg Leu
      50             55             60

Val Leu Thr Trp Phe Leu Pro Asn Asn Pro Val Asp Phe Gln Pro Glu

```

65					70					75					80
Asn	Leu	Pro	Cys	Phe	Ile	Arg	Asp	Arg	Asp	Gly	Phe	His	Val	Phe	Gly
				85					90					95	
Ala	Pro	Cys	Val	Asp	Gly	Tyr	Ser	Ile	Lys	Ile	Ala	Gly	Leu	Asp	Glu
			100					105					110		
Trp	Gly	Val	Pro	Leu	Ser	Leu	Asp	Pro	Pro	Met	Cys	Pro	Arg		
		115					120					125			

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<210> 147
<211> 488
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(478)
<223> RXN02263
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<400> 147																	
cctgggcaac ccaagtgtat gaaaacgccc tggaaaaagg cgctcggcacc acattgaacc																	60
tgtgggaatc acccgcaactg gcttgagaga agaaacaaca atg aaa att gcg gta																	115
Met Lys Ile Ala Val																	5
1																	
atc ggc ctt gga tca acc ggc tcc atg gca ctg tgg cac tta agt aac																	163
Ile Gly Leu Gly Ser Thr Gly Ser Met Ala Leu Trp His Leu Ser Asn																	20
10 15																	
atc cca ggt gta gag gcc atc ggc ttt gaa caa ttc ggc atc tcc cat																	211
Ile Pro Gly Val Glu Ala Ile Gly Phe Glu Gln Phe Gly Ile Ser His																	35
25 30																	
ggc tac ggc gca ttc aca ggg gag tcc cga ctg ttt cgc atg gcc tac																	259
Gly Tyr Gly Ala Phe Thr Gly Glu Ser Arg Leu Phe Arg Met Ala Tyr																	50
40 45																	
cac gaa ggc agc acc tac gtt ccg ttg ctc aaa cgc gca cga gca cta																	307
His Glu Gly Ser Thr Tyr Val Pro Leu Leu Lys Arg Ala Arg Ala Leu																	65
55 60																	
tgg tca tca ctg agc gag att tcc gga cgc gaa ctc ttc cac aac ttc																	355
Trp Ser Ser Leu Ser Glu Ile Ser Gly Arg Glu Leu Phe His Asn Phe																	85
70 75 80																	
ggt gtc tta agc acc ggc aag gaa gac gaa gca ccc ttc caa cgc ctg																	403
Gly Val Leu Ser Thr Gly Lys Glu Asp Glu Ala Pro Phe Gln Arg Leu																	100
90 95 100																	
gtg gaa tca gtg gaa cgt tat gag ctg cca cat gaa cga ctt acc gcc																	451
Val Glu Ser Val Glu Arg Tyr Glu Leu Pro His Glu Arg Leu Thr Ala																	115
105 110																	
gcg cag atg cgc agc gtt acc cag gtc tagacttccg																	488
Ala Gln Met Arg Ser Val Thr Gln Val																	
120 125																	

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<210> 148
<211> 126
<212> PRT
<213> Corynebacterium glutamicum
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<400> 148																
Met	Lys	Ile	Ala	Val	Ile	Gly	Leu	Gly	Ser	Thr	Gly	Ser	Met	Ala	Leu	
1				5					10					15		
Trp	His	Leu	Ser	Asn	Ile	Pro	Gly	Val	Glu	Ala	Ile	Gly	Phe	Glu	Gln	
			20					25					30			
Phe	Gly	Ile	Ser	His	Gly	Tyr	Gly	Ala	Phe	Thr	Gly	Glu	Ser	Arg	Leu	
		35					40					45				
Phe	Arg	Met	Ala	Tyr	His	Glu	Gly	Ser	Thr	Tyr	Val	Pro	Leu	Leu	Lys	
	50					55					60					
Arg	Ala	Arg	Ala	Leu	Trp	Ser	Ser	Leu	Ser	Glu	Ile	Ser	Gly	Arg	Glu	
65					70					75					80	
Leu	Phe	His	Asn	Phe	Gly	Val	Leu	Ser	Thr	Gly	Lys	Glu	Asp	Glu	Ala	
				85					90					95		
Pro	Phe	Gln	Arg	Leu	Val	Glu	Ser	Val	Glu	Arg	Tyr	Glu	Leu	Pro	His	
			100					105					110			
Glu	Arg	Leu	Thr	Ala	Ala	Gln	Met	Arg	Ser	Val	Thr	Gln	Val			
		115					120					125				

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<210> 149
<211> 460
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(460)  
<223> FRXA02263
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<400> 149
cctgggcaac ccaagtgtat gaaaacgccc tggaaaaaagg cgtcggcacc acattgaacc 60

tgtgggaatc acccgccactg gcttgagaga agaaacaaca atg aaa att gcg gta 115
Met Lys Ile Ala Val
1 5

atc ggc ctt gga tca acc ggc tcc atg gca ctg tgg cac tta agt aac 163
Ile Gly Leu Gly Ser Thr Gly Ser Met Ala Leu Trp His Leu Ser Asn
10 15 20

atc cca ggt gta gag gcc atc ggc ttt gaa caa ttc ggc atc tcc cat 211
Ile Pro Gly Val Glu Ala Ile Gly Phe Glu Gln Phe Gly Ile Ser His
25 30 35

ggc tac ggc gca ttc aca ggg gag tcc cga ctg ttt cgc atg gcc tac 259
Gly Tyr Gly Ala Phe Thr Gly Glu Ser Arg Leu Phe Arg Met Ala Tyr
40 45 50

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cac gaa ggc agc acc tac gtt ccg ttg ctc aaa cgc gca cga gca cta 307
 His Glu Gly Ser Thr Tyr Val Pro Leu Leu Lys Arg Ala Arg Ala Leu
 55 60 65

 tgg tca tca ctg agc gag att tcc gga cgc gaa ctc ttc cac aac ttc 355
 Trp Ser Ser Leu Ser Glu Ile Ser Gly Arg Glu Leu Phe His Asn Phe
 70 75 80 85

 ggt gtc tta agc acc ggc aag gaa gac gaa gca ccc ttc caa cgc ctg 403
 Gly Val Leu Ser Thr Gly Lys Glu Asp Glu Ala Pro Phe Gln Arg Leu
 90 95 100

 gtg gaa tca gtg gaa cgt tat gag ctg cca cat gaa cga ctt acc gcc 451
 Val Glu Ser Val Glu Arg Tyr Glu Leu Pro His Glu Arg Leu Thr Ala
 105 110 115

 gcg cag atg 460
 Ala Gln Met
 120

<210> 150
 <211> 120
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 150
 Met Lys Ile Ala Val Ile Gly Leu Gly Ser Thr Gly Ser Met Ala Leu
 1 5 10 15

 Trp His Leu Ser Asn Ile Pro Gly Val Glu Ala Ile Gly Phe Glu Gln
 20 25 30

 Phe Gly Ile Ser His Gly Tyr Gly Ala Phe Thr Gly Glu Ser Arg Leu
 35 40 45

 Phe Arg Met Ala Tyr His Glu Gly Ser Thr Tyr Val Pro Leu Leu Lys
 50 55 60

 Arg Ala Arg Ala Leu Trp Ser Ser Leu Ser Glu Ile Ser Gly Arg Glu
 65 70 75 80

 Leu Phe His Asn Phe Gly Val Leu Ser Thr Gly Lys Glu Asp Glu Ala
 85 90 95

 Pro Phe Gln Arg Leu Val Glu Ser Val Glu Arg Tyr Glu Leu Pro His
 100 105 110

 Glu Arg Leu Thr Ala Ala Gln Met
 115 120

<210> 151
 <211> 1251
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101) .. (1228)
 <223> RXA02176

<400> 151

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tggccctttt acttccaagc gcagaaagtt gcccgaagac atg acc gac ttc ccc 115
                                         Met Thr Asp Phe Pro
                                         1           5

acc ctg ccc tct gag ttc atc cct ggc gac ggc cgt ttc ggc tgc gga 163
Thr Leu Pro Ser Glu Phe Ile Pro Gly Asp Gly Arg Phe Gly Cys Gly
                        10                        15                        20

cct tcc aag gtt cga cca gaa cag att cag gct att gtc gac gga tcc 211
Pro Ser Lys Val Arg Pro Glu Gln Ile Gln Ala Ile Val Asp Gly Ser
                        25                        30                        35

gca tcc gtc atc ggt acc tca cac cgt cag ccg gca gta aaa aac gtc 259
Ala Ser Val Ile Gly Thr Ser His Arg Gln Pro Ala Val Lys Asn Val
                        40                        45                        50

gtg ggt tca atc cgc gag gga ctc tcc gac ctc ttc tcc ctt cca gaa 307
Val Gly Ser Ile Arg Glu Gly Leu Ser Asp Leu Phe Ser Leu Pro Glu
                        55                        60                        65

ggc tac gag atc atc ctt tcc cta ggt ggt gcg acc gca ttc tgg gat 355
Gly Tyr Glu Ile Ile Leu Ser Leu Gly Gly Ala Thr Ala Phe Trp Asp
                        70                        75                        80                        85

gca gca acc ttc gga ctc att gaa aag aag tcc ggt cac ctt tct ttc 403
Ala Ala Thr Phe Gly Leu Ile Glu Lys Lys Ser Gly His Leu Ser Phe
                        90                        95                        100

ggg gag ttc tcc tcc aag ttc gca aag gct tct aag ctt gct cct tgg 451
Gly Glu Phe Ser Ser Lys Phe Ala Lys Ala Ser Lys Leu Ala Pro Trp
                        105                        110                        115

ctc gac gag cca gag atc gtc acc gca gaa acc ggt gac tct ccg gcc 499
Leu Asp Glu Pro Glu Ile Val Thr Ala Glu Thr Gly Asp Ser Pro Ala
                        120                        125                        130

cca cag gca ttc gaa ggc gcc gat gtt att gca tgg gca cac aac gaa 547
Pro Gln Ala Phe Glu Gly Ala Asp Val Ile Ala Trp Ala His Asn Glu
                        135                        140                        145

acc tcc act ggc gcc atg gtt cca gtt ctt cgc ccc gaa ggc tct gaa 595
Thr Ser Thr Gly Ala Met Val Pro Val Leu Arg Pro Glu Gly Ser Glu
                        150                        155                        160                        165

ggc tcc ctg gtt gcc att gac gca acc tcc ggc gct ggt gga ctg cca 643
Gly Ser Leu Val Ala Ile Asp Ala Thr Ser Gly Ala Gly Gly Leu Pro
                        170                        175                        180

gta gac atc aag aac tcc gat gtt tac tac ttc tcc cca cag aag tgc 691
Val Asp Ile Lys Asn Ser Asp Val Tyr Tyr Phe Ser Pro Gln Lys Cys
                        185                        190                        195

ttc gca tcc gac ggt ggc ctg tgg ctt gca gcg atg agc cca gca gct 739
Phe Ala Ser Asp Gly Gly Leu Trp Leu Ala Ala Met Ser Pro Ala Ala
                        200                        205                        210

ctc gag cgc atc gag aag atc aac gct tcc gat cgc ttc atc cct gag 787

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Leu Glu Arg Ile Glu Lys Ile Asn Ala Ser Asp Arg Phe Ile Pro Glu
 215 220 225
 ttc ctc aac ctg cag acc gca gtg gat aac tcc ctg aag aac cag acc 835
 Phe Leu Asn Leu Gln Thr Ala Val Asp Asn Ser Leu Lys Asn Gln Thr
 230 235 240 245
 tac aac acc cca gct gtt gct acc ttg ctg atg ctg gac aac cag gtc 883
 Tyr Asn Thr Pro Ala Val Ala Thr Leu Leu Met Leu Asp Asn Gln Val
 250 255 260
 aag tgg atg aac tcc aac ggc ggc ctg gat gga atg gtt gct cgc acc 931
 Lys Trp Met Asn Ser Asn Gly Gly Leu Asp Gly Met Val Ala Arg Thr
 265 270 275
 aca gca agc tcc tcc gcc ctg tac aac tgg gct gag gct cgc gag gag 979
 Thr Ala Ser Ser Ala Leu Tyr Asn Trp Ala Glu Ala Arg Glu Glu
 280 285 290
 gca tcc cca tac gtg gca gat gca gct aag cgc tcc ctc gtt gtc ggc 1027
 Ala Ser Pro Tyr Val Ala Asp Ala Ala Lys Arg Ser Leu Val Val Gly
 295 300 305
 acc atc gac ttc gat gac tcc atc gac gca gca gtg atc gct aag ata 1075
 Thr Ile Asp Phe Asp Asp Ser Ile Asp Ala Ala Val Ile Ala Lys Ile
 310 315 320 325
 ctg cgc gca aac ggc atc ctg gac acc gag cct tac cgc aag ctg gga 1123
 Leu Arg Ala Asn Gly Ile Leu Asp Thr Glu Pro Tyr Arg Lys Leu Gly
 330 335 340
 cgc aac cag ctg cgc atc ggt atg ttc cca gcg atc gat tcc acc gat 1171
 Arg Asn Gln Leu Arg Ile Gly Met Phe Pro Ala Ile Asp Ser Thr Asp
 345 350 355
 gtg gaa aag ctc acc gga gca atc gac ttc atc ctc gat ggc ggt ttt 1219
 Val Glu Lys Leu Thr Gly Ala Ile Asp Phe Ile Leu Asp Gly Gly Phe
 360 365 370
 gca agg aag taataaccccc actttgaaaa aca 1251
 Ala Arg Lys
 375

<210> 152

<211> 376

<212> PRT

<213> Corynebacterium glutamicum

<400> 152

Met Thr Asp Phe Pro Thr Leu Pro Ser Glu Phe Ile Pro Gly Asp Gly
 1 5 10 15
 Arg Phe Gly Cys Gly Pro Ser Lys Val Arg Pro Glu Gln Ile Gln Ala
 20 25 30
 Ile Val Asp Gly Ser Ala Ser Val Ile Gly Thr Ser His Arg Gln Pro
 35 40 45
 Ala Val Lys Asn Val Val Gly Ser Ile Arg Glu Gly Leu Ser Asp Leu
 50 55 60

Phe Ser Leu Pro Glu Gly Tyr Glu Ile Ile Leu Ser Leu Gly Gly Ala
 65 70 75 80
 Thr Ala Phe Trp Asp Ala Ala Thr Phe Gly Leu Ile Glu Lys Lys Ser
 85 90 95
 Gly His Leu Ser Phe Gly Glu Phe Ser Ser Lys Phe Ala Lys Ala Ser
 100 105 110
 Lys Leu Ala Pro Trp Leu Asp Glu Pro Glu Ile Val Thr Ala Glu Thr
 115 120 125
 Gly Asp Ser Pro Ala Pro Gln Ala Phe Glu Gly Ala Asp Val Ile Ala
 130 135 140
 Trp Ala His Asn Glu Thr Ser Thr Gly Ala Met Val Pro Val Leu Arg
 145 150 155 160
 Pro Glu Gly Ser Glu Gly Ser Leu Val Ala Ile Asp Ala Thr Ser Gly
 165 170 175
 Ala Gly Gly Leu Pro Val Asp Ile Lys Asn Ser Asp Val Tyr Tyr Phe
 180 185 190
 Ser Pro Gln Lys Cys Phe Ala Ser Asp Gly Gly Leu Trp Leu Ala Ala
 195 200 205
 Met Ser Pro Ala Ala Leu Glu Arg Ile Glu Lys Ile Asn Ala Ser Asp
 210 215 220
 Arg Phe Ile Pro Glu Phe Leu Asn Leu Gln Thr Ala Val Asp Asn Ser
 225 230 235 240
 Leu Lys Asn Gln Thr Tyr Asn Thr Pro Ala Val Ala Thr Leu Leu Met
 245 250 255
 Leu Asp Asn Gln Val Lys Trp Met Asn Ser Asn Gly Gly Leu Asp Gly
 260 265 270
 Met Val Ala Arg Thr Thr Ala Ser Ser Ser Ala Leu Tyr Asn Trp Ala
 275 280 285
 Glu Ala Arg Glu Glu Ala Ser Pro Tyr Val Ala Asp Ala Ala Lys Arg
 290 295 300
 Ser Leu Val Val Gly Thr Ile Asp Phe Asp Asp Ser Ile Asp Ala Ala
 305 310 315 320
 Val Ile Ala Lys Ile Leu Arg Ala Asn Gly Ile Leu Asp Thr Glu Pro
 325 330 335
 Tyr Arg Lys Leu Gly Arg Asn Gln Leu Arg Ile Gly Met Phe Pro Ala
 340 345 350
 Ile Asp Ser Thr Asp Val Glu Lys Leu Thr Gly Ala Ile Asp Phe Ile
 355 360 365
 Leu Asp Gly Gly Phe Ala Arg Lys
 370 375

<210> 153
 <211> 1422
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1399)
 <223> RXN02758

<400> 153

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aatgtcgtgt tccgcgctca gacatgagac aattgttgcc gtg act gaa ctc atc    115
                               Val Thr Glu Leu Ile
                               1      5

cag aat gaa tcc caa gaa atc gct gag ctg gaa gcc ggc cag cag gtt    163
Gln Asn Glu Ser Gln Glu Ile Ala Glu Leu Glu Ala Gly Gln Gln Val
                10                15                20

gca ttg cgt gaa ggt tat ctt cct gcg gtg atc aca gtg agc ggt aaa    211
Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile Thr Val Ser Gly Lys
                25                30                35

gac cgc cca ggt gtg act gcc gcg ttc ttt agg gtc ttg tcc gct aat    259
Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg Val Leu Ser Ala Asn
                40                45                50

cag gtt cag gtc ttg gac gtt gag cag tca atg ttc cgt ggc ttt ttg    307
Gln Val Gln Val Leu Asp Val Glu Gln Ser Met Phe Arg Gly Phe Leu
                55                60                65

aac ttg gcg gcg ttt gtg ggt atc gca cct gag cgt gtc gag acc gtc    355
Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu Arg Val Glu Thr Val
                70                75                80                85

acc aca ggc ctg act gac acc ctc aag gtg cat gga cag tcc gtg gtg    403
Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His Gly Gln Ser Val Val
                90                95                100

gtg gag ctg cag gaa act gtg cag tcg tcc cgt cct cgt tct tcc cat    451
Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg Pro Arg Ser Ser His
                105                110                115

gtt gtt gtg gtg ttg ggt gat ccg gtt gat gcg ttg gat att tcc cgc    499
Val Val Val Val Leu Gly Asp Pro Val Asp Ala Leu Asp Ile Ser Arg
                120                125                130

att ggt cag acc ctg gcg gat tac gat gcc aac att gac acc att cgt    547
Ile Gly Gln Thr Leu Ala Asp Tyr Asp Ala Asn Ile Asp Thr Ile Arg
                135                140                145

ggt att tcg gat tac cct gtg acc ggc ctg gag ctg aag gtg act gtg    595
Gly Ile Ser Asp Tyr Pro Val Thr Gly Leu Glu Leu Lys Val Thr Val
                150                155                160                165

ccg gat gtc agc cct ggt ggt ggt gaa gcg atg cgt aag gcg ctt gct    643
Pro Asp Val Ser Pro Gly Gly Gly Glu Ala Met Arg Lys Ala Leu Ala
                170                175                180

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gct ctt acc tct gag ctg aat gtg gat att gcg att gag cgt tct ggt	691
Ala Leu Thr Ser Glu Leu Asn Val Asp Ile Ala Ile Glu Arg Ser Gly	
185 190 195	
ttg ctg cgt cgt tct aag cgt ctg gtg tgc ttc gat tgt gat tcc acg	739
Leu Leu Arg Arg Ser Lys Arg Leu Val Cys Phe Asp Cys Asp Ser Thr	
200 205 210	
ttg atc act ggt gag gtc att gag atg ctg gcg gct cac gcg ggc aag	787
Leu Ile Thr Gly Glu Val Ile Glu Met Leu Ala Ala His Ala Gly Lys	
215 220 225	
gaa gct gaa gtt gcg gca gtt act gag cgt gcg atg cgc ggt gag ctc	835
Glu Ala Glu Val Ala Ala Val Thr Glu Arg Ala Met Arg Gly Glu Leu	
230 235 240 245	
gat ttc gag gag tct ctg cgt gag cgt gtg aag gcg ttg gct ggt ttg	883
Asp Phe Glu Glu Ser Leu Arg Glu Arg Val Lys Ala Leu Ala Gly Leu	
250 255 260	
gat gcg tcg gtg atc gat gag gtc gct gcc gct att gag ctg acc cct	931
Asp Ala Ser Val Ile Asp Glu Val Ala Ala Ala Ile Glu Leu Thr Pro	
265 270 275	
ggt gcg cgc acc acg atc cgt acg ctg aac cgc atg ggt tac cag acc	979
Gly Ala Arg Thr Thr Ile Arg Thr Leu Asn Arg Met Gly Tyr Gln Thr	
280 285 290	
gct gtt gtt tcc ggt ggt ttc atc cag gtg ttg gaa ggt ttg gct gag	1027
Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu Glu Gly Leu Ala Glu	
295 300 305	
gag ttg gag ttg gat tat gtc cgc gcc aac act ttg gaa atc gtt gat	1075
Glu Leu Glu Leu Asp Tyr Val Arg Ala Asn Thr Leu Glu Ile Val Asp	
310 315 320 325	
ggc aag ctg acc ggc aac gtc acc gga aag atc gtt gac cgc gct gcg	1123
Gly Lys Leu Thr Gly Asn Val Thr Gly Lys Ile Val Asp Arg Ala Ala	
330 335 340	
aag gct gag ttc ctc cgt gag ttc gct gcg gat tct ggc ctg aag atg	1171
Lys Ala Glu Phe Leu Arg Glu Phe Ala Ala Asp Ser Gly Leu Lys Met	
345 350 355	
tac cag act gtc gct gtc ggt gat ggc gct aat gac atc gat atg ctc	1219
Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn Asp Ile Asp Met Leu	
360 365 370	
tcc gct gcg ggt ctg ggt gtt gct ttc aac gcg aag cct gcg ctg aag	1267
Ser Ala Ala Gly Leu Gly Val Ala Phe Asn Ala Lys Pro Ala Leu Lys	
375 380 385	
gag att gcg gat act tcc gtg aac cac cca ttc ctc gac gag gtt ttg	1315
Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe Leu Asp Glu Val Leu	
390 395 400 405	
cac atc atg ggc att tcc cgc gac gag atc gat ctg gcg gat cag gaa	1363
His Ile Met Gly Ile Ser Arg Asp Glu Ile Asp Leu Ala Asp Gln Glu	
410 415 420	

gac ggc act ttc cac cgc gtt cca ttg acc aat gcc taaagattcg 1409
 Asp Gly Thr Phe His Arg Val Pro Leu Thr Asn Ala
 425 430

tttctcgacg ccc 1422

<210> 154

<211> 433

<212> PRT

<213> Corynebacterium glutamicum

<400> 154

Val Thr Glu Leu Ile Gln Asn Glu Ser Gln Glu Ile Ala Glu Leu Glu
 1 5 10 15

Ala Gly Gln Gln Val Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile
 20 25 30

Thr Val Ser Gly Lys Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg
 35 40 45

Val Leu Ser Ala Asn Gln Val Gln Val Leu Asp Val Glu Gln Ser Met
 50 55 60

Phe Arg Gly Phe Leu Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu
 65 70 75 80

Arg Val Glu Thr Val Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His
 85 90 95

Gly Gln Ser Val Val Val Glu Leu Gln Glu Thr Val Gln Ser Arg
 100 105 110

Pro Arg Ser Ser His Val Val Val Val Leu Gly Asp Pro Val Asp Ala
 115 120 125

Leu Asp Ile Ser Arg Ile Gly Gln Thr Leu Ala Asp Tyr Asp Ala Asn
 130 135 140

Ile Asp Thr Ile Arg Gly Ile Ser Asp Tyr Pro Val Thr Gly Leu Glu
 145 150 155 160

Leu Lys Val Thr Val Pro Asp Val Ser Pro Gly Gly Gly Glu Ala Met
 165 170 175

Arg Lys Ala Leu Ala Ala Leu Thr Ser Glu Leu Asn Val Asp Ile Ala
 180 185 190

Ile Glu Arg Ser Gly Leu Leu Arg Arg Ser Lys Arg Leu Val Cys Phe
 195 200 205

Asp Cys Asp Ser Thr Leu Ile Thr Gly Glu Val Ile Glu Met Leu Ala
 210 215 220

Ala His Ala Gly Lys Glu Ala Glu Val Ala Ala Val Thr Glu Arg Ala
 225 230 235 240

Met Arg Gly Glu Leu Asp Phe Glu Glu Ser Leu Arg Glu Arg Val Lys
 245 250 255

Ala

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<220>
<221> CDS
<222> (101)..(490)
<223> FRXA02479
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<400> 155																		
atacatctca cccaattccc cataactaga caattgcccc gcaacgactg ataagtctcc																		60
aatgtcgtgt tccgcgctca gacatgagac aattgttgcc																		
												gtg	act	gaa	ctc	atc		115
												Val	Thr	Glu	Leu	Ile		
												1						5
cag aat gaa tcc caa gaa atc gct gag ctg gaa gcc ggc cag cag gtt																		163
Gln Asn Glu Ser Gln Glu Ile Ala Glu Leu Glu Ala Gly Gln Gln Val																		
										10					15		20	
gca ttg cgt gaa ggt tat ctt cct gcg gtg atc aca gtg agc ggt aaa																		211
Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile Thr Val Ser Gly Lys																		
										25					30		35	

gac cgc cca ggt gtg act gcc gcg ttc ttt agg gtc ttg tcc gct aat 259
 Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg Val Leu Ser Ala Asn
 40 45 50

cag gtt cag gtc ttg gac gtt gag cag tca atg ttc cgt ggc ttt ttg 307
 Gln Val Gln Val Leu Asp Val Glu Gln Ser Met Phe Arg Gly Phe Leu
 55 60 65

aac ttg gcg gcg ttt gtg ggt atc gca cct gag cgt gtc gag acc gtc 355
 Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu Arg Val Glu Thr Val
 70 75 80 85

acc aca ggc ctg act gac acc ctc aag gtg cat gga cag tcc gtg gtg 403
 Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His Gly Gln Ser Val Val
 90 95 100

gtg gag ctg cag gaa act gtg cag tcg tcc cgt cct cgt tct tcc cat 451
 Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg Pro Arg Ser Ser His
 105 110 115

gtt gtt gtg gtg ttg ggt gat ccg gtt gat gcg ctg gat 490
 Val Val Val Val Leu Gly Asp Pro Val Asp Ala Leu Asp
 120 125 130

<210> 156

<211> 130

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 156

Val Thr Glu Leu Ile Gln Asn Glu Ser Gln Glu Ile Ala Glu Leu Glu
 1 5 10 15

Ala Gly Gln Gln Val Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile
 20 25 30

Thr Val Ser Gly Lys Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg
 35 40 45

Val Leu Ser Ala Asn Gln Val Gln Val Leu Asp Val Glu Gln Ser Met
 50 55 60

Phe Arg Gly Phe Leu Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu
 65 70 75 80

Arg Val Glu Thr Val Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His
 85 90 95

Gly Gln Ser Val Val Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg
 100 105 110

Pro Arg Ser Ser His Val Val Val Val Leu Gly Asp Pro Val Asp Ala
 115 120 125

Leu Asp
 130

<210> 157

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<211> 558
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(535)
<223> FRXA02758
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<400> 157																
aaggcggttg ctggttttga tgcgctcggtg atcgatgagg tcgctgccgc tattgagctg																60
acccttggtg cgcgcaccac gatccgtacg gttgaaccgc atg ggt tac cag acc																115
Met Gly Tyr Gln Thr																5
1																
gct gtt gtt tcc ggt ggt ttc atc cag gtg ttg gaa ggt ttg gct gag																163
Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu Glu Gly Leu Ala Glu																20
10 15																
gag ttg gag ttg gat tat gtc cgc gcc aac act ttg gaa atc gtt gat																211
Glu Leu Glu Leu Asp Tyr Val Arg Ala Asn Thr Leu Glu Ile Val Asp																35
25 30																
ggc aag ctg acc ggc aac gtc acc gga aag atc gtt gac cgc gct gcg																259
Gly Lys Leu Thr Gly Asn Val Thr Gly Lys Ile Val Asp Arg Ala Ala																50
40 45																
aag gct gag ttc ctc cgt gag ttc gct gcg gat tct ggc ctg aag atg																307
Lys Ala Glu Phe Leu Arg Glu Phe Ala Ala Asp Ser Gly Leu Lys Met																65
55 60																
tac cag act gtc gct gtc ggt gat ggc gct aat gac atc gat atg ctc																355
Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn Asp Ile Asp Met Leu																85
70 75 80																
tcc gct gcg ggt ctg ggt gtt gct ttc aac gcg aag cct gcg ctg aag																403
Ser Ala Ala Gly Leu Gly Val Ala Phe Asn Ala Lys Pro Ala Leu Lys																100
90 95																
gag att gcg gat act tcc gtg aac cac cca ttc ctc gac gag gtt ttg																451
Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe Leu Asp Glu Val Leu																115
105 110																
cac atc atg ggc att tcc cgc gac gag atc gat ctg gcg gat cag gaa																499
His Ile Met Gly Ile Ser Arg Asp Glu Ile Asp Leu Ala Asp Gln Glu																130
120 125																
gac ggc act ttc cac cgc gtt cca ttg acc aat gcc taaagattcg																545
Asp Gly Thr Phe His Arg Val Pro Leu Thr Asn Ala																145
135 140																
tttctcgacg ccc																558

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<210> 158
<211> 145
<212> PRT
<213> Corynebacterium glutamicum
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<400> 158

Met Gly Tyr Gln Thr Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu
 1 5 10 15
 Glu Gly Leu Ala Glu Glu Leu Glu Leu Asp Tyr Val Arg Ala Asn Thr
 20 25 30
 Leu Glu Ile Val Asp Gly Lys Leu Thr Gly Asn Val Thr Gly Lys Ile
 35 40 45
 Val Asp Arg Ala Ala Lys Ala Glu Phe Leu Arg Glu Phe Ala Ala Asp
 50 55 60
 Ser Gly Leu Lys Met Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn
 65 70 75 80
 Asp Ile Asp Met Leu Ser Ala Ala Gly Leu Gly Val Ala Phe Asn Ala
 85 90 95
 Lys Pro Ala Leu Lys Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe
 100 105 110
 Leu Asp Glu Val Leu His Ile Met Gly Ile Ser Arg Asp Glu Ile Asp
 115 120 125
 Leu Ala Asp Gln Glu Asp Gly Thr Phe His Arg Val Pro Leu Thr Asn
 130 135 140
 Ala
 145

<210> 159
 <211> 205
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (72) .. (182)
 <223> FRXA02759

<400> 159
 tcttacttct aagctgaatg tgatattgcg attaagcgtt ctggtttgct gcgtcgttct 60
 aagcgtctgg tgtg ctt cga ttg tat ccc acg ttg atc act ggt gag gtc 110
 Val Leu Arg Leu Tyr Pro Thr Leu Ile Thr Gly Glu Val
 1 5 10
 att gag atg ctg gcg gct cac gcg ggc aag gaa gct aaa gtt gcg gca 158
 Ile Glu Met Leu Ala Ala His Ala Gly Lys Glu Ala Lys Val Ala Ala
 15 20 25
 gtt act gag cgt gcg atg cgc ggg tgagctcgat ttcgaggagt ctc 205
 Val Thr Glu Arg Ala Met Arg Gly
 30 35

<210> 160
 <211> 37
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 160

Val Leu Arg Leu Tyr Pro Thr Leu Ile Thr Gly Glu Val Ile Glu Met
 1 5 10 15

Leu Ala Ala His Ala Gly Lys Glu Ala Lys Val Ala Ala Val Thr Glu
 20 25 30

Arg Ala Met Arg Gly
 35

<210> 161

<211> 1188

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1165)

<223> RXA02501

<400> 161

cgccccgaaa gctttaccat ggatacgata ctcaatggag atatccatta tcggtttggc 60

gtctgtgctgc tcatgaacca ggaaggtttt tgtttgtctc atg agc tct gaa gga 115
 Met Ser Ser Glu Gly
 1 5

aga aac cac aac tgg gac tac gcc gcc atc ggc acc cca gag gat ttc 163
 Arg Asn His Asn Trp Asp Tyr Ala Ala Ile Gly Thr Pro Glu Asp Phe
 10 15 20

ctc gcc agc tgg agc gca tcc cgc gga aat cta cga cgc ttt ttc gaa 211
 Leu Ala Ser Trp Ser Ala Ser Arg Gly Asn Leu Arg Arg Phe Phe Glu
 25 30 35

gac cac gca gcc gcc ccc ata aac gat gcc gcc cag cgc caa gca ggt 259
 Asp His Ala Ala Ala Pro Ile Asn Asp Ala Ala Gln Arg Gln Ala Gly
 40 45 50

gaa gcc gca gca acc caa gcc gtc gca gcg atc tac ggc atg gag ctc 307
 Glu Ala Ala Ala Thr Gln Val Ala Ala Ile Tyr Gly Met Glu Leu
 55 60 65

aac gaa ttc aac gca ggt gtc gac gcc gtc gcc ggc gcc atc gaa tct 355
 Asn Glu Phe Asn Ala Gly Val Asp Ala Val Ala Gly Ala Ile Glu Ser
 70 75 80 85

gcc ggc gcc atc cac gtc agc atc ccc gat ccc gat gtc ccc caa gat 403
 Ala Gly Ala Ile His Val Ser Ile Pro Asp Pro Asp Val Pro Gln Asp
 90 95 100

gtc gga gcc gca gca ttt ttc gac gtc gac aac acc ctc atc caa ggc 451
 Val Gly Ala Ala Ala Phe Phe Asp Val Asp Asn Thr Leu Ile Gln Gly
 105 110 115

tcc tcc ctc atc gtt ttc gcc caa gga ctc ttc cgg aag aaa ttc ttc 499
 Ser Ser Leu Ile Val Phe Ala Gln Gly Leu Phe Arg Lys Lys Phe Phe
 120 125 130

acc atc aaa gaa atc ctc ccc gtg gtg tgg aaa caa gtg aaa ttc aaa 547
 Thr Ile Lys Glu Ile Leu Pro Val Val Trp Lys Gln Val Lys Phe Lys
 135 140 145

ctc acc ggc tcc gaa aac gcc gac gac gtc tcc cgc ggc cgc gaa caa 595
 Leu Thr Gly Ser Glu Asn Ala Asp Asp Val Ser Arg Gly Arg Glu Gln
 150 155 160 165

gcc ctc gaa ttc atc aaa ggc cgc ccc gtc caa gaa cta gtt gac ctc 643
 Ala Leu Glu Phe Ile Lys Gly Arg Pro Val Gln Glu Leu Val Asp Leu
 170 175 180

tgc gaa gaa atc gtc gac caa cgc atg gcc gac aaa atg tgg ccc ggc 691
 Cys Glu Glu Ile Val Asp Gln Arg Met Ala Asp Lys Met Trp Pro Gly
 185 190 195

acc aaa caa ctc gcc gac atg cac atc gcc gcc ggc cac caa gtc tgg 739
 Thr Lys Gln Leu Ala Asp Met His Ile Ala Ala Gly His Gln Val Trp
 200 205 210

ctc gtc tcc gca acc ccc gtc caa ctc gcc caa atc ctg gca caa cgc 787
 Leu Val Ser Ala Thr Pro Val Gln Leu Ala Gln Ile Leu Ala Gln Arg
 215 220 225

ctc ggc ttc acc gga gcg atc ggc aca gtc gca gaa gca aaa gat gga 835
 Leu Gly Phe Thr Gly Ala Ile Gly Thr Val Ala Glu Ala Lys Asp Gly
 230 235 240 245

gta ttc acc ggc cga ctc gtc ggc gac atc ctc cac gga ccc ggc aaa 883
 Val Phe Thr Gly Arg Leu Val Gly Asp Ile Leu His Gly Pro Gly Lys
 250 255 260

aga cac gca gtc gca gca ctc gca tcc atc gaa caa ctc gac ctc acc 931
 Arg His Ala Val Ala Ala Leu Ala Ser Ile Glu Gln Leu Asp Leu Thr
 265 270 275

cga tgc acc gcc tac tcc gac tcc atc aac gac ctc ccc atg ctc tcc 979
 Arg Cys Thr Ala Tyr Ser Asp Ser Ile Asn Asp Leu Pro Met Leu Ser
 280 285 290

atg gtc ggc acc gcc gtc gca gta aac ccc gac tcc aaa ctc cgc aaa 1027
 Met Val Gly Thr Ala Val Ala Val Asn Pro Asp Ser Lys Leu Arg Lys
 295 300 305

gaa gcc gaa acc cga ggc tgg gac gtc cgc gat ttc cga agc atc cgc 1075
 Glu Ala Glu Thr Arg Gly Trp Asp Val Arg Asp Phe Arg Ser Ile Arg
 310 315 320 325

aaa gcc acc cgc gaa tac gga atc ccc gcc ctg gtc acc gcc gca ttc 1123
 Lys Ala Thr Arg Glu Tyr Gly Ile Pro Ala Leu Val Thr Ala Ala Phe
 330 335 340

agt gtc gcc ggc tgg agt cta cgc cgc cga tgg aga aaa caa 1165
 Ser Val Ala Gly Trp Ser Leu Arg Arg Arg Trp Arg Lys Gln
 345 350 355

taacgcacag gagccgtttt aag 1188

<210> 162

<211> 355

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 162

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Met Ser Ser Glu Gly Arg Asn His Asn Trp Asp Tyr Ala Ala Ile Gly
  1           5           10           15

Thr Pro Glu Asp Phe Leu Ala Ser Trp Ser Ala Ser Arg Gly Asn Leu
          20           25           30

Arg Arg Phe Phe Glu Asp His Ala Ala Ala Pro Ile Asn Asp Ala Ala
          35           40           45

Gln Arg Gln Ala Gly Glu Ala Ala Ala Thr Gln Ala Val Ala Ala Ile
          50           55           60

Tyr Gly Met Glu Leu Asn Glu Phe Asn Ala Gly Val Asp Ala Val Ala
          65           70           75           80

Gly Ala Ile Glu Ser Ala Gly Ala Ile His Val Ser Ile Pro Asp Pro
          85           90           95

Asp Val Pro Gln Asp Val Gly Ala Ala Ala Phe Phe Asp Val Asp Asn
          100           105           110

Thr Leu Ile Gln Gly Ser Ser Leu Ile Val Phe Ala Gln Gly Leu Phe
          115           120           125

Arg Lys Lys Phe Phe Thr Ile Lys Glu Ile Leu Pro Val Val Trp Lys
          130           135           140

Gln Val Lys Phe Lys Leu Thr Gly Ser Glu Asn Ala Asp Asp Val Ser
          145           150           155           160

Arg Gly Arg Glu Gln Ala Leu Glu Phe Ile Lys Gly Arg Pro Val Gln
          165           170           175

Glu Leu Val Asp Leu Cys Glu Glu Ile Val Asp Gln Arg Met Ala Asp
          180           185           190

Lys Met Trp Pro Gly Thr Lys Gln Leu Ala Asp Met His Ile Ala Ala
          195           200           205

Gly His Gln Val Trp Leu Val Ser Ala Thr Pro Val Gln Leu Ala Gln
          210           215           220

Ile Leu Ala Gln Arg Leu Gly Phe Thr Gly Ala Ile Gly Thr Val Ala
          225           230           235           240

Glu Ala Lys Asp Gly Val Phe Thr Gly Arg Leu Val Gly Asp Ile Leu
          245           250           255

His Gly Pro Gly Lys Arg His Ala Val Ala Ala Leu Ala Ser Ile Glu
          260           265           270

Gln Leu Asp Leu Thr Arg Cys Thr Ala Tyr Ser Asp Ser Ile Asn Asp
          275           280           285

Leu Pro Met Leu Ser Met Val Gly Thr Ala Val Ala Val Asn Pro Asp
          290           295           300

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Ser Lys Leu Arg Lys Glu Ala Glu Thr Arg Gly Trp Asp Val Arg Asp
305 310 315 320

Phe Arg Ser Ile Arg Lys Ala Thr Arg Glu Tyr Gly Ile Pro Ala Leu
325 330 335

Val Thr Ala Ala Phe Ser Val Ala Gly Trp Ser Leu Arg Arg Arg Trp
340 345 350

Arg Lys Gln
355

<210> 163

<211> 558

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(535)

<223> RXN03105

<400> 163

ggttgggggtc atcaaaggat gcggacatcg ctgtgggggtt gtgtaataat tgcacctgtg 60

aggtgccttt ctggcaggtg aatcaggact ctaagcaagc ttg att ctt cca gtt 115
Leu Ile Leu Pro Val
1 5

cag gag ggc att tcc tat ttt ccc acg ccg tta cac ctg aat cac atc 163
Gln Glu Gly Ile Ser Tyr Phe Pro Thr Pro Leu His Leu Asn His Ile
10 15 20

ggg gga tcc agg tta agc gca cat gta gaa gat gaa gat ctc cgc ctc 211
Gly Gly Ser Arg Leu Ser Ala His Val Glu Asp Glu Asp Leu Arg Leu
25 30 35

gac cgg gac gca gtc tct gaa ttt ggt cgg aaa acc cac gaa ctc ttc 259
Asp Arg Asp Ala Val Ser Glu Phe Gly Arg Lys Thr His Glu Leu Phe
40 45 50

ccc ggg gtc aac cca gag ccc aac cgt ttc agc gtc cac tat gac acc 307
Pro Gly Val Asn Pro Glu Pro Asn Arg Phe Ser Val His Tyr Asp Thr
55 60 65

tac act gca gac aaa tct cca att atc gac gcg gtt gac aat gtc att 355
Tyr Thr Ala Asp Lys Ser Pro Ile Ile Asp Ala Val Asp Asn Val Ile
70 75 80 85

gtg ctc acc gga gga tcc gga cac gcc ttc aag ctc tct cca gct tat 403
Val Leu Thr Gly Gly Ser Gly His Ala Phe Lys Leu Ser Pro Ala Tyr
90 95 100

ggc gaa ctc gca gca caa cga gcg gtc gga aac acc tcg ccg ctg tac 451
Gly Glu Leu Ala Ala Gln Arg Ala Val Gly Asn Thr Ser Pro Leu Tyr
105 110 115

agc gaa gac ttt cgg atc gcc tcg cat gaa cca atc aaa gag cgg tgc 499
Ser Glu Asp Phe Arg Ile Ala Ser His Glu Pro Ile Lys Glu Arg Cys
120 125 130

acg tat aga aag cta acc ttt tta agt gcg cgg ttt taggggtgaga 545
 Thr Tyr Arg Lys Leu Thr Phe Leu Ser Ala Arg Phe
 135 140 145

atctaacgct gag 558

<210> 164

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 164

Leu Ile Leu Pro Val Gln Glu Gly Ile Ser Tyr Phe Pro Thr Pro Leu
 1 5 10 15

His Leu Asn His Ile Gly Gly Ser Arg Leu Ser Ala His Val Glu Asp
 20 25 30

Glu Asp Leu Arg Leu Asp Arg Asp Ala Val Ser Glu Phe Gly Arg Lys
 35 40 45

Thr His Glu Leu Phe Pro Gly Val Asn Pro Glu Pro Asn Arg Phe Ser
 50 55 60

Val His Tyr Asp Thr Tyr Thr Ala Asp Lys Ser Pro Ile Ile Asp Ala
 65 70 75 80

Val Asp Asn Val Ile Val Leu Thr Gly Gly Ser Gly His Ala Phe Lys
 85 90 95

Leu Ser Pro Ala Tyr Gly Glu Leu Ala Ala Gln Arg Ala Val Gly Asn
 100 105 110

Thr Ser Pro Leu Tyr Ser Glu Asp Phe Arg Ile Ala Ser His Glu Pro
 115 120 125

Ile Lys Glu Arg Cys Thr Tyr Arg Lys Leu Thr Phe Leu Ser Ala Arg
 130 135 140

Phe

145

<210> 165

<211> 687

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (62)..(664)

<223> RXS01130

<400> 165

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gatg gat ctg gct cgc aag ctt ggt ctt ctt gct ggc aag ctt gtc gac 109

Met Asp Leu Ala Arg Lys Leu Gly Leu Leu Ala Gly Lys Leu Val Asp

1

5

10

15


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gcc gcc cca gtc tcc att gag gtt gag gct cga ggc gag ctt tct tcc 157
Ala Ala Pro Val Ser Ile Glu Val Glu Ala Arg Gly Glu Leu Ser Ser
      20                      25                      30

gag cag gtc aat gca ctt ggt ttg tcc gct gtt cgt ggt ttg ttc tcc 205
Glu Gln Val Asn Ala Leu Gly Leu Ser Ala Val Arg Gly Leu Phe Ser
      35                      40                      45

gga att atc gaa gag tcc gtt act ttc gtc aac gct cct cgc att gct 253
Gly Ile Ile Glu Glu Ser Val Thr Phe Val Asn Ala Pro Arg Ile Ala
      50                      55                      60

gaa gag cgt ggc ctg gac atc tcc gtg aag acc aac tct gag tct gtt 301
Glu Glu Arg Gly Leu Asp Ile Ser Val Lys Thr Asn Ser Glu Ser Val
      65                      70                      75                      80

act cac cgt tcc gtc ctg cag gtc aag gtc att act ggc agc ggc gcg 349
Thr His Arg Ser Val Leu Gln Val Lys Val Ile Thr Gly Ser Gly Ala
      85                      90                      95

agc gca act gtt gtt ggt gcc ctg act ggt ctt gag cgc gtt gag aag 397
Ser Ala Thr Val Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys
      100                      105                      110

atc acc cgc atc aat ggc cgt ggc ctg gat ctg cgc gca gag ggt ctg 445
Ile Thr Arg Ile Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu
      115                      120                      125

aac ctc ttc ctg cag tac act gac gct cct ggt gca ctg ggt acc gtt 493
Asn Leu Phe Leu Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val
      130                      135                      140

ggt acc aag ctg ggt gct gct ggc atc aac atc gag gct gct gcg ttg 541
Gly Thr Lys Leu Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu
      145                      150                      155                      160

act cag gct gag aag ggt gac ggc gct gtc ctg atc ctg cgt gtt gag 589
Thr Gln Ala Glu Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu
      165                      170                      175

tcc gct gtc tct gaa gag ctg gaa gct gaa atc aac gct gag ttg ggt 637
Ser Ala Val Ser Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly
      180                      185                      190

gct act tcc ttc cag gtt gat ctt gac taattagaga tccatttgct 684
Ala Thr Ser Phe Gln Val Asp Leu Asp
      195                      200

tga 687

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<210> 166

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 166

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Met Asp Leu Ala Arg Lys Leu Gly Leu Leu Ala Gly Lys Leu Val Asp
  1              5              10              15

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<210> 167
<211> 604
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(604)  
<223> RXS03112
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[illegible]

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gct aac cct gct cgt gcg gct cag ctg aac gtt gag ttg gtt gag ttg 259
Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val Glu Leu Val Glu Leu
      40                      45                      50

gat gag ctg atg agc cgt tct gac ttt gtc acc att cac ctt cct aag 307
Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr Ile His Leu Pro Lys
      55                      60                      65

acc aag gaa act gct ggc atg ttt gat gcg cac ctc ctt gct aag tcc 355
Thr Lys Glu Thr Ala Gly Met Phe Asp Ala His Leu Leu Ala Lys Ser
      70                      75                      80                      85

aag aag ggc cag atc atc atc aac gct gct cgt ggt ggc ctt gtt gat 403
Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg Gly Gly Leu Val Asp
                      90                      95                      100

gag cag gct ttg gct gat gcg att gag tcc ggt cac att cgt ggc gct 451
Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly His Ile Arg Gly Ala
      105                      110                      115

ggt ttc gat gtg tac tcc acc gag cct tgc act gat tct cct ttg ttc 499
Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr Asp Ser Pro Leu Phe
      120                      125                      130

aag ttg cct cag gtt gtt gtg act cct cac ttg ggt gct tct act gaa 547
Lys Leu Pro Gln Val Val Val Thr Pro His Leu Gly Ala Ser Thr Glu
      135                      140                      145

gag gct caa gat cgt gcg ggt act gac att gct gat tct gtg ctc aag 595
Glu Ala Gln Asp Arg Ala Gly Thr Asp Ile Ala Asp Ser Val Leu Lys
      150                      155                      160                      165

gcg ctg gct
Ala Leu Ala
804

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<210> 168

<211> 168

<212> PRT

<213> Corynebacterium glutamicum

<400> 168

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Val Glu Ile Phe Gly Lys Thr Val Gly Ile Val Gly Phe Gly His Ile
  1                      5                      10                      15

Gly Gln Leu Phe Ala Gln Arg Leu Ala Ala Phe Glu Thr Thr Ile Val
      20                      25                      30

Ala Tyr Asp Pro Tyr Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val
      35                      40                      45

Glu Leu Val Glu Leu Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr
      50                      55                      60

Ile His Leu Pro Lys Thr Lys Glu Thr Ala Gly Met Phe Asp Ala His
      65                      70                      75                      80

Leu Leu Ala Lys Ser Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg
      85                      90                      95

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Gly Gly Leu Val Asp Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly
 100 105 110

His Ile Arg Gly Ala Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr
 115 120 125

Asp Ser Pro Leu Phe Lys Leu Pro Gln Val Val Val Thr Pro His Leu
 130 135 140

Gly Ala Ser Thr Glu Glu Ala Gln Asp Arg Ala Gly Thr Asp Ile Ala
 145 150 155 160

Asp Ser Val Leu Lys Ala Leu Ala
 165

<210> 169
 <211> 1458
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1435)
 <223> RXN00969

<400> 169
 ctatagtggc taggtaccct ttttgttttg gacacatgta ggggtggccga aacaaagtaa 60

taggacaaca acgctcgacc gcgattatatt ttggagaatc atg acc tca gca tct 115
 Met Thr Ser Ala Ser
 1 5

gcc cca agc ttt aac ccc ggc aag ggt ccc ggc tca gca gtc gga att 163
 Ala Pro Ser Phe Asn Pro Gly Lys Gly Pro Gly Ser Ala Val Gly Ile
 10 15 20

gcc ctt tta gga ttc gga aca gtc ggc act gag gtg atg cgt ctg atg 211
 Ala Leu Leu Gly Phe Gly Thr Val Gly Thr Glu Val Met Arg Leu Met
 25 30 35

acc gag tac ggt gat gaa ctt gcg cac cgc att ggt ggc cca ctg gag 259
 Thr Glu Tyr Gly Asp Glu Leu Ala His Arg Ile Gly Gly Pro Leu Glu
 40 45 50

gtt cgt ggc att gct gtt tct gat atc tca aag cca cgt gaa ggc gtt 307
 Val Arg Gly Ile Ala Val Ser Asp Ile Ser Lys Pro Arg Glu Gly Val
 55 60 65

gca cct gag ctg ctc act gag gac gct ttt gca ctc atc gag cgc gag 355
 Ala Pro Glu Leu Leu Thr Glu Asp Ala Phe Ala Leu Ile Glu Arg Glu
 70 75 80 85

gat gtt gac atc gtc gtt gag gtt atc ggc ggc att gag tac cca cgt 403
 Asp Val Asp Ile Val Val Glu Val Ile Gly Gly Ile Glu Tyr Pro Arg
 90 95 100

gag gta gtt ctc gca gct ctg aag gcc ggc aag tct gtt gtt acc gcc 451
 Glu Val Val Leu Ala Ala Leu Lys Ala Gly Lys Ser Val Val Thr Ala
 105 110 115

aat aag gct ctt gtt gca gct cac tct gct gag ctt gct gat gca gcg	499
Asn Lys Ala Leu Val Ala Ala His Ser Ala Glu Leu Ala Asp Ala Ala	
120 125 130	
 gaa gcc gca aac gtt gac ctg tac ttc gag gct gct gtt gca tgc gca	547
Glu Ala Ala Asn Val Asp Leu Tyr Phe Glu Ala Ala Val Ala Cys Ala	
135 140 145	
 att cca gtg gtt ggc cca ctg cgt cgc tcc ctg gct ggc gat cag atc	595
Ile Pro Val Val Gly Pro Leu Arg Arg Ser Leu Ala Gly Asp Gln Ile	
150 155 160 165	
 cag tct gtg atg ggc atc gtt aac ggc acc acc aac ttc atc ttg gac	643
Gln Ser Val Met Gly Ile Val Asn Gly Thr Thr Asn Phe Ile Leu Asp	
170 175 180	
 gcc atg gat tcc acc ggc gct gac tat gca gat tct ttg gct gag gca	691
Ala Met Asp Ser Thr Gly Ala Asp Tyr Ala Asp Ser Leu Ala Glu Ala	
185 190 195	
 act cgt ttg ggt tac gcc gaa gct gat cca act gca aac gtc gaa ggc	739
Thr Arg Leu Gly Tyr Ala Glu Ala Asp Pro Thr Ala Asn Val Glu Gly	
200 205 210	
 cat gac gcc gca tcc aag gct gca att ttg gca tgc atc gct ttc cac	787
His Asp Ala Ala Ser Lys Ala Ala Ile Leu Ala Cys Ile Ala Phe His	
215 220 225	
 acc cgt gtt acc gcg gat gat gtg tac tgc gaa ggt att agg aac atc	835
Thr Arg Val Thr Ala Asp Asp Val Tyr Cys Glu Gly Ile Arg Asn Ile	
230 235 240 245	
 aac gct gcc gac att gag gca gca cag cag gca ggc cac acc atc aag	883
Asn Ala Ala Asp Ile Glu Ala Ala Gln Gln Ala Gly His Thr Ile Lys	
250 255 260	
 ttg ttg gcc atc tgt gag aag ttc acc aac aag gaa gga aag tcg gct	931
Leu Leu Ala Ile Cys Glu Lys Phe Thr Asn Lys Glu Gly Lys Ser Ala	
265 270 275	
 att tct gct cgc gtg cac ccg act cta tta cct gtg tcc cac cca ctg	979
Ile Ser Ala Arg Val His Pro Thr Leu Leu Pro Val Ser His Pro Leu	
280 285 290	
 gcg tcg gta aac aag tcc ttt aat gca atc ttt gtt gaa gca gaa gca	1027
Ala Ser Val Asn Lys Ser Phe Asn Ala Ile Phe Val Glu Ala Glu Ala	
295 300 305	
 gct ggt cgc ctg atg ttc tac gga aac ggt gca ggt ggc gcg cca acc	1075
Ala Gly Arg Leu Met Phe Tyr Gly Asn Gly Ala Gly Gly Ala Pro Thr	
310 315 320 325	
 gcg tct gct gtg ctt ggc gac gtc gtt ggt gcc gca cga aac aag gtg	1123
Ala Ser Ala Val Leu Gly Asp Val Val Gly Ala Ala Arg Asn Lys Val	
330 335 340	
 cac ggt ggc cgt gct cca ggt gag tcc acc tac gct aac ctg ccg atc	1171
His Gly Gly Arg Ala Pro Gly Glu Ser Thr Tyr Ala Asn Leu Pro Ile	
345 350 355	

gct gat ttc ggt gag acc acc act cgt tac cac ctc gac atg gat gtg 1219
 Ala Asp Phe Gly Glu Thr Thr Thr Arg Tyr His Leu Asp Met Asp Val
 360 365 370

gaa gat cgc gtg ggg gtt ttg gct gaa ttg gct agc ctg ttc tct gag 1267
 Glu Asp Arg Val Gly Val Leu Ala Glu Leu Ala Ser Leu Phe Ser Glu
 375 380 385

caa gga atc tcc ctg cgt aca atc cga cag gaa gag cgc gat gat gat 1315
 Gln Gly Ile Ser Leu Arg Thr Ile Arg Gln Glu Glu Arg Asp Asp Asp
 390 395 400 405

gca cgt ctg atc gtg gtc acc cac tct gcg ctg gaa tct gat ctt tcc 1363
 Ala Arg Leu Ile Val Val Thr His Ser Ala Leu Glu Ser Asp Leu Ser
 410 415 420

cgc acc gtt gaa ctg ctg aag gct aag cct gtt gtt aag gca atc aac 1411
 Arg Thr Val Glu Leu Leu Lys Ala Lys Pro Val Val Lys Ala Ile Asn
 425 430 435

agt gtg atc cgc ctc gaa agg gac taattttact gacatggcaa ttg 1458
 Ser Val Ile Arg Leu Glu Arg Asp
 440 445

<210> 170

<211> 445

<212> PRT

<213> Corynebacterium glutamicum

<400> 170

Met Thr Ser Ala Ser Ala Pro Ser Phe Asn Pro Gly Lys Gly Pro Gly
 1 5 10 15

Ser Ala Val Gly Ile Ala Leu Leu Gly Phe Gly Thr Val Gly Thr Glu
 20 25 30

Val Met Arg Leu Met Thr Glu Tyr Gly Asp Glu Leu Ala His Arg Ile
 35 40 45

Gly Gly Pro Leu Glu Val Arg Gly Ile Ala Val Ser Asp Ile Ser Lys
 50 55 60

Pro Arg Glu Gly Val Ala Pro Glu Leu Leu Thr Glu Asp Ala Phe Ala
 65 70 75 80

Leu Ile Glu Arg Glu Asp Val Asp Ile Val Val Glu Val Ile Gly Gly
 85 90 95

Ile Glu Tyr Pro Arg Glu Val Val Leu Ala Ala Leu Lys Ala Gly Lys
 100 105 110

Ser Val Val Thr Ala Asn Lys Ala Leu Val Ala Ala His Ser Ala Glu
 115 120 125

Leu Ala Asp Ala Ala Glu Ala Ala Asn Val Asp Leu Tyr Phe Glu Ala
 130 135 140

Ala Val Ala Cys Ala Ile Pro Val Val Gly Pro Leu Arg Arg Ser Leu
 145 150 155 160

Ala Gly Asp Gln Ile Gln Ser Val Met Gly Ile Val Asn Gly Thr Thr
 165 170 175
 Asn Phe Ile Leu Asp Ala Met Asp Ser Thr Gly Ala Asp Tyr Ala Asp
 180 185 190
 Ser Leu Ala Glu Ala Thr Arg Leu Gly Tyr Ala Glu Ala Asp Pro Thr
 195 200 205
 Ala Asn Val Glu Gly His Asp Ala Ala Ser Lys Ala Ala Ile Leu Ala
 210 215 220
 Cys Ile Ala Phe His Thr Arg Val Thr Ala Asp Asp Val Tyr Cys Glu
 225 230 235 240
 Gly Ile Arg Asn Ile Asn Ala Ala Asp Ile Glu Ala Ala Gln Gln Ala
 245 250 255
 Gly His Thr Ile Lys Leu Leu Ala Ile Cys Glu Lys Phe Thr Asn Lys
 260 265 270
 Glu Gly Lys Ser Ala Ile Ser Ala Arg Val His Pro Thr Leu Leu Pro
 275 280 285
 Val Ser His Pro Leu Ala Ser Val Asn Lys Ser Phe Asn Ala Ile Phe
 290 295 300
 Val Glu Ala Glu Ala Ala Gly Arg Leu Met Phe Tyr Gly Asn Gly Ala
 305 310 315 320
 Gly Gly Ala Pro Thr Ala Ser Ala Val Leu Gly Asp Val Val Gly Ala
 325 330 335
 Ala Arg Asn Lys Val His Gly Gly Arg Ala Pro Gly Glu Ser Thr Tyr
 340 345 350
 Ala Asn Leu Pro Ile Ala Asp Phe Gly Glu Thr Thr Thr Arg Tyr His
 355 360 365
 Leu Asp Met Asp Val Glu Asp Arg Val Gly Val Leu Ala Glu Leu Ala
 370 375 380
 Ser Leu Phe Ser Glu Gln Gly Ile Ser Leu Arg Thr Ile Arg Gln Glu
 385 390 395 400
 Glu Arg Asp Asp Asp Ala Arg Leu Ile Val Val Thr His Ser Ala Leu
 405 410 415
 Glu Ser Asp Leu Ser Arg Thr Val Glu Leu Leu Lys Ala Lys Pro Val
 420 425 430
 Val Lys Ala Ile Asn Ser Val Ile Arg Leu Glu Arg Asp
 435 440 445

<210> 171

<211> 493

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(493)

<223> FRXA00974

<400> 171

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ctatagtggc taggtaccct ttttgttttg gacacatgta ggggtggccga aacaaagtaa 60

taggacaaca acgctcgacc gcgattatTT ttggagaatc atg acc tca gca tct 115
                Met Thr Ser Ala Ser
                1                    5

gcc cca agc ttt aac ccc ggc aag ggt ccc ggc tca gca gtc gga att 163
Ala Pro Ser Phe Asn Pro Gly Lys Gly Pro Gly Ser Ala Val Gly Ile
                10                    15                    20

gcc ctt tta gga ttc gga aca gtc ggc act gag gtg atg cgt ctg atg 211
Ala Leu Leu Gly Phe Gly Thr Val Gly Thr Glu Val Met Arg Leu Met
                25                    30                    35

acc gag tac ggt gat gaa ctt gcg cac cgc att ggt ggc cca ctg gag 259
Thr Glu Tyr Gly Asp Glu Leu Ala His Arg Ile Gly Gly Pro Leu Glu
                40                    45                    50

gtt cgt ggc att gct gtt tct gat atc tca aag cca cgt gaa ggc gtt 307
Val Arg Gly Ile Ala Val Ser Asp Ile Ser Lys Pro Arg Glu Gly Val
                55                    60                    65

gca cct gag ctg ctc act gag gac gct ttt gca ctc atc gag cgc gag 355
Ala Pro Glu Leu Leu Thr Glu Asp Ala Phe Ala Leu Ile Glu Arg Glu
                70                    75                    80                    85

gat gtt gac atc gtc gtt gag gtt atc ggc ggc att gag tac cca cgt 403
Asp Val Asp Ile Val Val Glu Val Ile Gly Gly Ile Glu Tyr Pro Arg
                90                    95                    100

gag gta gtt ctc gca gct ctg aag gcc ggc aag tct gtt gtt acc gcc 451
Glu Val Val Leu Ala Ala Leu Lys Ala Gly Lys Ser Val Val Thr Ala
                105                    110                    115

aat aag gct ctt gtt gca gct cac tct gct gag ctt gct gat 493
Asn Lys Ala Leu Val Ala Ala His Ser Ala Glu Leu Ala Asp
                120                    125                    130

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<210> 172

<211> 131

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 172

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Met Thr Ser Ala Ser Ala Pro Ser Phe Asn Pro Gly Lys Gly Pro Gly
 1                    5                    10                    15

Ser Ala Val Gly Ile Ala Leu Leu Gly Phe Gly Thr Val Gly Thr Glu
 20                    25                    30

Val Met Arg Leu Met Thr Glu Tyr Gly Asp Glu Leu Ala His Arg Ile
 35                    40                    45

Gly Gly Pro Leu Glu Val Arg Gly Ile Ala Val Ser Asp Ile Ser Lys
 50                    55                    60

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Pro Arg Glu Gly Val Ala Pro Glu Leu Leu Thr Glu Asp Ala Phe Ala
 65 70 75 80

Leu Ile Glu Arg Glu Asp Val Asp Ile Val Val Glu Val Ile Gly Gly
 85 90 95

Ile Glu Tyr Pro Arg Glu Val Val Leu Ala Ala Leu Lys Ala Gly Lys
 100 105 110

Ser Val Val Thr Ala Asn Lys Ala Leu Val Ala Ala His Ser Ala Glu
 115 120 125

Leu Ala Asp
 130

<210> 173
 <211> 1050
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1027)
 <223> RXA00970

<400> 173
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aacagtgtga tccgcctcga aagggaactaa ttttactgac atg gca att gaa ctg 115
 Met Ala Ile Glu Leu
 1 5

aac gtc ggt cgt aag gtt acc gtc acg gta cct gga tct tct gca aac 163
 Asn Val Gly Arg Lys Val Thr Val Thr Val Pro Gly Ser Ser Ala Asn
 10 15 20

ctc gga cct ggc ttt gac act tta ggt ttg gca ctg tcg gta tac gac 211
 Leu Gly Pro Gly Phe Asp Thr Leu Gly Leu Ala Leu Ser Val Tyr Asp
 25 30 35

act gtc gaa gtg gaa att att cca tct ggc ttg gaa gtg gaa gtt ttt 259
 Thr Val Glu Val Glu Ile Ile Pro Ser Gly Leu Glu Val Glu Val Phe
 40 45 50

ggc gaa ggc caa ggc gaa gtc cct ctt gat ggc tcc cac ctg gtg gtt 307
 Gly Glu Gly Gln Gly Glu Val Pro Leu Asp Gly Ser His Leu Val Val
 55 60 65

aaa gct att cgt gct ggc ctg aag gca gct gac gct gaa gtt cct gga 355
 Lys Ala Ile Arg Ala Gly Leu Lys Ala Ala Asp Ala Glu Val Pro Gly
 70 75 80 85

ttg cga gtg gtg tgc cac aac aac att ccg cag tct cgt ggt ctt ggc 403
 Leu Arg Val Val Cys His Asn Asn Ile Pro Gln Ser Arg Gly Leu Gly
 90 95 100

tcc tct gct gca gcg gcg gtt gct ggt gtt gct gca gct aat ggt ttg 451
 Ser Ser Ala Ala Ala Ala Val Ala Gly Val Ala Ala Ala Asn Gly Leu
 105 110 115

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gcg gat ttc ccg ctg act caa gag cag att gtt cag ttg tcc tct gcc 499
Ala Asp Phe Pro Leu Thr Gln Glu Gln Ile Val Gln Leu Ser Ser Ala
      120                      125                      130

ttt gaa ggc cac cca gat aat gct gcg gct tct gtg ctg ggt gga gca 547
Phe Glu Gly His Pro Asp Asn Ala Ala Ala Ser Val Leu Gly Gly Ala
      135                      140                      145

gtg gtg tcg tgg aca aat ctg tct atc gac ggc aag agc cag cca cag 595
Val Val Ser Trp Thr Asn Leu Ser Ile Asp Gly Lys Ser Gln Pro Gln
      150                      155                      160                      165

tat gct gct gta cca ctt gag gtg cag gac aat att cgt gcg act gcg 643
Tyr Ala Ala Val Pro Leu Glu Val Gln Asp Asn Ile Arg Ala Thr Ala
      170                      175                      180

ctg gtt cct aat ttc cac gca tcc acc gaa gct gtg cgc cga gtc ctt 691
Leu Val Pro Asn Phe His Ala Ser Thr Glu Ala Val Arg Arg Val Leu
      185                      190                      195

ccc act gaa gtc act cac atc gat gcg cga ttt aac gtg tcc cgc gtt 739
Pro Thr Glu Val Thr His Ile Asp Ala Arg Phe Asn Val Ser Arg Val
      200                      205                      210

gca gtg atg atc gtt gcg ttg cag cag cgt cct gat ttg ctg tgg gag 787
Ala Val Met Ile Val Ala Leu Gln Gln Arg Pro Asp Leu Leu Trp Glu
      215                      220                      225

ggg act cgt gac cgt ctg cac cag cct tat cgt gca gaa gtg ttg cct 835
Gly Thr Arg Asp Arg Leu His Gln Pro Tyr Arg Ala Glu Val Leu Pro
      230                      235                      240                      245

att acc tct gag tgg gta aac cgc ctg cgc aac cgt ggc tac gcg gca 883
Ile Thr Ser Glu Trp Val Asn Arg Leu Arg Asn Arg Gly Tyr Ala Ala
      250                      255                      260

tac ctt tcc ggt gcc ggc cca acc gcc atg gtg ctg tcc act gag cca 931
Tyr Leu Ser Gly Ala Gly Pro Thr Ala Met Val Leu Ser Thr Glu Pro
      265                      270                      275

att cca gac aag gtt ttg gaa gat gct cgt gag tct ggc att aag gtg 979
Ile Pro Asp Lys Val Leu Glu Asp Ala Arg Glu Ser Gly Ile Lys Val
      280                      285                      290

ctt gag ctt gag gtt gcg gga cca gtc aag gtt gaa gtt aac caa cct 1027
Leu Glu Leu Glu Val Ala Gly Pro Val Lys Val Glu Val Asn Gln Pro
      295                      300                      305

taggcccaac aaggaaggcc ccc 1050

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<210> 174

<211> 309

<212> PRT

<213> Corynebacterium glutamicum

<400> 174

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Met Ala Ile Glu Leu Asn Val Gly Arg Lys Val Thr Val Thr Val Pro
  1                      5                      10                      15

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Gly Ser Ser Ala Asn Leu Gly Pro Gly Phe Asp Thr Leu Gly Leu Ala
 20 25 30
 Leu Ser Val Tyr Asp Thr Val Glu Val Glu Ile Ile Pro Ser Gly Leu
 35 40 45
 Glu Val Glu Val Phe Gly Glu Gly Gln Gly Glu Val Pro Leu Asp Gly
 50 55 60
 Ser His Leu Val Val Lys Ala Ile Arg Ala Gly Leu Lys Ala Ala Asp
 65 70 75 80
 Ala Glu Val Pro Gly Leu Arg Val Val Cys His Asn Asn Ile Pro Gln
 85 90 95
 Ser Arg Gly Leu Gly Ser Ser Ala Ala Ala Val Ala Gly Val Ala
 100 105 110
 Ala Ala Asn Gly Leu Ala Asp Phe Pro Leu Thr Gln Glu Gln Ile Val
 115 120 125
 Gln Leu Ser Ser Ala Phe Glu Gly His Pro Asp Asn Ala Ala Ala Ser
 130 135 140
 Val Leu Gly Gly Ala Val Val Ser Trp Thr Asn Leu Ser Ile Asp Gly
 145 150 155 160
 Lys Ser Gln Pro Gln Tyr Ala Ala Val Pro Leu Glu Val Gln Asp Asn
 165 170 175
 Ile Arg Ala Thr Ala Leu Val Pro Asn Phe His Ala Ser Thr Glu Ala
 180 185 190
 Val Arg Arg Val Leu Pro Thr Glu Val Thr His Ile Asp Ala Arg Phe
 195 200 205
 Asn Val Ser Arg Val Ala Val Met Ile Val Ala Leu Gln Gln Arg Pro
 210 215 220
 Asp Leu Leu Trp Glu Gly Thr Arg Asp Arg Leu His Gln Pro Tyr Arg
 225 230 235 240
 Ala Glu Val Leu Pro Ile Thr Ser Glu Trp Val Asn Arg Leu Arg Asn
 245 250 255
 Arg Gly Tyr Ala Ala Tyr Leu Ser Gly Ala Gly Pro Thr Ala Met Val
 260 265 270
 Leu Ser Thr Glu Pro Ile Pro Asp Lys Val Leu Glu Asp Ala Arg Glu
 275 280 285
 Ser Gly Ile Lys Val Leu Glu Leu Glu Val Ala Gly Pro Val Lys Val
 290 295 300
 Glu Val Asn Gln Pro
 305

<210> 175
 <211> 1566
 <212> DNA

$\langle 220 \rangle$

<221> CDS

<222> (101) . . (1543)

<223> RXA00330

<400> 175

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gggggagtat tgtgtcaccc cttgggatag ggttatatcc gtg gac tac att tcg 115
Val Asp Tyr Ile Ser
1 5

acg cgt gat gcc agc cgt acc cct gcc cgc ttc agt gat att ttg ctg 163
Thr Arg Asp Ala Ser Arg Thr Pro Ala Arg Phe Ser Asp Ile Leu Leu
10 15 20

ggc ggt cta gca cca gac ggc gga ctg tac ctg cct gca acc tac cct 211
Gly Gly Leu Ala Pro Asp Gly Gly Leu Tyr Leu Pro Ala Thr Tyr Pro
25 30 35

caa cta gat gat gcc cag ctg agt aaa tgg cgt gag gta tta gcc aac 259
Gln Leu Asp Asp Ala Gln Leu Ser Lys Trp Arg Glu Val Leu Ala Asn
40 45 50

gaa gga tac gca gct ttg gct gct gaa gtt atc tcc ctg ttt gtt gat 307
Glu Gly Tyr Ala Ala Leu Ala Ala Glu Val Ile Ser Leu Phe Val Asp
55 60 65

gac atc cca gta gaa gac atc aag gcg atc acc gca cgc gcc tac acc 355
Asp Ile Pro Val Glu Asp Ile Lys Ala Ile Thr Ala Arg Ala Tyr Thr
70 75 80 85

tac	ccg	aag	ttc	aac	agc	gaa	gac	atc	gtt	cct	gtc	acc	gaa	ctc	gag	403
Tyr	Pro	Lys	Phe	Asn	Ser	Glu	Asp	Ile	Val	Pro	Val	Thr	Glu	Leu	Glu	
				90					95					100		

gac aac att tac ctg ggc cac ctt tcc gaa ggc cca acc gct gca ttc 451
Asp Asn Ile Tyr Leu Gly His Leu Ser Glu Gly Pro Thr Ala Ala Phe
105 110 115

aaa gac atg gcc atg cag ctg ctc ggc gaa ctt ttc gaa tac gag ctt 499
Lys Asp Met Ala Met Gln Leu Leu Gly Glu Leu Phe Glu Tyr Glu Leu
120 125 130

cgc cgc cgc aac gaa acc atc aac atc ctg ggc gct acc tct ggc gat 547
Arg Arg Arg Asn Glu Thr Ile Asn Ile Leu Gly Ala Thr Ser Gly Asp
135 140 145

acc ggc tcc tct gcg gaa tac gcc atg cgc ggc cgc gag gga atc cgc 595
Thr Gly Ser Ser Ala Glu Tyr Ala Met Arg Gly Arg Glu Gly Ile Arg
150 155 160 165

gta ttc atg ctg acc cca gct ggc cgc atg acc cca ttc cag caa gca 643
Val Phe Met Leu Thr Pro Ala Gly Arg Met Thr Pro Phe Gln Gln Ala
170 175 180

cag atg ttt ggc ctt gac gat cca aac atc ttc aac atc gcc ctc gac 691
Gln Met Phe Gly Leu Asp Asp Pro Asn Ile Phe Asn Ile Ala Leu Asp
185 190 195

ggc gtt ttc gac gat tgc caa gac gta gtc aag gct gtc tcc gcc gac	739
Gly Val Phe Asp Asp Cys Gln Asp Val Val Lys Ala Val Ser Ala Asp	
200 205 210	
gca gaa ttc aaa aaa gac aac cgc atc ggt gcc gtg aac tcc atc aac	787
Ala Glu Phe Lys Lys Asp Asn Arg Ile Gly Ala Val Asn Ser Ile Asn	
215 220 225	
tgg gca cgc ctt atg gca cag gtt gtg tac tac gtt tcc tca tgg atc	835
Trp Ala Arg Leu Met Ala Gln Val Val Tyr Tyr Val Ser Ser Trp Ile	
230 235 240 245	
cgc acc aca acc agc aat gac caa aag gtc agc ttc tcc gta cca acc	883
Arg Thr Thr Thr Ser Asn Asp Gln Lys Val Ser Phe Ser Val Pro Thr	
250 255 260	
ggc aac ttc ggt gac att tgc gca ggc cac atc gcc cgc caa atg gga	931
Gly Asn Phe Gly Asp Ile Cys Ala Gly His Ile Ala Arg Gln Met Gly	
265 270 275	
ctt ccc atc gat cgc ctc atc gtg gcc acc aac gaa aac gat gtg ctc	979
Leu Pro Ile Asp Arg Leu Ile Val Ala Thr Asn Glu Asn Asp Val Leu	
280 285 290	
gac gag ttc ttc cgt acc ggc gac tac cga gtc cgc agc tcc gca gac	1027
Asp Glu Phe Phe Arg Thr Gly Asp Tyr Arg Val Arg Ser Ser Ala Asp	
295 300 305	
acc cac gag acc tcc tca cct tcg atg gat atc tcc cgc gcc tcc aac	1075
Thr His Glu Thr Ser Ser Pro Ser Met Asp Ile Ser Arg Ala Ser Asn	
310 315 320 325	
ttc gag cgt ttc atc ttc gac ctg ctc ggc cgc gac gcc acc cgc gtc	1123
Phe Glu Arg Phe Ile Phe Asp Leu Leu Gly Arg Asp Ala Thr Arg Val	
330 335 340	
aac gat cta ttt ggt acc cag gtt cgc caa ggc gga ttc tca ctg gct	1171
Asn Asp Leu Phe Gly Thr Gln Val Arg Gln Gly Gly Phe Ser Leu Ala	
345 350 355	
gat gac gcc aac ttt gag aag gct gca gca gaa tac ggt ttc gcc tcc	1219
Asp Asp Ala Asn Phe Glu Lys Ala Ala Ala Glu Tyr Gly Phe Ala Ser	
360 365 370	
gga cga tcc acc cat gct gac cgt gtg gca acc atc gct gac gtg cat	1267
Gly Arg Ser Thr His Ala Asp Arg Val Ala Thr Ile Ala Asp Val His	
375 380 385	
tcc cgc ctc gac gta cta atc gat ccc cac acc gcc gac ggc gtt cac	1315
Ser Arg Leu Asp Val Leu Ile Asp Pro His Thr Ala Asp Gly Val His	
390 395 400 405	
gtg gca cgc cag tgg agg gac gag gtc aac acc cca atc atc gtc cta	1363
Val Ala Arg Gln Trp Arg Asp Glu Val Asn Thr Pro Ile Ile Val Leu	
410 415 420	
gaa act gca ctc cca gtg aaa ttt gcc gac acc atc gtc gaa gca att	1411
Glu Thr Ala Leu Pro Val Lys Phe Ala Asp Thr Ile Val Glu Ala Ile	
425 430 435	

ggt gaa gca cct caa act cca gag cgt ttc gcc gcg atc atg gat gct 1459
 Gly Glu Ala Pro Gln Thr Pro Glu Arg Phe Ala Ala Ile Met Asp Ala
 440 445 450

cca ttc aag gtt tcc gac cta cca aac gac acc gat gca gtt aag cag 1507
 Pro Phe Lys Val Ser Asp Leu Pro Asn Asp Thr Asp Ala Val Lys Gln
 455 460 465

tac ata gtc gat gcg att gca aac act tcc gtg aag taacttgctt 1553
 Tyr Ile Val Asp Ala Ile Ala Asn Thr Ser Val Lys
 470 475 480

tacgccaaagg cct 1566

<210> 176

<211> 481

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 176

Val Asp Tyr Ile Ser Thr Arg Asp Ala Ser Arg Thr Pro Ala Arg Phe
 1 5 10 15

Ser Asp Ile Leu Leu Gly Gly Leu Ala Pro Asp Gly Gly Leu Tyr Leu
 20 25 30

Pro Ala Thr Tyr Pro Gln Leu Asp Asp Ala Gln Leu Ser Lys Trp Arg
 35 40 45

Glu Val Leu Ala Asn Glu Gly Tyr Ala Ala Leu Ala Ala Glu Val Ile
 50 55 60

Ser Leu Phe Val Asp Asp Ile Pro Val Glu Asp Ile Lys Ala Ile Thr
 65 70 75 80

Ala Arg Ala Tyr Thr Tyr Pro Lys Phe Asn Ser Glu Asp Ile Val Pro
 85 90 95

Val Thr Glu Leu Glu Asp Asn Ile Tyr Leu Gly His Leu Ser Glu Gly
 100 105 110

Pro Thr Ala Ala Phe Lys Asp Met Ala Met Gln Leu Leu Gly Glu Leu
 115 120 125

Phe Glu Tyr Glu Leu Arg Arg Arg Asn Glu Thr Ile Asn Ile Leu Gly
 130 135 140

Ala Thr Ser Gly Asp Thr Gly Ser Ser Ala Glu Tyr Ala Met Arg Gly
 145 150 155 160

Arg Glu Gly Ile Arg Val Phe Met Leu Thr Pro Ala Gly Arg Met Thr
 165 170 175

Pro Phe Gln Gln Ala Gln Met Phe Gly Leu Asp Asp Pro Asn Ile Phe
 180 185 190

Asn Ile Ala Leu Asp Gly Val Phe Asp Asp Cys Gln Asp Val Val Lys
 195 200 205

Ala Val Ser Ala Asp Ala Glu Phe Lys Lys Asp Asn Arg Ile Gly Ala

210	215	220
Val Asn Ser Ile Asn Trp Ala Arg Leu Met	Ala Gln Val Val Tyr Tyr	
225	230	235 240
Val Ser Ser Trp Ile Arg Thr Thr Thr Ser	Asn Asp Gln Lys Val Ser	
	245	250 255
Phe Ser Val Pro Thr Gly Asn Phe Gly Asp	Ile Cys Ala Gly His Ile	
	260	265 270
Ala Arg Gln Met Gly Leu Pro Ile Asp Arg	Leu Ile Val Ala Thr Asn	
	275	280 285
Glu Asn Asp Val Leu Asp Glu Phe Phe Arg	Thr Gly Asp Tyr Arg Val	
	290	295 300
Arg Ser Ser Ala Asp Thr His Glu Thr Ser	Ser Pro Ser Met Asp Ile	
	305	310 315 320
Ser Arg Ala Ser Asn Phe Glu Arg Phe Ile	Phe Asp Leu Leu Gly Arg	
	325	330 335
Asp Ala Thr Arg Val Asn Asp Leu Phe Gly	Thr Gln Val Arg Gln Gly	
	340	345 350
Gly Phe Ser Leu Ala Asp Asp Ala Asn Phe	Glu Lys Ala Ala Ala Glu	
	355	360 365
Tyr Gly Phe Ala Ser Gly Arg Ser Thr His	Ala Asp Arg Val Ala Thr	
	370	375 380
Ile Ala Asp Val His Ser Arg Leu Asp Val	Leu Ile Asp Pro His Thr	
	385	390 395 400
Ala Asp Gly Val His Val Ala Arg Gln Trp	Arg Asp Glu Val Asn Thr	
	405	410 415
Pro Ile Ile Val Leu Glu Thr Ala Leu Pro	Val Lys Phe Ala Asp Thr	
	420	425 430
Ile Val Glu Ala Ile Gly Glu Ala Pro Gln	Thr Pro Glu Arg Phe Ala	
	435	440 445
Ala Ile Met Asp Ala Pro Phe Lys Val Ser	Asp Leu Pro Asn Asp Thr	
	450	455 460
Asp Ala Val Lys Gln Tyr Ile Val Asp Ala	Ile Ala Asn Thr Ser Val	
	465	470 475 480

Lys

<210> 177

<211> 1254

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1231)

<223> RXN00403

<400> 177

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tttttcagac tcgtgagaat gcaaactaga ctagacagag ctgtccatat acactggacg 60

aagtttttagt cttgtccacc cagaacaggc gggtatttttc atg ccc acc ctc gcg 115
                                         Met Pro Thr Leu Ala
                                         1           5

cct tca ggt caa ctt gaa atc caa gcg atc ggt gat gtc tcc acc gaa 163
Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu
                10                15                20

gcc gga gca atc att aca aac gct gaa atc gcc tat cac cgc tgg ggt 211
Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly
                25                30                35

gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa 259
Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu
                40                45                50

cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg 307
His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu
                55                60                65

ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt 355
Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys
                70                75                80                85

acc aac gtc atc ggt ggt tgc aac ggt tcc acc gga cct ggc tcc atg 403
Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met
                90                95                100

cat cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc acg tcc att 451
His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile
                105                110                115

cgt gat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc 499
Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile
                120                125                130

acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc 547
Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr
                135                140                145

cta gag tgg gcc gca atg tac cca gaa act gtt ggc gca gct gct gtt 595
Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Ala Val
                150                155                160                165

ctt gca gtt tct gca cgc gcc agc gcc tgg caa atc ggc att caa tcc 643
Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser
                170                175                180

gcc caa att aag gcg att gaa aac gac cac cac tgg cac gaa ggc aac 691
Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn
                185                190                195

tac tac gaa tcc ggc tgc aac cca gcc acc gga ctc ggc gcc gcc cga 739
Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg
                200                205                210

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cgc atc gcc cac ctc acc tac cgt ggc gaa cta gaa atc gac gaa cgc 787
 Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg
 215 220 225

 ttc ggc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc 835
 Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg
 230 235 240 245

 aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca 883
 Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala
 250 255 260

 gac aag cta gta cag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc 931
 Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr
 265 270 275

 gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac 979
 Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn
 280 285 290

 aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat 1027
 Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp
 295 300 305

 acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac 1075
 Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn
 310 315 320 325

 ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac 1123
 Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His
 330 335 340

 gat gct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac 1171
 Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn
 345 350 355

 ttc ttc agc ctc atc tcc cca gac gaa gac aac cct tcg acc tac atc 1219
 Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser Thr Tyr Ile
 360 365 370

 gag ttc tac atc taataggtat ttacgacaaa tag 1254
 Glu Phe Tyr Ile
 375

<210> 178

<211> 377

<212> PRT

<213> Corynebacterium glutamicum

<400> 178

Met Pro Thr Leu Ala Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly
 1 5 10 15

Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala
 20 25 30

Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
 35 40 45

Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
 50 55 60
 Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
 65 70 75 80
 Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
 85 90 95
 Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
 100 105 110
 Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
 115 120 125
 Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
 130 135 140
 Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
 145 150 155 160
 Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
 165 170 175
 Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His
 180 185 190
 Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
 195 200 205
 Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
 210 215 220
 Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
 225 230 235 240
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr
 245 250 255
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
 260 265 270
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
 275 280 285
 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
 290 295 300
 Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu
 305 310 315 320
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
 325 330 335
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp
 340 345 350
 Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn
 355 360 365
 Pro Ser Thr Tyr Ile Glu Phe Tyr Ile

375

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<220>  
<221> CDS  
<222> (101) .. (1210)  
<223> FRXA00403
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tttttcagac tcgtgagaat gcaaactaga ctagacagag ctgtccatat acactggacg 60

cct tca ggt caa ctt gaa atc caa gcg atc ggt gat gtc tcc acc gaa 163
Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu
10 15 20

gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa 259
Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu
40 45 50

ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt 355
Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys
70 75 80 85

cat cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc acg tcc att 451
His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile
105 110 115

acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc 547
Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr
135 140 145

ctt gca gtt tct gca cgc gcc agc gcc tgg caa atc ggc att caa tcc 643

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Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser
      170      175      180

gcc caa att aag gcg att gaa aac gac cac cac tgg cac gaa ggc aac 691
Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn
      185      190      195

tac tac gaa tcc ggc tgc aac cca gcc acc gga ctc ggc gcc gcc cga 739
Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg
      200      205      210

cgc atc gcc cac ctc acc tac cgt ggc gaa cta gaa atc gac gaa cgc 787
Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg
      215      220      225

ttc ggc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc 835
Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg
      230      235      240      245

aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca 883
Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala
      250      255      260

gac aag cta gta cag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc 931
Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr
      265      270      275

gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac 979
Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn
      280      285      290

aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat 1027
Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp
      295      300      305

acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac 1075
Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn
      310      315      320      325

ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac 1123
Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His
      330      335      340

gat gct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac 1171
Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn
      345      350      355

ttc ttc agc ctc atc tcc cca gac gaa gac aac cct tcg 1210
Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser
      360      365      370

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<210> 180

<211> 370

<212> PRT

<213> Corynebacterium glutamicum

<400> 180

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Met Pro Thr Leu Ala Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly
  1              5              10              15

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Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala
 20 25 30
 Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
 35 40 45
 Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
 50 55 60
 Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
 65 70 75 80
 Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
 85 90 95
 Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
 100 105 110
 Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
 115 120 125
 Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
 130 135 140
 Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
 145 150 155 160
 Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
 165 170 175
 Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His
 180 185 190
 Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
 195 200 205
 Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
 210 215 220
 Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
 225 230 235 240
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr
 245 250 255
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
 260 265 270
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
 275 280 285
 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
 290 295 300
 Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu
 305 310 315 320
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
 325 330 335
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp

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          340          345          350
Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn
      355          360          365

Pro Ser
  370

<210> 181
<211> 771
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(748)
<223> RXC01207

<400> 181
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atttttgaac aatccgtaca ccaacttcag gagaaaaaca gtg agc aga atc tat 115
                               Val Ser Arg Ile Tyr
                               1 5

gac tgt gcc gac caa gac tcc cgt gca gca ggc cta aag gcg gct gtc 163
Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly Leu Lys Ala Ala Val
      10          15          20

gat gca gtc aaa gcc ggt cag ctc gtt gtc ctt ccc acg gat acc ctt 211
Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu Pro Thr Asp Thr Leu
      25          30          35

tat gga ctc ggc tgc gac gct ttc aac aac gag gca gta gcc aac ctt 259
Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu Ala Val Ala Asn Leu
      40          45          50

ctg gcc acc aaa cac cgt ggc ccc gat atg ccc gtt cca gtg ctc gtc 307
Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro Val Pro Val Leu Val
      55          60          65

ggc agc tgg gac acc att caa gga ctt gtg cac tcc tat tct gcg cag 355
Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His Ser Tyr Ser Ala Gln
      70          75          80          85

gca aaa gcg ctt gtg gag gcg ttc tgg cct ggt gga ctg tcc atc atc 403
Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly Gly Leu Ser Ile Ile
      90          95          100

gtt ccg cag gca cca agc ctt ccg tgg aac ctt ggc gat acc cgt ggc 451
Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu Gly Asp Thr Arg Gly
      105          110          115

acc gta atg ctg cgc atg cca ctg cac cca gtt gcc att gaa ttg ctg 499
Thr Val Met Leu Arg Met Pro Leu His Pro Val Ala Ile Glu Leu Leu
      120          125          130

cgc caa acc gga cca atg gct gtc tcc tcc gcc aac atc tcc gga cat 547
Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala Asn Ile Ser Gly His
      135          140          145

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act cct cca acc acc gtg ctg gag gct cgt cag cag ctc aac caa aat 595
 Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln Gln Leu Asn Gln Asn
 150 155 160 165

gtc gct gtc tac ctc gat ggt ggc gaa tgc gcg ctg gcc acc cct tca 643
 Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala Leu Ala Thr Pro Ser
 170 175 180

acc atc gtg gat att tca ggc ccc gca cca aag att ttg cgt gag ggt 691
 Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys Ile Leu Arg Glu Gly
 185 190 195

gcc atc agc gca gaa cgc gtt ggc gaa gta ctt gga gtg tcg gca gaa 739
 Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu Gly Val Ser Ala Glu
 200 205 210

agc ctg cgc taaatgggag tcggtttcgc ggg 771
 Ser Leu Arg
 215

<210> 182

<211> 216

<212> PRT

<213> Corynebacterium glutamicum

<400> 182

Val Ser Arg Ile Tyr Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly
 1 5 10 15

Leu Lys Ala Ala Val Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu
 20 25 30

Pro Thr Asp Thr Leu Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu
 35 40 45

Ala Val Ala Asn Leu Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro
 50 55 60

Val Pro Val Leu Val Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His
 65 70 75 80

Ser Tyr Ser Ala Gln Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly
 85 90 95

Gly Leu Ser Ile Ile Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu
 100 105 110

Gly Asp Thr Arg Gly Thr Val Met Leu Arg Met Pro Leu His Pro Val
 115 120 125

Ala Ile Glu Leu Leu Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala
 130 135 140

Asn Ile Ser Gly His Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln
 145 150 155 160

Gln Leu Asn Gln Asn Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala
 165 170 175

Leu Ala Thr Pro Ser Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys
 180 185 190

Ile Leu Arg Glu Gly Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu
 195 200 205

Gly Val Ser Ala Glu Ser Leu Arg
 210 215

<210> 183

<211> 1419

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (1396)

<223> RXC00152

<400> 183

gtcattgata tccaaggcac gaccgcgatt gtatggaaag aagcctaaat ttttaacaat 60

caaatagtac tggccattcc caactaaaac tggagtaacg atg aca gga cta atc 115
 Met Thr Gly Leu Ile
 1 5

ctc gcc ata gtt ttc ctg gtc ttt gtc gcc gtc gtg gtg atc aag tcc 163
 Leu Ala Ile Val Phe Leu Val Phe Val Ala Val Val Val Ile Lys Ser
 10 15 20

ata gcc ctg att ccc cag ggt gaa gcc gcc gtc att gaa cgc ctt ggt 211
 Ile Ala Leu Ile Pro Gln Gly Glu Ala Ala Val Ile Glu Arg Leu Gly
 25 30 35

agc tac acc cgc acc gtt tca ggt ggc ctg acc ctg ctg gtt cca ttc 259
 Ser Tyr Thr Arg Thr Val Ser Gly Gly Leu Thr Leu Leu Val Pro Phe
 40 45 50

gtg gac cga gta cgc gca agg atc gac acc cgt gag cgc gtg gtc tca 307
 Val Asp Arg Val Arg Ala Arg Ile Asp Thr Arg Glu Arg Val Val Ser
 55 60 65

ttc cca ccg cag gct gtt att acc caa gac aac ctg acc gtg gcc atc 355
 Phe Pro Pro Gln Ala Val Ile Thr Gln Asp Asn Leu Thr Val Ala Ile
 70 75 80 85

gat atc gtg gtg acc ttc caa atc aac gaa cca gag cgc gcc atc tac 403
 Asp Ile Val Val Thr Phe Gln Ile Asn Glu Pro Glu Arg Ala Ile Tyr
 90 95 100

ggc gtg gac aac tac atc gtc ggt gtg gag cag att tct gta gca aca 451
 Gly Val Asp Asn Tyr Ile Val Gly Val Glu Gln Ile Ser Val Ala Thr
 105 110 115

ctt cga gac gtt gtc ggt ggc atg acc ctg gaa gaa acc ctc act tca 499
 Leu Arg Asp Val Val Gly Gly Met Thr Leu Glu Glu Thr Leu Thr Ser
 120 125 130

cgt gac gtg atc aac cgc cgc ctc cgt ggc gag ctc gat gca gca acc 547
 Arg Asp Val Ile Asn Arg Arg Leu Arg Gly Glu Leu Asp Ala Ala Thr

135	140	145	
acc aaa tgg ggc ctg cgc atc agc cgt gtg gaa cta aag gca att gat			595
Thr Lys Trp Gly Leu Arg Ile Ser Arg Val Glu Leu Lys Ala Ile Asp			
150	155	160	165
ccg cca cca tcc atc cag caa tcg atg gaa aag cag atg aag gca gac			643
Pro Pro Pro Ser Ile Gln Gln Ser Met Glu Lys Gln Met Lys Ala Asp			
	170	175	180
cgt gaa aag cgc gcc acc att ttg acc gca gaa ggt cag cgc gaa gcc			691
Arg Glu Lys Arg Ala Thr Ile Leu Thr Ala Glu Gly Gln Arg Glu Ala			
	185	190	195
gac atc aaa act gcc gaa ggt gaa aag caa gcc aag atc ctc caa gct			739
Asp Ile Lys Thr Ala Glu Gly Glu Lys Gln Ala Lys Ile Leu Gln Ala			
	200	205	210
gag ggt gaa aag cac gca tcc atc ctg aac gca gaa gca gaa cgc caa			787
Glu Gly Glu Lys His Ala Ser Ile Leu Asn Ala Glu Ala Glu Arg Gln			
	215	220	225
gcg atg atc ctg cgc gcc gaa ggt gaa cgc gca gca cgc tac ctc cag			835
Ala Met Ile Leu Arg Ala Glu Gly Glu Arg Ala Ala Arg Tyr Leu Gln			
	230	235	240
gcg cag ggt gaa gcc cga gca atc caa aag gtc aac gca gca atc aag			883
Ala Gln Gly Glu Ala Arg Ala Ile Gln Lys Val Asn Ala Ala Ile Lys			
	250	255	260
tct gcc aag ttg acc cca gag gtt ctt gct tat caa tac ctc gaa aag			931
Ser Ala Lys Leu Thr Pro Glu Val Leu Ala Tyr Gln Tyr Leu Glu Lys			
	265	270	275
ctt cct aag atc gca gag ggc aac gcc tcc aag atg tgg gtc atc cca			979
Leu Pro Lys Ile Ala Glu Gly Asn Ala Ser Lys Met Trp Val Ile Pro			
	280	285	290
agc cag ttc tcc gat tct ctg gaa ggt ttt gcg aag cag ttc ggc gca			1027
Ser Gln Phe Ser Asp Ser Leu Glu Gly Phe Ala Lys Gln Phe Gly Ala			
	295	300	305
aag gat gca gaa ggt gtc ttc cgc tac gaa cca aac acc gtg gat gaa			1075
Lys Asp Ala Glu Gly Val Phe Arg Tyr Glu Pro Asn Thr Val Asp Glu			
	310	315	320
gaa acc cgc gac atc gca aac gcc gac aac gtg gaa gac tgg ttc tcc			1123
Glu Thr Arg Asp Ile Ala Asn Ala Asp Asn Val Glu Asp Trp Phe Ser			
	330	335	340
acc gaa tca gac cct gaa atc gca gca gca gtc gcc gca gca aac gcc			1171
Thr Glu Ser Asp Pro Glu Ile Ala Ala Ala Val Ala Ala Asn Ala			
	345	350	355
gtg gcc aac aag cca gtc gat cca gaa ccc ggt gag atc ctt tcc aag			1219
Val Ala Asn Lys Pro Val Asp Pro Glu Pro Gly Glu Ile Leu Ser Lys			
	360	365	370
aag acc gca cga cgc gtt gaa cct gaa gca gta ttg gag gct ttg caa			1267
Lys Thr Ala Arg Arg Val Glu Pro Glu Ala Val Leu Glu Ala Leu Gln			
	375	380	385

aac gga acc act aca caa cct gag gtt gag gca gca cct cct acc gca 1315
 Asn Gly Thr Thr Thr Gln Pro Glu Val Glu Ala Ala Pro Pro Thr Ala
 390 395 400 405

aac ttc gcc caa gaa ttc cct gca cca cag gca aac cct gaa gat tac 1363
 Asn Phe Ala Gln Glu Phe Pro Ala Pro Gln Ala Asn Pro Glu Asp Tyr
 410 415 420

tcc gac caa cac cga gag aat cct tac gga aac taatcaggca taagaaaagg 1416
 Ser Asp Gln His Arg Glu Asn Pro Tyr Gly Asn
 425 430

cgg 1419

<210> 184

<211> 432

<212> PRT

<213> Corynebacterium glutamicum

<400> 184

Met Thr Gly Leu Ile Leu Ala Ile Val Phe Leu Val Phe Val Ala Val
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Val Val Ile Lys Ser Ile Ala Leu Ile Pro Gln Gly Glu Ala Ala Val
 20 25 30

Ile Glu Arg Leu Gly Ser Tyr Thr Arg Thr Val Ser Gly Gly Leu Thr
 35 40 45

Leu Leu Val Pro Phe Val Asp Arg Val Arg Ala Arg Ile Asp Thr Arg
 50 55 60

Glu Arg Val Val Ser Phe Pro Pro Gln Ala Val Ile Thr Gln Asp Asn
 65 70 75 80

Leu Thr Val Ala Ile Asp Ile Val Val Thr Phe Gln Ile Asn Glu Pro
 85 90 95

Glu Arg Ala Ile Tyr Gly Val Asp Asn Tyr Ile Val Gly Val Glu Gln
 100 105 110

Ile Ser Val Ala Thr Leu Arg Asp Val Val Gly Gly Met Thr Leu Glu
 115 120 125

Glu Thr Leu Thr Ser Arg Asp Val Ile Asn Arg Arg Leu Arg Gly Glu
 130 135 140

Leu Asp Ala Ala Thr Thr Lys Trp Gly Leu Arg Ile Ser Arg Val Glu
 145 150 155 160

Leu Lys Ala Ile Asp Pro Pro Pro Ser Ile Gln Gln Ser Met Glu Lys
 165 170 175

Gln Met Lys Ala Asp Arg Glu Lys Arg Ala Thr Ile Leu Thr Ala Glu
 180 185 190

Gly Gln Arg Glu Ala Asp Ile Lys Thr Ala Glu Gly Glu Lys Gln Ala
 195 200 205

Lys Ile Leu Gln Ala Glu Gly Glu Lys His Ala Ser Ile Leu Asn Ala
 210 215 220
 Glu Ala Glu Arg Gln Ala Met Ile Leu Arg Ala Glu Gly Glu Arg Ala
 225 230 235 240
 Ala Arg Tyr Leu Gln Ala Gln Gly Glu Ala Arg Ala Ile Gln Lys Val
 245 250 255
 Asn Ala Ala Ile Lys Ser Ala Lys Leu Thr Pro Glu Val Leu Ala Tyr
 260 265 270
 Gln Tyr Leu Glu Lys Leu Pro Lys Ile Ala Glu Gly Asn Ala Ser Lys
 275 280 285
 Met Trp Val Ile Pro Ser Gln Phe Ser Asp Ser Leu Glu Gly Phe Ala
 290 295 300
 Lys Gln Phe Gly Ala Lys Asp Ala Glu Gly Val Phe Arg Tyr Glu Pro
 305 310 315 320
 Asn Thr Val Asp Glu Glu Thr Arg Asp Ile Ala Asn Ala Asp Asn Val
 325 330 335
 Glu Asp Trp Phe Ser Thr Glu Ser Asp Pro Glu Ile Ala Ala Val
 340 345 350
 Ala Ala Ala Asn Ala Val Ala Asn Lys Pro Val Asp Pro Glu Pro Gly
 355 360 365
 Glu Ile Leu Ser Lys Lys Thr Ala Arg Arg Val Glu Pro Glu Ala Val
 370 375 380
 Leu Glu Ala Leu Gln Asn Gly Thr Thr Thr Gln Pro Glu Val Glu Ala
 385 390 395 400
 Ala Pro Pro Thr Ala Asn Phe Ala Gln Glu Phe Pro Ala Pro Gln Ala
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<211> 1170

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1147)

<223> RXA00115

<400> 185

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 cgtatattgt gacctacacc ccatactgtt aggagttttc atg ctc gac aat agt 115
 Met Leu Asp Asn Ser

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ttt	tac	acc	gca	gag	gtt	cag	ggc	cca	tac	gaa	acc	gct	tcc	att	ggc		163
Phe	Tyr	Thr	Ala	Glu	Val	Gln	Gly	Pro	Tyr	Glu	Thr	Ala	Ser	Ile	Gly		
				10					15					20			
cgg	ctc	gaa	ctc	gaa	gaa	ggg	ggg	gtg	att	gag	gat	tgc	tgg	ttg	gct		211
Arg	Leu	Glu	Leu	Glu	Glu	Gly	Gly	Val	Ile	Glu	Asp	Cys	Trp	Leu	Ala		
			25					30					35				
tac	gct	aca	gct	gga	acg	ctc	aac	gag	gac	aag	tcc	aac	gcc	atc	ctc		259
Tyr	Ala	Thr	Ala	Gly	Thr	Leu	Asn	Glu	Asp	Lys	Ser	Asn	Ala	Ile	Leu		
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att	cgc	acg	tgg	tac	tcc	gga	acc	cat	cag	acc	tgg	ttc	cag	cag	tac		307
Ile	Pro	Thr	Trp	Tyr	Ser	Gly	Thr	His	Gln	Thr	Trp	Phe	Gln	Gln	Tyr		
	55					60					65						
atc	ggc	act	gat	cat	gcg	ctg	gat	cca	tca	aag	tat	ttc	atc	atc	tcc		355
Ile	Gly	Thr	Asp	His	Ala	Leu	Asp	Pro	Ser	Lys	Tyr	Phe	Ile	Ile	Ser		
	70				75					80					85		
atc	aac	caa	atc	ggg	aat	ggg	ttg	tcg	gtc	tcc	cct	gcc	aac	acg	gct		403
Ile	Asn	Gln	Ile	Gly	Asn	Gly	Leu	Ser	Val	Ser	Pro	Ala	Asn	Thr	Ala		
				90					95					100			
gat	gac	agc	atc	tcg	atg	tcc	aag	ttc	cgc	aat	gtt	cgc	att	ggg	gat		451
Asp	Asp	Ser	Ile	Ser	Met	Ser	Lys	Phe	Pro	Asn	Val	Arg	Ile	Gly	Asp		
			105					110					115				
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Asp	Val	Val	Ala	Gln	Asp	Arg	Leu	Leu	Arg	Gln	Glu	Phe	Gly	Ile	Thr		
			120				125					130					
gag	ctc	ttt	gcc	gtc	gtt	ggg	ggg	tcg	atg	ggg	gcg	cag	caa	acc	tat		547
Glu	Leu	Phe	Ala	Val	Val	Gly	Gly	Ser	Met	Gly	Ala	Gln	Gln	Thr	Tyr		
	135					140					145						
gag	tgg	att	gtt	cgc	ttc	cct	gac	caa	gtt	cat	cga	gca	gct	ccg	atc		595
Glu	Trp	Ile	Val	Arg	Phe	Pro	Asp	Gln	Val	His	Arg	Ala	Ala	Pro	Ile		
	150				155					160					165		
gcg	ggc	act	gcg	aag	aac	act	cct	cat	gat	ttc	atc	ttc	acc	cag	act		643
Ala	Gly	Thr	Ala	Lys	Asn	Thr	Pro	His	Asp	Phe	Ile	Phe	Thr	Gln	Thr		
				170					175					180			
ctt	aat	gag	acc	gtt	gag	gcc	gat	cca	ggg	ttc	aat	ggc	ggc	gaa	tac		691
Leu	Asn	Glu	Thr	Val	Glu	Ala	Asp	Pro	Gly	Phe	Asn	Gly	Gly	Glu	Tyr		
			185					190					195				
tcc	tcc	cat	gaa	gag	gta	gct	gat	gga	ctt	cgc	cgt	caa	tcg	cat	ctt		739
Ser	Ser	His	Glu	Glu	Val	Ala	Asp	Gly	Leu	Arg	Arg	Gln	Ser	His	Leu		
			200				205					210					
tgg	gct	gcc	atg	gga	ttt	tcc	aca	gag	ttc	tgg	aag	cag	gag	gca	tgg		787
Trp	Ala	Ala	Met	Gly	Phe	Ser	Thr	Glu	Phe	Trp	Lys	Gln	Glu	Ala	Trp		
	215					220					225						
cgt	cgc	ctg	gga	ctt	gaa	agt	aag	gag	tca	gtg	ctc	gcg	gac	ttc	ctg		835
Arg	Arg	Leu	Gly	Leu	Glu	Ser	Lys	Glu	Ser	Val	Leu	Ala	Asp	Phe	Leu		
	230				235					240					245		

gat ccg ctg ttc atg tcc atg gat cct aat acc ttg ctc aac aac gct 883
Asp Pro Leu Phe Met Ser Met Asp Pro Asn Thr Leu Leu Asn Asn Ala
250 255 260

tgg aag tgg cag cat ggc gat gtc tct cgc cac acc ggc ggc gac ttg 931
Trp Lys Trp Gln His Gly Asp Val Ser Arg His Thr Gly Gly Asp Leu
265 270 275

gca gcg gct ctt ggc cga gtg aag gct aag acc ttc gtt atg ccc atc 979
Ala Ala Ala Leu Gly Arg Val Lys Ala Lys Thr Phe Val Met Pro Ile
280 285 290

agc gag gac atg ttc ttt cct gtt cgt gac tgt gcc gca gaa caa gca 1027
Ser Glu Asp Met Phe Phe Pro Val Arg Asp Cys Ala Ala Glu Gln Ala
295 300 305

ctc atc cca ggc agc gag ctt cga gtg atc gaa gac atc gcc ggt cac 1075
Leu Ile Pro Gly Ser Glu Leu Arg Val Ile Glu Asp Ile Ala Gly His
310 315 320 325

ctt ggg ctt ttt aac gtc tct gag aat tac atc cca cag atc gac aaa 1123
Leu Gly Leu Phe Asn Val Ser Glu Asn Tyr Ile Pro Gln Ile Asp Lys
330 335 340

aat ctg aaa gag ctg ttc gag agc taaacactga tgtcaaagag cct 1170
Asn Leu Lys Glu Leu Phe Glu Ser
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<210> 186

<211> 349

<212> PRT

<213> Corynebacterium glutamicum

<400> 186

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Asp Cys Trp Leu Ala Tyr Ala Thr Ala Gly Thr Leu Asn Glu Asp Lys
35 40 45

Ser Asn Ala Ile Leu Ile Pro Thr Trp Tyr Ser Gly Thr His Gln Thr
50 55 60

Trp Phe Gln Gln Tyr Ile Gly Thr Asp His Ala Leu Asp Pro Ser Lys
65 70 75 80

Tyr Phe Ile Ile Ser Ile Asn Gln Ile Gly Asn Gly Leu Ser Val Ser
85 90 95

Pro Ala Asn Thr Ala Asp Asp Ser Ile Ser Met Ser Lys Phe Pro Asn
100 105 110

Val Arg Ile Gly Asp Asp Val Val Ala Gln Asp Arg Leu Leu Arg Gln
115 120 125

Glu Phe Gly Ile Thr Glu Leu Phe Ala Val Val Gly Gly Ser Met Gly

130	135	140
Ala Gln Gln Thr Tyr Glu Trp Ile Val Arg Phe Pro Asp Gln Val His		
145	150	155 160
Arg Ala Ala Pro Ile Ala Gly Thr Ala Lys Asn Thr Pro His Asp Phe		
	165	170 175
Ile Phe Thr Gln Thr Leu Asn Glu Thr Val Glu Ala Asp Pro Gly Phe		
	180	185 190
Asn Gly Gly Glu Tyr Ser Ser His Glu Glu Val Ala Asp Gly Leu Arg		
	195	200 205
Arg Gln Ser His Leu Trp Ala Ala Met Gly Phe Ser Thr Glu Phe Trp		
	210	215 220
Lys Gln Glu Ala Trp Arg Arg Leu Gly Leu Glu Ser Lys Glu Ser Val		
	225	230 235 240
Leu Ala Asp Phe Leu Asp Pro Leu Phe Met Ser Met Asp Pro Asn Thr		
	245	250 255
Leu Leu Asn Asn Ala Trp Lys Trp Gln His Gly Asp Val Ser Arg His		
	260	265 270
Thr Gly Gly Asp Leu Ala Ala Ala Leu Gly Arg Val Lys Ala Lys Thr		
	275	280 285
Phe Val Met Pro Ile Ser Glu Asp Met Phe Phe Pro Val Arg Asp Cys		
	290	295 300
Ala Ala Glu Gln Ala Leu Ile Pro Gly Ser Glu Leu Arg Val Ile Glu		
	305	310 315 320
Asp Ile Ala Gly His Leu Gly Leu Phe Asn Val Ser Glu Asn Tyr Ile		
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Pro Gln Ile Asp Lys Asn Leu Lys Glu Leu Phe Glu Ser		
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<211> 1254

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1231)

<223> RXN00403

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Met Pro Thr Leu Ala	
1 5	

cct tca ggt caa ctt gaa atc caa gcg atc ggt gat gtc tcc acc gaa	163
Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu	

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gcc	gga	gca	atc	att	aca	aac	gct	gaa	atc	gcc	tat	cac	cgc	tgg	ggt					211									
Ala	Gly	Ala	Ile	Ile	Thr	Asn	Ala	Glu	Ile	Ala	Tyr	His	Arg	Trp	Gly														
			25					30					35																
gaa	tac	cgc	gta	gat	aaa	gaa	gga	cgc	agc	aat	gtc	gtt	ctc	atc	gaa					259									
Glu	Tyr	Arg	Val	Asp	Lys	Glu	Gly	Arg	Ser	Asn	Val	Val	Leu	Ile	Glu														
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cac	gcc	ctc	act	gga	gat	tcc	aac	gca	gcc	gat	tgg	tgg	gct	gac	ttg					307									
His	Ala	Leu	Thr	Gly	Asp	Ser	Asn	Ala	Ala	Asp	Trp	Trp	Ala	Asp	Leu														
		55				60					65																		
ctc	ggt	ccc	ggc	aaa	gcc	atc	aac	act	gat	att	tac	tgc	gtg	atc	tgt					355									
Leu	Gly	Pro	Gly	Lys	Ala	Ile	Asn	Thr	Asp	Ile	Tyr	Cys	Val	Ile	Cys														
	70				75			80							85														
acc	aac	gtc	atc	ggt	ggt	tgc	aac	ggt	tcc	acc	gga	cct	ggc	tcc	atg					403									
Thr	Asn	Val	Ile	Gly	Gly	Cys	Asn	Gly	Ser	Thr	Gly	Pro	Gly	Ser	Met														
				90				95						100															
cat	cca	gat	gga	aat	ttc	tgg	ggt	aat	cgc	ttc	ccc	gcc	acg	tcc	att					451									
His	Pro	Asp	Gly	Asn	Phe	Trp	Gly	Asn	Arg	Phe	Pro	Ala	Thr	Ser	Ile														
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cgt	gat	cag	gta	aac	gcc	gaa	aaa	caa	ttc	ctc	gac	gca	ctc	ggc	atc					499									
Arg	Asp	Gln	Val	Asn	Ala	Glu	Lys	Gln	Phe	Leu	Asp	Ala	Leu	Gly	Ile														
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acc	acg	gtc	gcc	gca	gta	ctt	ggt	ggt	tcc	atg	ggt	ggt	gcc	cgc	acc					547									
Thr	Thr	Val	Ala	Ala	Val	Leu	Gly	Gly	Ser	Met	Gly	Gly	Ala	Arg	Thr														
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Leu	Glu	Trp	Ala	Ala	Met	Tyr	Pro	Glu	Thr	Val	Gly	Ala	Ala	Ala	Val														
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ctt	gca	gtt	tct	gca	cgc	gcc	agc	gcc	tgg	caa	atc	ggc	att	caa	tcc					643									
Leu	Ala	Val	Ser	Ala	Arg	Ala	Ser	Ala	Trp	Gln	Ile	Gly	Ile	Gln	Ser														
			170					175						180															
gcc	caa	att	aag	gcg	att	gaa	aac	gac	cac	cac	tgg	cac	gaa	ggc	aac					691									
Ala	Gln	Ile	Lys	Ala	Ile	Glu	Asn	Asp	His	His	Trp	His	Glu	Gly	Asn														
			185					190					195																
tac	tac	gaa	tcc	ggc	tgc	aac	cca	gcc	acc	gga	ctc	ggc	gcc	gcc	cga					739									
Tyr	Tyr	Glu	Ser	Gly	Cys	Asn	Pro	Ala	Thr	Gly	Leu	Gly	Ala	Ala	Arg														
		200				205						210																	
cgc	atc	gcc	cac	ctc	acc	tac	cgt	ggc	gaa	cta	gaa	atc	gac	gaa	cgc					787									
Arg	Ile	Ala	His	Leu	Thr	Tyr	Arg	Gly	Glu	Leu	Glu	Ile	Asp	Glu	Arg														
	215					220					225																		
ttc	ggc	acc	aaa	gcc	caa	aag	aac	gaa	aac	cca	ctc	ggt	ccc	tac	cgc					835									
Phe	Gly	Thr	Lys	Ala	Gln	Lys	Asn	Glu	Asn	Pro	Leu	Gly	Pro	Tyr	Arg														
	230				235					240					245														
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Lys	Pro	Asp	Gln	Arg	Phe	Ala	Val	Glu	Ser	Tyr	Leu	Asp	Tyr	Gln	Ala														
			250					255						260															

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 Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr
 265 270 275

 gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac 979
 Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn
 280 285 290

 aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat 1027
 Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp
 295 300 305

 acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac 1075
 Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn
 310 315 320 325

 ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac 1123
 Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His
 330 335 340

 gat gct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac 1171
 Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn
 345 350 355

 ttc ttc agc ctc atc tcc cca gac gaa gac aac cct tcg acc tac atc 1219
 Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser Thr Tyr Ile
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 Glu Phe Tyr Ile
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<210> 188

<211> 377

<212> PRT

<213> Corynebacterium glutamicum

<400> 188

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 Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
 35 40 45

 Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
 50 55 60

 Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
 65 70 75 80

 Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
 85 90 95

 Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
 100 105 110

Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
 115 120 125
 Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
 130 135 140
 Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
 145 150 155 160
 Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
 165 170 175
 Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His
 180 185 190
 Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
 195 200 205
 Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
 210 215 220
 Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
 225 230 235 240
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr
 245 250 255
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
 260 265 270
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
 275 280 285
 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
 290 295 300
 Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu
 305 310 315 320
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
 325 330 335
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp
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 Pro Ser Thr Tyr Ile Glu Phe Tyr Ile
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 <213> Corynebacterium glutamicum

<220>
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 <223> FRXA00403

<400> 189

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Met Pro Thr Leu Ala
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cct tca ggt caa ctt gaa atc caa gcg atc ggt gat gtc tcc acc gaa 163
Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu
10 15 20

gcc gga gca atc att aca aac gct gaa atc gcc tat cac cgc tgg ggt 211
Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly
25 30 35

gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa 259
Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu
40 45 50

cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg 307
His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu
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ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt 355
Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys
70 75 80 85

acc aac gtc atc ggt ggt tgc aac ggt tcc acc gga cct ggc tcc atg 403
Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met
90 95 100

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His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile
105 110 115

cgt gat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc 499
Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile
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acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc 547
Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr
135 140 145

cta gag tgg gcc gca atg tac cca gaa act gtt ggc gca gct gct gtt 595
Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Ala Val
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Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser
170 175 180

gcc caa att aag gcg att gaa aac gac cac cac tgg cac gaa ggc aac 691
Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn
185 190 195

tac tac gaa tcc ggc tgc aac cca gcc acc gga ctc ggc gcc gcc cga 739
Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg
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cgc atc gcc cac ctc acc tac cgt ggc gaa cta gaa atc gac gaa cgc 787

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Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg
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 230 235 240 245
 aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca 883
 Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala
 250 255 260
 gac aag cta gta cag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc 931
 Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr
 265 270 275
 gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac 979
 Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn
 280 285 290
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 Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp
 295 300 305
 acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac 1075
 Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn
 310 315 320 325
 ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac 1123
 Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His
 330 335 340
 gat gct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac 1171
 Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn
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 Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser
 360 365 370

<210> 190

<211> 370

<212> PRT

<213> Corynebacterium glutamicum

<400> 190

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 35 40 45
 Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
 50 55 60
 Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
 65 70 75 80

Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
 85 90 95
 Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
 100 105 110
 Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
 115 120 125
 Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
 130 135 140
 Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
 145 150 155 160
 Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
 165 170 175
 Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His
 180 185 190
 Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
 195 200 205
 Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
 210 215 220
 Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
 225 230 235 240
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr
 245 250 255
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
 260 265 270
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
 275 280 285
 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
 290 295 300
 Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu
 305 310 315 320
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
 325 330 335
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp
 340 345 350
 Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn
 355 360 365
 Pro Ser
 370

<210> 191

<211> 687

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(664)

<223> RXS03158

<400> 191

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caaagctcac cgaaggcacc aacgccaagt tggttgttga caacaccttg gcatcccat 60
acctgcagca gccactaaaa ctcggcgcac acgcaagtcc ttg cac tcc acc acc 115
                                   Leu His Ser Thr Thr
                                   1      5

aag tac atc gaa gga cac tcc gac gtt gtt ggc ggc ctt gtg ggt acc 163
Lys Tyr Ile Glu Gly His Ser Asp Val Val Gly Gly Leu Val Gly Thr
                                   10      15      20

aac gac cag gaa atg gac gaa gaa ctg ctg ttc atg cag ggc ggc atc 211
Asn Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile
                                   25      30      35

gga ccg atc cca tca gtt ttc gat gca tac ctg acc gcc cgt ggc ctc 259
Gly Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu
                                   40      45      50

aag acc ctt gca gtg cgc atg gat cgc cac tgc gac aac gca gaa aag 307
Lys Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys
                                   55      60      65

atc gcg gaa ttc ctg gac tcc cgc cca gag gtc tcc acc gtg ctc tac 355
Ile Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr
                                   70      75      80      85

cca ggt ctg aag aac cac cca ggc cac gaa gtc gca gcg aag cag atg 403
Pro Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met
                                   90      95      100

aag cgc ttc ggc ggc atg atc tcc gtc cgt ttc gca ggc ggc gaa gaa 451
Lys Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu
                                   105      110      115

gca gct aag aag ttc tgt acc tcc acc aaa ctg atc tgt ctg gcc gag 499
Ala Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu
                                   120      125      130

tcc ctc ggt ggc gtg gaa tcc ctc ctg gag cac cca gca acc atg acc 547
Ser Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr
                                   135      140      145

cac cag tca gct gcc ggc tct cag ctc gag gtt ccc cgc gac ctc gtg 595
His Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val
                                   150      155      160      165

cgc atc tcc att ggt att gaa gac att gaa gac ctg ctc gca gat gtc 643
Arg Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val
                                   170      175      180

gag cag gcc ctc aat aac ctt tagaaactat ttggcggcaa gca 687
Glu Gln Ala Leu Asn Asn Leu
                                   185

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<210> 192

<211> 188

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 192

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 1 5 10 15

Gly Leu Val Gly Thr Asn Asp Gln Glu Met Asp Glu Glu Leu Leu Phe
 20 25 30

Met Gln Gly Gly Ile Gly Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu
 35 40 45

Thr Ala Arg Gly Leu Lys Thr Leu Ala Val Arg Met Asp Arg His Cys
 50 55 60

Asp Asn Ala Glu Lys Ile Ala Glu Phe Leu Asp Ser Arg Pro Glu Val
 65 70 75 80

Ser Thr Val Leu Tyr Pro Gly Leu Lys Asn His Pro Gly His Glu Val
 85 90 95

Ala Ala Lys Gln Met Lys Arg Phe Gly Gly Met Ile Ser Val Arg Phe
 100 105 110

Ala Gly Gly Glu Glu Ala Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu
 115 120 125

Ile Cys Leu Ala Glu Ser Leu Gly Gly Val Glu Ser Leu Leu Glu His
 130 135 140

Pro Ala Thr Met Thr His Gln Ser Ala Ala Gly Ser Gln Leu Glu Val
 145 150 155 160

Pro Arg Asp Leu Val Arg Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp
 165 170 175

Leu Leu Ala Asp Val Glu Gln Ala Leu Asn Asn Leu
 180 185

<210> 193

<211> 617

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1) .. (594)

<223> FRXA00254

<400> 193

cag cca cta aaa ctc ggc gca cac gca gtc ttg cac tcc acc acc aag 48
 Gln Pro Leu Lys Leu Gly Ala His Ala Val Leu His Ser Thr Thr Lys
 1 5 10 15

tac atc gga gga cac tcc gac gtt gtt ggc ggc ctt gtg gtt acc aac 96

Tyr Ile Gly Gly His Ser Asp Val Val Gly Gly Leu Val Val Thr Asn
 20 25 30
 gac cag gaa atg gac gaa gaa ctg ctg ttc atg cag ggc ggc atc gga 144
 Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile Gly
 35 40 45
 ccg atc cca tca gtt ttc gat gca tac ctg acc gcc cgt ggc ctc aag 192
 Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu Lys
 50 55 60
 acc ctt gca gtg cgc atg gat cgc cac tgc gac aac gca gaa aag atc 240
 Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys Ile
 65 70 75 80
 gcg gaa ttc ctg gac tcc cgc cca gag gtc tcc acc gtg ctc tac cca 288
 Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr Pro
 85 90 95
 ggt ctg aag aac cac cca ggc cac gaa gtc gca gcg aag cag atg aag 336
 Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met Lys
 100 105 110
 cgc ttc ggc ggc atg atc tcc gtc cgt ttc gca ggc ggc gaa gaa gca 384
 Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu Ala
 115 120 125
 gct aag aag ttc tgt acc tcc acc aaa ctg atc tgt ctg gcc gag tcc 432
 Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu Ser
 130 135 140
 ctc ggt ggc gtg gaa tcc ctc ctg gag cac cca gca acc atg acc cac 480
 Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr His
 145 150 155 160
 cag tca gct gcc ggc tct cag ctc gag gtt ccc cgc gac ctc gtg cgc 528
 Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val Arg
 165 170 175
 atc tcc att ggt att gaa gac att gaa gac ctg ctc gca gat gtc gag 576
 Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val Glu
 180 185 190
 cag gcc ctc aat aac ctt tagaaactat ttggcggcaa gca 617
 Gln Ala Leu Asn Asn Leu
 195

<210> 194

<211> 198

<212> PRT

<213> Corynebacterium glutamicum

<400> 194

Gln Pro Leu Lys Leu Gly Ala His Ala Val Leu His Ser Thr Thr Lys
 1 5 10 15
 Tyr Ile Gly Gly His Ser Asp Val Val Gly Gly Leu Val Val Thr Asn
 20 25 30
 Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile Gly

35	40	45
Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu Lys		
50	55	60
Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys Ile		
65	70	75
Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr Pro		
	85	90
Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met Lys		
	100	105
Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu Ala		
	115	120
Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu Ser		
	130	135
Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr His		
	145	150
Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val Arg		
	165	170
Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val Glu		
	180	185
Gln Ala Leu Asn Asn Leu		
	195	

<210> 195

<211> 1170

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1147)

<223> RXA02532

<400> 195

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tgtgcaagcg ggacggccag ccagaactcc tgggtgcgcg	atg aac cca cct atc	115
	Met Asn Pro Pro Ile	
	1 5	

acg ttg tcc agc act tat gtt cat gat tca gaa aaa gct tat ggg cgc	163
Thr Leu Ser Ser Thr Tyr Val His Asp Ser Glu Lys Ala Tyr Gly Arg	
	10 15 20

gat ggc aat gat gga tgg ggt gca ttt gag gct gcc atg gga act cta	211
Asp Gly Asn Asp Gly Trp Gly Ala Phe Glu Ala Ala Met Gly Thr Leu	
	25 30 35

gat ggt ggg ttc gcg gta tct tat tct tca ggt ttg gca gcg gca acg	259
Asp Gly Gly Phe Ala Val Ser Tyr Ser Ser Gly Leu Ala Ala Ala Thr	
	40 45 50

tcg att gct gat ttg gtt cct act ggt ggc aca gtt gtt tta cct aaa	307
Ser Ile Ala Asp Leu Val Pro Thr Gly Gly Thr Val Val Leu Pro Lys	
55 60 65	
gct gcc tat tat ggc gtg acc aat att ttc gcc agg atg gaa gcc cgc	355
Ala Ala Tyr Tyr Gly Val Thr Asn Ile Phe Ala Arg Met Glu Ala Arg	
70 75 80 85	
gga agg ctg aag gtt cga act gtt gat gca gac aat acc gaa gaa gtg	403
Gly Arg Leu Lys Val Arg Thr Val Asp Ala Asp Asn Thr Glu Glu Val	
90 95 100	
att gct gct gct caa ggt gca gat gtg gtg tgg gtg gaa tcg atc gct	451
Ile Ala Ala Ala Gln Gly Ala Asp Val Val Trp Val Glu Ser Ile Ala	
105 110 115	
aat ccg acg atg gtg gta gct gat atc cct gca ata gtc gac ggt gtg	499
Asn Pro Thr Met Val Val Ala Asp Ile Pro Ala Ile Val Asp Gly Val	
120 125 130	
cgt ggg ctt gga gtt ttg act gtc gtt gac gcg act ttc gca acg cca	547
Arg Gly Leu Gly Val Leu Thr Val Val Asp Ala Thr Phe Ala Thr Pro	
135 140 145	
ctt cgt caa cgt cca ttg gaa ctt ggt gct gat att gtg ctt tac tcg	595
Leu Arg Gln Arg Pro Leu Glu Leu Gly Ala Asp Ile Val Leu Tyr Ser	
150 155 160 165	
gca acc aaa ctt atc ggt gga cac tct gat ctt ctt ctt gga gtc gca	643
Ala Thr Lys Leu Ile Gly Gly His Ser Asp Leu Leu Leu Gly Val Ala	
170 175 180	
gtg tgc aag tct gag cac cat gcg cag ttt ctt gcc act cac cgt cat	691
Val Cys Lys Ser Glu His His Ala Gln Phe Leu Ala Thr His Arg His	
185 190 195	
gat cat ggt tca gtg ccg gga ggt ctt gaa gcg ttt ctt gct ctc cgt	739
Asp His Gly Ser Val Pro Gly Gly Leu Glu Ala Phe Leu Ala Leu Arg	
200 205 210	
gga ttg tat tcc ttg gcg gtg cgt ctt gat cga gca gaa tcc aac gca	787
Gly Leu Tyr Ser Leu Ala Val Arg Leu Asp Arg Ala Glu Ser Asn Ala	
215 220 225	
gca gaa ctt tcg cgg cga ctt aac gcg cat cct tcg gtt acc cgc gtc	835
Ala Glu Leu Ser Arg Arg Leu Asn Ala His Pro Ser Val Thr Arg Val	
230 235 240 245	
aat tat cca gga ctt cct gat gat ccc caa cat gaa aaa gcc gtg cga	883
Asn Tyr Pro Gly Leu Pro Asp Asp Pro Gln His Glu Lys Ala Val Arg	
250 255 260	
gtc cta ccc tct gga tgt gga aac atg ttg tca ttt gag ctt gat gca	931
Val Leu Pro Ser Gly Cys Gly Asn Met Leu Ser Phe Glu Leu Asp Ala	
265 270 275	
aca cct gaa cga act gat gag att ctc gaa agc ctg tca ctt tta acc	979
Thr Pro Glu Arg Thr Asp Glu Ile Leu Glu Ser Leu Ser Leu Leu Thr	
280 285 290	

cac gcg acc agt tgg gga ggt gtg gaa aca gcc att gaa cgt cgc acc 1027
 His Ala Thr Ser Trp Gly Gly Val Glu Thr Ala Ile Glu Arg Arg Thr
 295 300 305
 agg cgg gat gct gaa gtg gtg gca gaa gta ccg atg act ctt tgc cgc 1075
 Arg Arg Asp Ala Glu Val Val Ala Glu Val Pro Met Thr Leu Cys Arg
 310 315 320 325
 gtt tcc gta gga att gaa gac gtt gaa gat cta tgg gaa gac ctc aac 1123
 Val Ser Val Gly Ile Glu Asp Val Glu Asp Leu Trp Glu Asp Leu Asn
 330 335 340
 gcc tca atc gac aaa gtt ctg ggt tagaactcgt agccagtaac cag 1170
 Ala Ser Ile Asp Lys Val Leu Gly
 345

<210> 196

<211> 349

<212> PRT

<213> Corynebacterium glutamicum

<400> 196

Met Asn Pro Pro Ile Thr Leu Ser Ser Thr Tyr Val His Asp Ser Glu
 1 5 10 15
 Lys Ala Tyr Gly Arg Asp Gly Asn Asp Gly Trp Gly Ala Phe Glu Ala
 20 25 30
 Ala Met Gly Thr Leu Asp Gly Gly Phe Ala Val Ser Tyr Ser Ser Gly
 35 40 45
 Leu Ala Ala Ala Thr Ser Ile Ala Asp Leu Val Pro Thr Gly Gly Thr
 50 55 60
 Val Val Leu Pro Lys Ala Ala Tyr Tyr Gly Val Thr Asn Ile Phe Ala
 65 70 75 80
 Arg Met Glu Ala Arg Gly Arg Leu Lys Val Arg Thr Val Asp Ala Asp
 85 90 95
 Asn Thr Glu Glu Val Ile Ala Ala Ala Gln Gly Ala Asp Val Val Trp
 100 105 110
 Val Glu Ser Ile Ala Asn Pro Thr Met Val Val Ala Asp Ile Pro Ala
 115 120 125
 Ile Val Asp Gly Val Arg Gly Leu Gly Val Leu Thr Val Val Asp Ala
 130 135 140
 Thr Phe Ala Thr Pro Leu Arg Gln Arg Pro Leu Glu Leu Gly Ala Asp
 145 150 155 160
 Ile Val Leu Tyr Ser Ala Thr Lys Leu Ile Gly Gly His Ser Asp Leu
 165 170 175
 Leu Leu Gly Val Ala Val Cys Lys Ser Glu His His Ala Gln Phe Leu
 180 185 190
 Ala Thr His Arg His Asp His Gly Ser Val Pro Gly Gly Leu Glu Ala
 195 200 205

Phe Leu Ala Leu Arg Gly Leu Tyr Ser Leu Ala Val Arg Leu Asp Arg
 210 215 220
 Ala Glu Ser Asn Ala Ala Glu Leu Ser Arg Arg Leu Asn Ala His Pro
 225 230 235 240
 Ser Val Thr Arg Val Asn Tyr Pro Gly Leu Pro Asp Asp Pro Gln His
 245 250 255
 Glu Lys Ala Val Arg Val Leu Pro Ser Gly Cys Gly Asn Met Leu Ser
 260 265 270
 Phe Glu Leu Asp Ala Thr Pro Glu Arg Thr Asp Glu Ile Leu Glu Ser
 275 280 285
 Leu Ser Leu Leu Thr His Ala Thr Ser Trp Gly Gly Val Glu Thr Ala
 290 295 300
 Ile Glu Arg Arg Thr Arg Arg Asp Ala Glu Val Val Ala Glu Val Pro
 305 310 315 320
 Met Thr Leu Cys Arg Val Ser Val Gly Ile Glu Asp Val Glu Asp Leu
 325 330 335
 Trp Glu Asp Leu Asn Ala Ser Ile Asp Lys Val Leu Gly
 340 345

<210> 197
 <211> 861
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(838)
 <223> RXS03159

<400> 197
 aggggctagt tttacacaaa agtggacagc ttggtctatc attgccagaa gaccggctct 60
 tttagggcca tagaattctg attacaggag ttgatctacc ttg tct ttt gac cca 115
 Leu Ser Phe Asp Pro
 1 5
 aac acc cag ggt ttc tcc act gca tcg att cac gct ggg tat gag cca 163
 Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His Ala Gly Tyr Glu Pro
 10 15 20
 gac gac tac tac ggt tcg att aac acc cca atc tat gcc tcc acc acc 211
 Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile Tyr Ala Ser Thr Thr
 25 30 35
 ttc gcg cag aac gct cca aac gaa ctg cgc aaa ggc tac gag tac acc 259
 Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys Gly Tyr Glu Tyr Thr
 40 45 50
 cgt gtg ggc aac ccc acc atc gtg gca tta gag cag acc gtc gca gca 307
 Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu Gln Thr Val Ala Ala
 55 60 65

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ctc gaa ggc gca aag tat ggc cgc gca ttc tcc tcc ggc atg gct gca 355
Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser Ser Gly Met Ala Ala
  70                75                80                85

acc gac atc ctg ttc cgc atc atc ctc aag ccg ggc gat cac atc gtc 403
Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro Gly Asp His Ile Val
                90                95                100

ctc ggc aac gat gct tac ggc gga acc tac cgc ctg atc gac acc gta 451
Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg Leu Ile Asp Thr Val
                105                110                115

ttc acc gca tgg ggc gtc gaa tac acc gtt gtt gat acc tcc gtc gtg 499
Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val Asp Thr Ser Val Val
                120                125                130

gaa gag gtc aag gca gcg atc aag gac aac acc aag ctg atc tgg gtg 547
Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr Lys Leu Ile Trp Val
                135                140                145

gaa acc cca acc aac cca gca ctt ggc atc acc gac atc gaa gca gta 595
Glu Thr Pro Thr Asn Pro Ala Leu Gly Ile Thr Asp Ile Glu Ala Val
                150                155                160                165

gca aag ctc acc gaa ggc acc aac gcc aag ttg gtt gtt gac aac acc 643
Ala Lys Leu Thr Glu Gly Thr Asn Ala Lys Leu Val Val Asp Asn Thr
                170                175                180

ttg gca tcc cca tac ctg cag cag cca cta aaa ctc ggc gca cac gca 691
Leu Ala Ser Pro Tyr Leu Gln Gln Pro Leu Lys Leu Gly Ala His Ala
                185                190                195

agt cct tgc act cca cca cca agt aca tcg aag gac act ccg acg ttg 739
Ser Pro Cys Thr Pro Pro Pro Ser Thr Ser Lys Asp Thr Pro Thr Leu
                200                205                210

ttg gcg gcc ttg tgg gta cca acg acc agg aaa tgg acg aag aac tgc 787
Leu Ala Ala Leu Trp Val Pro Thr Thr Arg Lys Trp Thr Lys Asn Cys
                215                220                225

tgt tca tgc agg gcg gca tcg gac cga tcc cat cag ttt tcg atg cat 835
Cys Ser Cys Arg Ala Ala Ser Asp Arg Ser His Gln Phe Ser Met His
                230                235                240                245

acc tgaccgcccg tggcctcaag acc 861
Thr

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<210> 198

<211> 246

<212> PRT

<213> Corynebacterium glutamicum

<400> 198

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Leu Ser Phe Asp Pro Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His
  1                5                10                15

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Ala Gly Tyr Glu Pro Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile
                20                25                30

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tttagggcca tagaattctg attacaggag ttgatctacc ttg tct ttt gac cca 115
Leu Ser Phe Asp Pro
1 5

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aac acc cag ggt ttc tcc act gca tcg att cac gct ggg tat gag cca 163
Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His Ala Gly Tyr Glu Pro
      10                      15                      20

gac gac tac tac ggt tcg att aac acc cca atc tat gcc tcc acc acc 211
Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile Tyr Ala Ser Thr Thr
      25                      30                      35

ttc gcg cag aac gct cca aac gaa ctg cgc aaa ggc tac gag tac acc 259
Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys Gly Tyr Glu Tyr Thr
      40                      45                      50

cgt gtg ggc aac ccc acc atc gtg gca tta gag cag acc gtc gca gca 307
Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu Gln Thr Val Ala Ala
      55                      60                      65

ctc gaa ggc gca aag tat ggc cgc gca ttc tcc tcc ggc atg gct gca 355
Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser Ser Gly Met Ala Ala
      70                      75                      80                      85

acc gac atc ctg ttc cgc atc atc ctc aag ccg ggc gat cac atc gtc 403
Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro Gly Asp His Ile Val
      90                      95                      100

ctc ggc aac gat gct tac ggc gga acc tac cgc ctg atc gac acc gta 451
Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg Leu Ile Asp Thr Val
      105                      110                      115

ttc acc gca tgg ggc gtc gaa tac acc gtt gtt gat acc tcc gtc gtg 499
Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val Asp Thr Ser Val Val
      120                      125                      130

gaa gag gtc aag gca gcg atc aag gac aac acc aag gct gat ctt ggt 547
Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr Lys Ala Asp Leu Gly
      135                      140                      145

gga aac ccc aac caa ccc agc act ttg gca tta ccc gac atc gaa gca 595
Gly Asn Pro Asn Gln Pro Ser Thr Leu Ala Leu Pro Asp Ile Glu Ala
      150                      155                      160                      165

gtg tgc aaa act tca ccc gaa agg cac caa ccc caa gct tgt tgt ttg 643
Val Cys Lys Thr Ser Pro Glu Arg His Gln Pro Gln Ala Cys Cys Leu
      170                      175                      180

aca aca cct tcg cat tcc cca tac ctg cag can cca ctt aaa ant tnn 691
Thr Thr Pro Ser His Ser Pro Tyr Leu Gln Xaa Pro Leu Lys Xaa Xaa
      185                      190                      195

gng cac acg cag
Xaa His Thr Gln
      200

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<210> 200

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 200

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Leu Ser Phe Asp Pro Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His
  1                      5                      10                      15

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Ala Gly Tyr Glu Pro Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile
 20 25 30

Tyr Ala Ser Thr Thr Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys
 35 40 45

Gly Tyr Glu Tyr Thr Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu
 50 55 60

Gln Thr Val Ala Ala Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser
 65 70 75 80

Ser Gly Met Ala Ala Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro
 85 90 95

Gly Asp His Ile Val Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg
 100 105 110

Leu Ile Asp Thr Val Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val
 115 120 125

Asp Thr Ser Val Val Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr
 130 135 140

Lys Ala Asp Leu Gly Gly Asn Pro Asn Gln Pro Ser Thr Leu Ala Leu
 145 150 155 160

Pro Asp Ile Glu Ala Val Cys Lys Thr Ser Pro Glu Arg His Gln Pro
 165 170 175

Gln Ala Cys Cys Leu Thr Thr Pro Ser His Ser Pro Tyr Leu Gln Xaa
 180 185 190

Pro Leu Lys Xaa Xaa Xaa His Thr Gln
 195 200

<210> 201
 <211> 1113
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1090)
 <223> RXA00216

<400> 201
 gtgttgctcg cggccaggca gcagtgtgt acctgcctga cgcggatggt gacatcggtc 60

ttggatcagg caccatctgc cacacggagt cttaagaaaa ttg ggc gct tat ggt 115
 Leu Gly Ala Tyr Gly
 1 5

tta ggt gag ctt cct gga aaa tcc gcc gcg gaa gcc gcc gac att att 163
 Leu Gly Glu Leu Pro Gly Lys Ser Ala Ala Glu Ala Ala Asp Ile Ile
 10 15 20

cag ggt gaa acg ggc gat ctt ctc cat att cct cag ctt ccg gcg cga 211
 Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro Gln Leu Pro Ala Arg

25										30					35					
ggt	ttg	ggt	gct	gat	ctg	atc	ggt	cga	acc	gtc	ggt	ctg	ctg	gac	atg	259				
Gly	Leu	Gly	Ala	Asp	Leu	Ile	Gly	Arg	Thr	Val	Gly	Leu	Leu	Asp	Met					
40						45						50								
atc	aac	gtt	gat	cgc	ggg	gcc	cga	tct	tgg	gtg	atg	agc	aca	cgc	ccc	307				
Ile	Asn	Val	Asp	Arg	Gly	Ala	Arg	Ser	Trp	Val	Met	Ser	Thr	Arg	Pro					
55						60						65								
agc	aga	ttg	acg	cac	ctg	acc	ggc	gat	ttc	ctt	gac	atg	gat	ttg	gat	355				
Ser	Arg	Leu	Thr	His	Leu	Thr	Gly	Asp	Phe	Leu	Asp	Met	Asp	Leu	Asp					
70						75						80			85					
gcg	tgc	gag	gaa	acc	tgg	gga	acg	ggc	gtc	gac	aag	cta	aaa	atc	caa	403				
Ala	Cys	Glu	Glu	Thr	Trp	Gly	Thr	Gly	Val	Asp	Lys	Leu	Lys	Ile	Gln					
			90						95						100					
gtt	gct	ggt	ccc	tgg	act	tta	ggt	gcg	cgc	att	gag	ttg	gcc	aat	ggc	451				
Val	Ala	Gly	Pro	Trp	Thr	Leu	Gly	Ala	Arg	Ile	Glu	Leu	Ala	Asn	Gly					
			105						110						115					
cat	cgc	gtt	ttg	tct	gat	cgc	ggt	gcg	atg	cgt	gat	ctc	acg	cag	gcg	499				
His	Arg	Val	Leu	Ser	Asp	Arg	Gly	Ala	Met	Arg	Asp	Leu	Thr	Gln	Ala					
120						125						130								
ctg	atc	gcc	ggc	atc	gat	gcg	cat	gca	cgc	aag	gtt	gct	ggg	cga	ttt	547				
Leu	Ile	Ala	Gly	Ile	Asp	Ala	His	Ala	Arg	Lys	Val	Ala	Gly	Arg	Phe					
135						140						145								
cgc	gcc	gaa	gtg	cag	gtg	caa	att	gat	gag	ccg	gag	ctg	aaa	tcg	ctt	595				
Arg	Ala	Glu	Val	Gln	Val	Gln	Ile	Asp	Glu	Pro	Glu	Leu	Lys	Ser	Leu					
150						155						160			165					
atc	gac	ggc	tcc	ctc	cct	ggc	act	tcc	acc	ttt	gac	att	att	cct	gcg	643				
Ile	Asp	Gly	Ser	Leu	Pro	Gly	Thr	Ser	Thr	Phe	Asp	Ile	Ile	Pro	Ala					
			170						175						180					
gtg	aat	gtc	gct	gat	gcc	agt	gaa	cgt	ttg	cag	cag	gtc	ttt	agc	tcg	691				
Val	Asn	Val	Ala	Asp	Ala	Ser	Glu	Arg	Leu	Gln	Gln	Val	Phe	Ser	Ser					
			185						190						195					
att	gag	ggg	ccg	aca	tat	ctc	aac	ctc	acc	ggc	cag	att	cct	act	tgg	739				
Ile	Glu	Gly	Pro	Thr	Tyr	Leu	Asn	Leu	Thr	Gly	Gln	Ile	Pro	Thr	Trp					
200						205						210								
gat	gtg	gct	cgg	ggt	gcg	ggc	gcc	gat	act	gtg	cag	att	tcc	atg	gat	787				
Asp	Val	Ala	Arg	Gly	Ala	Gly	Ala	Asp	Thr	Val	Gln	Ile	Ser	Met	Asp					
215						220						225								
caa	gtc	cgt	gga	aat	gaa	cat	ttg	gat	ggt	ttt	ggt	gaa	acc	atc	acc	835				
Gln	Val	Arg	Gly	Asn	Glu	His	Leu	Asp	Gly	Phe	Gly	Glu	Thr	Ile	Thr					
230						235						240			245					
agt	gga	att	cgt	ctt	ggt	ttg	ggc	att	acg	aca	gga	aaa	gat	gtc	gta	883				
Ser	Gly	Ile	Arg	Leu	Gly	Leu	Gly	Ile	Thr	Thr	Gly	Lys	Asp	Val	Val					
			250						255						260					
gat	gaa	ctg	ctc	gag	cga	ccg	cgg	caa	aag	gcc	gtt	gag	gta	gca	cgc	931				
Asp	Glu	Leu	Leu	Glu	Arg	Pro	Arg	Gln	Lys	Ala	Val	Glu	Val	Ala	Arg					
			265						270						275					

ttt ttt gat cgt tta ggt gtg ggc cga aac tat ctc gtg gat gct gtt 979
 Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr Leu Val Asp Ala Val
 280 285 290
 gat att cat ccg ggt gag gat ttg gtg cag ggg acc atc acc gag gcc 1027
 Asp Ile His Pro Gly Glu Asp Leu Val Gln Gly Thr Ile Thr Glu Ala
 295 300 305
 gcg cag gct tat cgc atg gcc cgg gtg atg tcg gag atg ttg tcg aag 1075
 Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser Glu Met Leu Ser Lys
 310 315 320 325
 gat tca tgc gac ctt taaggcttta ccggcgctgg gtg 1113
 Asp Ser Cys Asp Leu
 330

<210> 202

<211> 330

<212> PRT

<213> Corynebacterium glutamicum

<400> 202

Leu Gly Ala Tyr Gly Leu Gly Glu Leu Pro Gly Lys Ser Ala Ala Glu
 1 5 10 15
 Ala Ala Asp Ile Ile Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro
 20 25 30
 Gln Leu Pro Ala Arg Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val
 35 40 45
 Gly Leu Leu Asp Met Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val
 50 55 60
 Met Ser Thr Arg Pro Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu
 65 70 75 80
 Asp Met Asp Leu Asp Ala Cys Glu Glu Thr Trp Gly Thr Gly Val Asp
 85 90 95
 Lys Leu Lys Ile Gln Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile
 100 105 110
 Glu Leu Ala Asn Gly His Arg Val Leu Ser Asp Arg Gly Ala Met Arg
 115 120 125
 Asp Leu Thr Gln Ala Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys
 130 135 140
 Val Ala Gly Arg Phe Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro
 145 150 155 160
 Glu Leu Lys Ser Leu Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe
 165 170 175
 Asp Ile Ile Pro Ala Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln
 180 185 190
 Gln Val Phe Ser Ser Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly

195					200					205						
Gln	Ile	Pro	Thr	Trp	Asp	Val	Ala	Arg	Gly	Ala	Gly	Ala	Asp	Thr	Val	
210					215					220						
Gln	Ile	Ser	Met	Asp	Gln	Val	Arg	Gly	Asn	Glu	His	Leu	Asp	Gly	Phe	
225					230					235					240	
Gly	Glu	Thr	Ile	Thr	Ser	Gly	Ile	Arg	Leu	Gly	Leu	Gly	Ile	Thr	Thr	
245					250					255						
Gly	Lys	Asp	Val	Val	Asp	Glu	Leu	Leu	Glu	Arg	Pro	Arg	Gln	Lys	Ala	
260					265					270						
Val	Glu	Val	Ala	Arg	Phe	Phe	Asp	Arg	Leu	Gly	Val	Gly	Arg	Asn	Tyr	
275					280					285						
Leu	Val	Asp	Ala	Val	Asp	Ile	His	Pro	Gly	Glu	Asp	Leu	Val	Gln	Gly	
290					295					300						
Thr	Ile	Thr	Glu	Ala	Ala	Gln	Ala	Tyr	Arg	Met	Ala	Arg	Val	Met	Ser	
305					310					315					320	
Glu	Met	Leu	Ser	Lys	Asp	Ser	Cys	Asp	Leu							
325					330											

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(600)
 <223> RXN00402

<400> 203																
act	gac	gaa	aag	gat	gga	aag	cca	gta	ttg	ccc	tac	ttc	gtc	act	cca	48
Thr	Asp	Glu	Lys	Asp	Gly	Lys	Pro	Val	Leu	Pro	Tyr	Phe	Val	Thr	Pro	
1				5					10					15		
gat gct gct tac cac gga ttg aag tac gca gac ctt ggt gca cca gcc															96	
Asp	Ala	Ala	Tyr	His	Gly	Leu	Lys	Tyr	Ala	Asp	Leu	Gly	Ala	Pro	Ala	
			20					25					30			
ttc ggc ctc aag gtt cgc gtt ggc ctt cta cgc gac acc ggc tcc acc															144	
Phe	Gly	Leu	Lys	Val	Arg	Val	Gly	Leu	Leu	Arg	Asp	Thr	Gly	Ser	Thr	
		35					40					45				
ctc tcc gca ttc aac gca tgg gct gca gtc cag ggc atc gac acc ctt															192	
Leu	Ser	Ala	Phe	Asn	Ala	Trp	Ala	Ala	Val	Gln	Gly	Ile	Asp	Thr	Leu	
	50					55					60					
tcc ctg cgc ctg gag cgc cac aac gaa aac gcc atc aag gtt gca gaa															240	
Ser	Leu	Arg	Leu	Glu	Arg	His	Asn	Glu	Asn	Ala	Ile	Lys	Val	Ala	Glu	
	65				70				75						80	
ttc ctc aac aac cac gag aag gtg gaa aag gtt aac ttc gca ggc ctg															288	
Phe	Leu	Asn	Asn	His	Glu	Lys	Val	Glu	Lys	Val	Asn	Phe	Ala	Gly	Leu	
				85					90					95		

aag gat tcc cct tgg tac gca acc aag gaa aag ctt ggc ctg aag tac 336
Lys Asp Ser Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr
100 105 110

acc ggc tcc gtt ctc acc ttc gag atc aag ggc ggc aag gat gag gct 384
Thr Gly Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala
115 120 125

tgg gca ttt atc gac gcc ctg aag cta cac tcc aac ctt gca aac atc 432
Trp Ala Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile
130 135 140

ggc gat gtt cgc tcc ctc gtt gtt cac cca gca acc acc acc cat tca 480
Gly Asp Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser
145 150 155 160

cag tcc gac gaa gct ggc ctg gca cgc gcg ggc gtt acc cag tcc acc 528
Gln Ser Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr
165 170 175

gtc cgc ctg tcc gtt ggc atc gag acc att gat gat atc atc gct gac 576
Val Arg Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp
180 185 190

ctc gaa ggc ggc ttt gct gca atc tagctttaaa tagactcacc cca 623
Leu Glu Gly Gly Phe Ala Ala Ile
195 200

<210> 204

<211> 200

<212> PRT

<213> Corynebacterium glutamicum

<400> 204

Thr Asp Glu Lys Asp Gly Lys Pro Val Leu Pro Tyr Phe Val Thr Pro
1 5 10 15

Asp Ala Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala
20 25 30

Phe Gly Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr
35 40 45

Leu Ser Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu
50 55 60

Ser Leu Arg Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu
65 70 75 80

Phe Leu Asn Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu
85 90 95

Lys Asp Ser Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr
100 105 110

Thr Gly Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala
115 120 125

Trp Ala Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile

130		135		140
Gly Asp Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser				
145		150		155
Gln Ser Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr				
	165		170	175
Val Arg Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp				
	180		185	190
Leu Glu Gly Gly Phe Ala Ala Ile				
	195		200	

<210> 205

<211> 599

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(576)

<223> FRXA00402

<400> 205

gta ttg ccc tac ttc gtc act cca gat gct gct tac cac gga ttg aag	48
Val Leu Pro Tyr Phe Val Thr Pro Asp Ala Ala Tyr His Gly Leu Lys	
1 5 10 15	
tac gca gac ctt ggt gca cca gcc ttc ggc ctc aag gtt cgc gtt ggc	96
Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu Lys Val Arg Val Gly	
20 25 30	
ctt cta cgc gac acc ggc tcc acc ctc tcc gca ttc aac gca tgg gct	144
Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala Phe Asn Ala Trp Ala	
35 40 45	
gca gtc cag ggc atc gac acc ctt tcc ctg cgc ctg gag cgc cac aac	192
Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg Leu Glu Arg His Asn	
50 55 60	
gaa aac gcc atc aag gtt gca gaa ttc ctc aac aac cac gag aag gtg	240
Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn Asn His Glu Lys Val	
65 70 75 80	
gaa aag gtt aac ttc gca ggc ctg aag gat tcc cct tgg tac gca acc	288
Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser Pro Trp Tyr Ala Thr	
85 90 95	
aag gaa aag ctt ggc ctg aag tac acc ggc tcc gtt ctc acc ttc gag	336
Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu	
100 105 110	
atc aag ggc ggc aag gat gag gct tgg gca ttt atc gac gcc ctg aag	384
Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys	
115 120 125	
cta cac tcc aac ctt gca aac atc ggc gat gtt cgc tcc ctc gtt gtt	432
Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val Arg Ser Leu Val Val	
130 135 140	

cac cca gca acc acc acc cat tca cag tcc gac gaa gct ggc ctg gca 480
 His Pro Ala Thr Thr Thr His Ser Gln Ser Asp Glu Ala Gly Leu Ala
 145 150 155 160

cgc gcg ggc gtt acc cag tcc acc gtc cgc ctg tcc gtt ggc atc gag 528
 Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu Ser Val Gly Ile Glu
 165 170 175

acc att gat gat atc atc gct gac ctc gaa ggc ggc ttt gct gca atc 576
 Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly Gly Phe Ala Ala Ile
 180 185 190

tagctttaaa tagactcacc cca 599

<210> 206

<211> 192

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 206

Val Leu Pro Tyr Phe Val Thr Pro Asp Ala Ala Tyr His Gly Leu Lys
 1 5 10 15

Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu Lys Val Arg Val Gly
 20 25 30

Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala Phe Asn Ala Trp Ala
 35 40 45

Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg Leu Glu Arg His Asn
 50 55 60

Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn Asn His Glu Lys Val
 65 70 75 80

Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser Pro Trp Tyr Ala Thr
 85 90 95

Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu
 100 105 110

Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys
 115 120 125

Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val Arg Ser Leu Val Val
 130 135 140

His Pro Ala Thr Thr Thr His Ser Gln Ser Asp Glu Ala Gly Leu Ala
 145 150 155 160

Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu Ser Val Gly Ile Glu
 165 170 175

Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly Gly Phe Ala Ala Ile
 180 185 190

<210> 207
 <211> 613
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(613)
 <223> RXA00405

<400> 207

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agaataaatt tataccacac agtctattgc aatagaccaa gctgttcagt aggggtgcatg 60

ggagaagaat ttcttaataa aaactcttaa ggacctccaa atg cca aag tac gac 115
                                         Met Pro Lys Tyr Asp
                                         1           5

aat tcc aat gct gac cag tgg ggc ttt gaa acc cgc tcc att cac gca 163
Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu Thr Arg Ser Ile His Ala
                        10                        15                        20

ggc cag tca gta gac gca cag acc agc gca cga aac ctt ccg atc tac 211
Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg Asn Leu Pro Ile Tyr
                        25                        30                        35

caa tcc acc gct ttc gtg ttc gac tcc gct gag cac gcc aag cag cgt 259
Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu His Ala Lys Gln Arg
                        40                        45                        50

ttc gca ctt gag gat cta ggc cct gtt tac tcc cgc ctc acc aac cca 307
Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser Arg Leu Thr Asn Pro
                        55                        60                        65

acc gtt gag gct ttg gaa aac cgc atc gct tcc ctc gaa ggt ggc gtc 355
Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser Leu Glu Gly Gly Val
                        70                        75                        80                        85

cac gct gta gcg ttc tcc tcc gga cag gcc gca acc acc aac gcc att 403
His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala Thr Thr Asn Ala Ile
                        90                        95                        100

ttg aac ctg gca gga gcg ggc gac cac atc gtc acc tcc cca cgc ctc 451
Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val Thr Ser Pro Arg Leu
                        105                        110                        115

tac ggt ggc acc gag act cta ttc ctt atc act ctt aac cgc ctg ggt 499
Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr Leu Asn Arg Leu Gly
                        120                        125                        130

atc gat gtt tcc ttc gtg gaa aac ccc gac gac cct gag tcc tgg cag 547
Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp Pro Glu Ser Trp Gln
                        135                        140                        145

gca gcc gtt cag cca aac acc aaa gca ttc ttc ggc gag act ttc gcc 595
Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe Gly Glu Thr Phe Ala
                        150                        155                        160                        165

aac cca cag gca gac gtc 613
Asn Pro Gln Ala Asp Val
                        170

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<210> 208

<211> 171

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 208

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Met Pro Lys Tyr Asp Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu Thr
  1           5           10           15

Arg Ser Ile His Ala Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg
          20           25           30

Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu
      35           40           45

His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser
  50           55           60

Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser
  65           70           75           80

Leu Glu Gly Gly Val His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala
          85           90           95

Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val
      100           105           110

Thr Ser Pro Arg Leu Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr
      115           120           125

Leu Asn Arg Leu Gly Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp
      130           135           140

Pro Glu Ser Trp Gln Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe
      145           150           155           160

Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val
      165           170

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<210> 209

<211> 551

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(528)

<223> RXA02197

<400> 209

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gcc gaa cgc atg cgc ttt agc ttc cca cgc cag cag cgc ggc agg ttc      48
Ala Glu Arg Met Arg Phe Ser Phe Pro Arg Gln Gln Arg Gly Arg Phe
  1           5           10           15

ttg tgc atc gcg gat ttc att cgc cca cgc gag caa gct gtc aag gac      96
Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp
          20           25           30

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ggc caa gtg gac gtc atg cca ttc cag ctg gtc acc atg ggt aat cct 144
Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro
      35              40              45

att gct gat ttc gcc aac gag ttg ttc gca gcc aat gaa tac cgc gag 192
Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu
      50              55              60

tac ttg gaa gtt cac ggc atc ggc gtg cag ctc acc gaa gca ttg gcc 240
Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala
      65              70              75              80

gag tac tgg cac tcc cga gtg cgc agc gaa ctc aag ctg aac gac ggt 288
Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly
      85              90              95

gga tct gtc gct gat ttt gat cca gaa gac aag acc aag ttc ttc gac 336
Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp
      100             105             110

ctg gat tac cgc ggc gcc cgc ttc tcc ttt ggt tac ggt tct tgc cct 384
Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro
      115             120             125

gat ctg gaa gac cgc gca aag ctg gtg gaa ttg ctc gag cca ggc cgt 432
Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Glu Glu Pro Gly Arg
      130             135             140

atc ggc gtg gag ttg tcc gag gaa ctc cag ctg cac cca gag cag tcc 480
Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser
      145             150             155             160

aca gac gcg ttt gtg ctc tac cac cca gag gca aag tac ttt aac gtc 528
Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val
      165             170             175

taacaccttt gagagggaaa act 551

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<210> 210

<211> 176

<212> PRT

<213> Corynebacterium glutamicum

<400> 210

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Ala Glu Arg Met Arg Phe Ser Phe Pro Arg Gln Gln Arg Gly Arg Phe
  1              5              10              15

Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp
      20              25              30

Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro
      35              40              45

Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu
      50              55              60

Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala
      65              70              75              80

Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly

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85										90					95						
Gly	Ser	Val	Ala	Asp	Phe	Asp	Pro	Glu	Asp	Lys	Thr	Lys	Phe	Phe	Asp						
			100					105					110								
Leu	Asp	Tyr	Arg	Gly	Ala	Arg	Phe	Ser	Phe	Gly	Tyr	Gly	Ser	Cys	Pro						
		115					120					125									
Asp	Leu	Glu	Asp	Arg	Ala	Lys	Leu	Val	Glu	Leu	Leu	Glu	Pro	Gly	Arg						
		130				135						140									
Ile	Gly	Val	Glu	Leu	Ser	Glu	Glu	Leu	Gln	Leu	His	Pro	Glu	Gln	Ser						
145					150				155						160						
Thr	Asp	Ala	Phe	Val	Leu	Tyr	His	Pro	Glu	Ala	Lys	Tyr	Phe	Asn	Val						
				165					170					175							

<210> 211
 <211> 2599
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2599)
 <223> RXN02198

<400> 211
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 agttcgggaa ttgtctaate cgtactaagc tgtctacaca atg tct act tca gtt 115
 Met Ser Thr Ser Val
 1 5
 act tca cca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg 163
 Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala
 10 15 20
 ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc 211
 Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu
 25 30 35
 caa ggc ttt gac ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg 259
 Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly
 40 45 50
 tgt aat gag att ctc aac gac acc cgc cct gat gtg ttg agg cag att 307
 Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile
 55 60 65
 cac cgc gcc tac ttt gag gcg gga gct gac ttg gtt gag acc aat act 355
 His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr
 70 75 80 85
 ttt ggt tgc aac ctg ccg aac ttg gcg gat tat gac atc gct gat cgt 403
 Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg
 90 95 100

tgc cgt gag ctt gcc tac aag ggc act gca gtg gct agg gaa gtg gct	451
Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala	
105 110 115	
gat gag atg ggg ccg ggc cga aac ggc atg cgg cgt ttc gtg gtt ggt	499
Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly	
120 125 130	
tcc ctg gga cct gga acg aag ctt cca tcg ctg ggc cat gca ccg tat	547
Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr	
135 140 145	
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Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala Gln Asp Leu Leu Gln	
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Val Lys Ala Ala Val His Gly Val Gln Asp Ala Met Ala Glu Leu Asp	
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Thr Phe Leu Pro Ile Ile Cys His Val Thr Val Glu Thr Thr Gly Thr	
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Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu Thr Ala Leu Gln Pro	
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Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala Thr Gly Pro Asp Glu	
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Met Ser Glu His Leu Arg Tyr Leu Ser Lys His Ala Asp Ile Pro Val	
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Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu Gly Lys Asn Gly Ala	
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Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln Ala Leu Ala Gly Phe	
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Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly Cys Cys Gly Thr Thr	
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Pro Glu His Ile Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu	
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Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln	
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Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val Ala Ser Leu Tyr Thr	
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Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg	
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Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly	
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Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly	
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Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala Thr Ser Ser Thr Leu	
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Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu	
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Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp	
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ggc gat ggc cct gag tcc cgc tac cag cgc atc atg aaa ctg gta aag	1555
Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys	
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Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln	
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Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp	
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Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp	
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Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp	
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Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro	
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Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn	
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Tyr	Asp	Arg	Arg	Thr	Glu	Asp	Tyr	Asp	Pro	Leu	Gln	Glu	Phe	Met	Gln		
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Gln	Leu	Ala	Ala	Met	Pro	Leu	Phe	Glu	Arg	Leu	Ala	Gln	Arg	Ile	Ile		
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Lys	Thr	Val	Gly	Glu	Leu	Phe	Gly	Ser	Gly	Gln	Met	Gln	Leu	Pro	Phe		
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gtg	ctg	caa	tcg	gca	gaa	acc	atg	aaa	act	gcg	gtg	gcc	tat	ttg	gaa	2323	
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Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu
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Val Glu Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr
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Asp Ile Ala Asp Arg Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val
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Ala Arg Glu Val Ala Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg
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Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu
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Gly His Ala Pro Tyr Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala
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Leu Gly Ile Ile Asp Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala
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Gln Asp Leu Leu Gln Val Lys Ala Ala Val His Gly Val Gln Asp Ala
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Met Ala Glu Leu Asp Thr Phe Leu Pro Ile Ile Cys His Val Thr Val
 195 200 205

Glu Thr Thr Gly Thr Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu
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Thr Ala Leu Gln Pro Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala
 225 230 235 240

Thr Gly Pro Asp Glu Met Ser Glu His Leu Arg Tyr Leu Ser Lys His
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Ala Asp Ile Pro Val Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu
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Gly Lys Asn Gly Ala Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln

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Lys	Arg	Leu	Ile	Asp	Asp	Ile	Thr	Gly	Ser	Tyr	Gly	Leu	Asp	Ile	Lys	
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Asp	Ile	Val	Val	Asp	Cys	Leu	Thr	Phe	Pro	Ile	Ser	Thr	Gly	Gln	Glu	
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Lys	Lys	Leu	Tyr	Pro	Glu	Ile	His	Thr	Thr	Leu	Gly	Leu	Ser	Asn	Ile	
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Ser	Phe	Gly	Leu	Asn	Pro	Ala	Ala	Arg	Gln	Val	Leu	Asn	Ser	Val	Phe	
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Leu	Asn	Glu	Cys	Ile	Glu	Ala	Gly	Leu	Asp	Ser	Ala	Ile	Ala	His	Ser	
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Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val
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 Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu
 625 630 635 640
 Gln Glu Phe Met Gln Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys
 645 650 655
 Asp Ala Arg Ala Glu Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu
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 Ala Gln Arg Ile Ile Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu
 675 680 685
 Glu Ala Gly Met Lys Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp
 690 695 700
 Leu Leu Asn Gly Met Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln
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 Met Gln Leu Pro Phe Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala
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 Val Ala Tyr Leu Glu Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly
 740 745 750
 Ser Ala Gln Ala Glu Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys
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 Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser
 770 775 780
 Asn Asn Gly Tyr Asp Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser
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 Ser Gly Leu Leu Val Lys Ser Thr Val Val Met Lys Gln Thr Ile Ser
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Asp

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act	tca	cca	gcc	cac	aac	aac	gca	cat	tcc	tcc	gaa	ttt	ttg	gat	gcg	163
Thr	Ser	Pro	Ala	His	Asn	Asn	Ala	His	Ser	Ser	Glu	Phe	Leu	Asp	Ala	
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Leu	Ala	Asn	His	Val	Leu	Ile	Gly	Asp	Gly	Ala	Met	Gly	Thr	Gln	Leu	
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Gln	Gly	Phe	Asp	Leu	Asp	Val	Glu	Lys	Asp	Phe	Leu	Asp	Leu	Glu	Gly	
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Cys	Asn	Glu	Ile	Leu	Asn	Asp	Thr	Arg	Pro	Asp	Val	Leu	Arg	Gln	Ile	
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Phe	Gly	Cys	Asn	Leu	Pro	Asn	Leu	Ala	Asp	Tyr	Asp	Ile	Ala	Asp	Arg	
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Cys	Arg	Glu	Leu	Ala	Tyr	Lys	Gly	Thr	Ala	Val	Ala	Arg	Glu	Val	Ala	
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Asp	Glu	Met	Gly	Pro	Gly	Arg	Asn	Gly	Met	Arg	Arg	Phe	Val	Val	Gly	
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Ala	Asp	Leu	Arg	Gly	His	Tyr	Lys	Glu	Ala	Ala	Leu	Gly	Ile	Ile	Asp	
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ggc	ggc	ggc	gat	gcc	ttt	ttg	att	gag	act	gct	cag	gac	ttg	ctt	cag	643
Gly	Gly	Gly	Asp	Ala	Phe	Leu	Ile	Glu	Thr	Ala	Gln	Asp	Leu	Leu	Gln	
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Val	Lys	Ala	Ala	Val	His	Gly	Val	Gln	Asp	Ala	Met	Ala	Glu	Leu	Asp	
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aca	ttc	ttg	ccc	att	att	tgc	cac	gtc	acc	gta	gag	acc	acc	ggc	acc	739
Thr	Phe	Leu	Pro	Ile	Ile	Cys	His	Val	Thr	Val	Glu	Thr	Thr	Gly	Thr	
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Met	Leu	Met	Gly	Ser	Glu	Ile	Gly	Ala	Ala	Leu	Thr	Ala	Leu	Gln	Pro	
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Leu	Gly	Ile	Asp	Met	Ile											

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Met Ser Glu His Leu Arg Tyr Leu Ser Lys His Ala Asp Ile Pro Val	250	255	260	
tcg gtg atg cct aac gca ggt ctt cct gtc ctg ggt aaa aac ggt gca				931
Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu Gly Lys Asn Gly Ala	265	270	275	
gaa tac cca ctt gag gct gag gat ttg gcg cag gcg ctg gct gga ttc				979
Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln Ala Leu Ala Gly Phe	280	285	290	
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Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly Cys Cys Gly Thr Thr	295	300	305	
cct gag cac atc cgt gcg gtc cgc gat gcg gtg gtt ggt gtt cca gag				1075
Pro Glu His Ile Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu	310	315	320	325
cag gaa acc tcc aca ctg acc aag atc cct gca ggc cct gtt gag cag				1123
Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln	330	335	340	
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Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val Ala Ser Leu Tyr Thr	345	350	355	
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Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg	360	365	370	
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Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly	375	380	385	
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Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly	390	395	400	405
gca cac atg ctg gat ctt tgt gtg gat tac gtg gga cga gac ggc acc				1363
Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Thr	410	415	420	
gcc gat atg gcg acc ttg gca gca ctt ctt gct acc agc tcc act ttg				1411
Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala Thr Ser Ser Thr Leu	425	430	435	
cca atc atg att gac tcc acc gag cca gag gtt att cgc aca ggc ctt				1459
Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu	440	445	450	
gag cac ttg ggt gga cga agc atc gtt aac tcc gtc aac ttt gaa gac				1507
Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp	455	460	465	
ggc gat ggc cct gag tcc cgc tac cag cgc atc atg aaa ctg gta aag				1555
Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys	470	475	480	485

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Ala	Arg	Thr	Ala	Glu	His	Lys	Val	Arg	Ile	Ala	Lys	Arg	Leu	Ile	Asp	
			505					510					515			
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Asp	Ile	Thr	Gly	Ser	Tyr	Gly	Leu	Asp	Ile	Lys	Asp	Ile	Val	Val	Asp	
		520					525					530				
tgc	ctg	acc	ttc	ccg	atc	tct	act	ggc	cag	gaa	gaa	acc	agg	cga	gat	1747
Cys	Leu	Thr	Phe	Pro	Ile	Ser	Thr	Gly	Gln	Glu	Glu	Thr	Arg	Arg	Asp	
	535					540					545					
ggc	att	gaa	acc	atc	gaa	gcc	atc	cgc	gag	ctg	aag	aag	ctc	tac	cca	1795
Gly	Ile	Glu	Thr	Ile	Glu	Ala	Ile	Arg	Glu	Leu	Lys	Lys	Leu	Tyr	Pro	
550					555					560					565	
gaa	atc	cac	acc	acc	ctg	ggt	ctg	tcc	aat	att	tcc	ttc	ggc	ctg	aac	1843
Glu	Ile	His	Thr	Thr	Leu	Gly	Leu	Ser	Asn	Ile	Ser	Phe	Gly	Leu	Asn	
				570					575					580		
cct	gct	gca	cgc	cag	gtt	ctt	aac	tct	gtg	ttc	ctc	aat	gag	tgc	att	1891
Pro	Ala	Ala	Arg	Gln	Val	Leu	Asn	Ser	Val	Phe	Leu	Asn	Glu	Cys	Ile	
			585					590					595			
gag	gct	ggt	ctg	gac	tct	gcg	att	gcg	cac	agc	tcc	aag	att	ttg	ccg	1939
Glu	Ala	Gly	Leu	Asp	Ser	Ala	Ile	Ala	His	Ser	Ser	Lys	Ile	Leu	Pro	
		600					605					610				
atg	aac	cgc	att	gat	gat	cgc	cag	cgc	gaa	gtg	gcg	ttg	gat	atg	gtc	1987
Met	Asn	Arg	Ile	Asp	Asp	Arg	Gln	Arg	Glu	Val	Ala	Leu	Asp	Met	Val	
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tat	gat	cgc	cgc	acc	gag	gat	tac	gat	ccg	ctg	cag	gaa	ttc	atg	cag	2035
Tyr	Asp	Arg	Arg	Thr	Glu	Asp	Tyr	Asp	Pro	Leu	Gln	Glu	Phe	Met	Gln	
630					635					640					645	
ctg	ttt	gag	ggc	gtt	tct	gct	gcc	gat	gcc	aag	gat	gct	cgc	gct	gaa	2083
Leu	Phe	Glu	Gly	Val	Ser	Ala	Ala	Asp	Ala	Lys	Asp	Ala	Arg	Ala	Glu	
			650						655					660		
cag	ctg	gcc	gct	atg	cct	ttg	ttt	gag	cgt	ttg	gca	cag	cgc	atc	atc	2131
Gln	Leu	Ala	Ala	Met	Pro	Leu	Phe	Glu	Arg	Leu	Ala	Gln	Arg	Ile	Ile	
			665					670					675			
gac	ggc	gat	aag	aat	ggc	ctt	gag	gat	gat	ctg	gaa	gca	ggc	atg	aag	2179
Asp	Gly	Asp	Lys	Asn	Gly	Leu	Glu	Asp	Asp	Leu	Glu	Ala	Gly	Met	Lys	
		680					685					690				
gag	aag	tct	cct	att	gcg	atc	atc	aac	gag	gac	ctt	ctc	aac	ggc	atg	2227
Glu	Lys	Ser	Pro	Ile	Ala	Ile	Ile	Asn	Glu	Asp	Leu	Leu	Asn	Gly	Met	
	695					700					705					
aag	acc	gtg	ggt	gag	ctg	ttt	ggt	tcc	gga	cag	atg	cag	ctg	cca	ttc	2275
Lys	Thr	Val	Gly	Glu	Leu	Phe	Gly	Ser	Gly	Gln	Met	Gln	Leu	Pro	Phe	
710					715					720					725	

gtg ctg caa tcg gca gaa acc atg aaa act gcg gtg gcc tat ttg gaa 2323
 Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu
 730 735 740

ccg ttc atg gaa gag gaa gca gaa gct acc gga tct gcg cag gca gag 2371
 Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu
 745 750 755

ggc aag ggc aaa atc gtc gtg gcc acc gtc aag ggt gac gtg cac gat 2419
 Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp
 760 765 770

atc ggc aag aac ttg gtg gac atc att ttg tcc aac aac ggt tac gac 2467
 Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp
 775 780 785

gtg gtg aac ttg ggc atc aag cag cca ctg tcc gcc atg ttg gaa gca 2515
 Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala
 790 795 800 805

gcg gaa gaa cac aaa gca gac gtc atc ggc atg tcg gga ctt ctt gtg 2563
 Ala Glu Glu His Lys Ala Asp Val Ile Gly Met Ser Gly Leu Leu Val
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 Lys Ser Thr Val Val
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<211> 826

<212> PRT

<213> Corynebacterium glutamicum

<400> 214

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 20 25 30

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 35 40 45

Leu Asp Leu Glu Gly Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp
 50 55 60

Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu
 65 70 75 80

Val Glu Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr
 85 90 95

Asp Ile Ala Asp Arg Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val
 100 105 110

Ala Arg Glu Val Ala Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg
 115 120 125

Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu
 130 135 140

Gly	His	Ala	Pro	Tyr	Ala	Asp	Leu	Arg	Gly	His	Tyr	Lys	Glu	Ala	Ala	
145					150					155					160	
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				165					170					175		
Gln	Asp	Leu	Leu	Gln	Val	Lys	Ala	Ala	Val	His	Gly	Val	Gln	Asp	Ala	
			180					185					190			
Met	Ala	Glu	Leu	Asp	Thr	Phe	Leu	Pro	Ile	Ile	Cys	His	Val	Thr	Val	
		195					200					205				
Glu	Thr	Thr	Gly	Thr	Met	Leu	Met	Gly	Ser	Glu	Ile	Gly	Ala	Ala	Leu	
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Thr	Ala	Leu	Gln	Pro	Leu	Gly	Ile	Asp	Met	Ile	Gly	Leu	Asn	Cys	Ala	
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Thr	Gly	Pro	Asp	Glu	Met	Ser	Glu	His	Leu	Arg	Tyr	Leu	Ser	Lys	His	
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Ala	Asp	Ile	Pro	Val	Ser	Val	Met	Pro	Asn	Ala	Gly	Leu	Pro	Val	Leu	
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Gly	Lys	Asn	Gly	Ala	Glu	Tyr	Pro	Leu	Glu	Ala	Glu	Asp	Leu	Ala	Gln	
	275						280					285				
Ala	Leu	Ala	Gly	Phe	Val	Ser	Glu	Tyr	Gly	Leu	Ser	Met	Val	Gly	Gly	
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Cys	Cys	Gly	Thr	Thr	Pro	Glu	His	Ile	Arg	Ala	Val	Arg	Asp	Ala	Val	
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Val	Gly	Val	Pro	Glu	Gln	Glu	Thr	Ser	Thr	Leu	Thr	Lys	Ile	Pro	Ala	
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Gly	Pro	Val	Glu	Gln	Ala	Ser	Arg	Glu	Val	Glu	Lys	Glu	Asp	Ser	Val	
			340					345					350			
Ala	Ser	Leu	Tyr	Thr	Ser	Val	Pro	Leu	Ser	Gln	Glu	Thr	Gly	Ile	Ser	
		355					360					365				
Met	Ile	Gly	Glu	Arg	Thr	Asn	Ser	Asn	Gly	Ser	Lys	Ala	Phe	Arg	Glu	
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Gly	Arg	Asp	Gly	Thr	Ala	Asp	Met	Ala	Thr	Leu	Ala	Ala	Leu	Leu	Ala	
			420					425					430			
Thr	Ser	Ser	Thr	Leu	Pro	Ile	Met	Ile	Asp	Ser	Thr	Glu	Pro	Glu	Val	
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Ile	Arg	Thr	Gly	Leu	Glu	His	Leu	Gly	Gly	Arg	Ser	Ile	Val	Asn	Ser	
	450					455					460					

Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile
 465 470 475 480
 Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile
 485 490 495
 Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala
 500 505 510
 Lys Arg Leu Ile Asp Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys
 515 520 525
 Asp Ile Val Val Asp Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu
 530 535 540
 Glu Thr Arg Arg Asp Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu
 545 550 555 560
 Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile
 565 570 575
 Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe
 580 585 590
 Leu Asn Glu Cys Ile Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser
 595 600 605
 Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val
 610 615 620
 Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu
 625 630 635 640
 Gln Glu Phe Met Gln Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys
 645 650 655
 Asp Ala Arg Ala Glu Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu
 660 665 670
 Ala Gln Arg Ile Ile Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu
 675 680 685
 Glu Ala Gly Met Lys Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp
 690 695 700
 Leu Leu Asn Gly Met Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln
 705 710 715 720
 Met Gln Leu Pro Phe Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala
 725 730 735
 Val Ala Tyr Leu Glu Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly
 740 745 750
 Ser Ala Gln Ala Glu Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys
 755 760 765
 Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser
 770 775 780
 Asn Asn Gly Tyr Asp Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser

785					790					795					800
Ala	Met	Leu	Glu	Ala	Ala	Glu	Glu	His	Lys	Ala	Asp	Val	Ile	Gly	Met
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Ser	Gly	Leu	Leu	Val	Lys	Ser	Thr	Val	Val						
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<213> *Corynebacterium glutamicum*

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<222> (101)..(598)  
<223> RXN03074
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Met Thr Gln Ser Ala																	5
1																	
cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac																	163
Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn																	20
10 15																	
gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa																	211
Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu																	35
25 30																	
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Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu																	50
40 45																	
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Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile																	65
55 60																	
gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca																	355
Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala																	85
70 75 80																	
gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca																	403
Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala																	100
90 95																	
att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc																	451
Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala																	115
105 110																	
ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga																	499
Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg																	130
120 125																	
gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac																	547
Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr																	145
135 140																	

gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
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 Gln

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<211> 166

<212> PRT

<213> Corynebacterium glutamicum

<400> 216

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Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
 35 40 45

Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
 50 55 60

Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
 65 70 75 80

Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
 85 90 95

Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
 100 105 110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
 115 120 125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
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Glu Ala Pro Ile Lys Gln
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<210> 217

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<222> (101)..(598)

<223> FRXA02906

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<213> Corynebacterium glutamicum

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1 5 10 15
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Gly	Gly	Ala	Thr	Glu	Phe	His	Gly	Ile	Ile	Thr	Thr	Val	Lys	Cys	Phe
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Gln	Asp	Asn	Ala	Leu	Leu	Lys	Ser	Ile	Leu	Ser	Glu	Asp	Asn	Pro	Gly
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Gly	Val	Leu	Val	Ile	Asp	Gly	Asp	Ala	Ser	Val	His	Thr	Ala	Leu	Val
65					70					75					
Gly	Asp	Ile	Ile	Ala	Gly	Leu	Gly	Lys	Asp	His	Gly	Trp	Ser	Gly	Val
85					90					95					
Ile	Val	Asn	Gly	Ala	Ile	Arg	Asp	Ser	Ala	Val	Ile	Gly	Thr	Met	Thr
100					105					110					
Phe	Gly	Cys	Lys	Ala	Leu	Gly	Thr	Asn	Pro	Arg	Lys	Ser	Thr	Lys	Thr
115					120					125					
Gly	Ser	Gly	Glu	Arg	Asp	Val	Val	Val	Ser	Ile	Gly	Gly	Ile	Asp	Phe
130					135					140					
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<212> DNA

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<223> RXN00132

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gac	ttc	aag	ggt	gcc	gat	ctt	tca	cta	gca	gag	gca	gga	cgt	cac	cag	163
Asp	Phe	Lys	Val	Ala	Asp	Leu	Ser	Leu	Ala	Glu	Ala	Gly	Arg	His	Gln	
				10					15					20		

att	cgt	ctt	gca	gag	tat	gag	atg	cca	ggt	ctc	atg	cag	ttg	cgc	aag	211
Ile	Arg	Leu	Ala	Glu	Tyr	Glu	Met	Pro	Gly	Leu	Met	Gln	Leu	Arg	Lys	
			25					30				35				

gaa	ttc	gca	gac	gag	cag	cct	ttg	aag	ggc	gcc	cga	att	gct	ggt	tct	259
Glu	Phe	Ala	Asp	Glu	Gln	Pro	Leu	Lys	Gly	Ala	Arg	Ile	Ala	Gly	Ser	
		40					45				50					

atc	cac	atg	acg	gtc	cag	acc	gcc	gtg	ctt	att	gag	acc	ctc	act	gct	307
Ile	His	Met	Thr	Val	Gln	Thr	Ala	Val	Leu	Ile	Glu	Thr	Leu	Thr	Ala	

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ttg ggc gct gag gtt cgt tgg gct tcc tgc aac att ttc tcc acc cag			355
Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn Ile Phe Ser Thr Gln			
70	75	80	85
gat gag gct gca gcg gct atc gtt gtc ggc tcc ggc acc gtc gaa gag			403
Asp Glu Ala Ala Ala Ile Val Val Gly Ser Gly Thr Val Glu Glu			
	90	95	100
cca gct ggt gtt cca gta ttc gcg tgg aag ggt gag tca ctg gag gag			451
Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly Glu Ser Leu Glu Glu			
	105	110	115
tac tgg tgg tgc atc aac cag atc ttc agc tgg ggc gat gag ctg cca			499
Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp Gly Asp Glu Leu Pro			
	120	125	130
aac atg atc ctc gac gac ggc ggt gac gcc acc atg gct gtt att cgc			547
Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr Met Ala Val Ile Arg			
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ggt cgc gaa tac gag cag gct ggt ctg gtt cca cca gca gag gcc aac			595
Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro Pro Ala Glu Ala Asn			
	150	155	160
gat tcc gat gag tac atc gca ttc ttg ggc atg ctg cgt gag gtt ctt			643
Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met Leu Arg Glu Val Leu			
	170	175	180
gct gca gag cct ggc aag tgg ggc aag atc gct gag gcc gtt aag ggt			691
Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala Glu Ala Val Lys Gly			
	185	190	195
gtc acc gag gaa acc acc acc ggt gtg cac cgc ctg tac cac ttc gct			739
Val Thr Glu Glu Thr Thr Thr Gly Val His Arg Leu Tyr His Phe Ala			
	200	205	210
gaa gaa ggc gtg ctg cct ttc cca gcg atg aac gtc aac gac gct gtc			787
Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn Val Asn Asp Ala Val			
	215	220	225
acc aag tcc aag ttt gat aac aag tac ggc acc cgc cac tcc ctg atc			835
Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr Arg His Ser Leu Ile			
	230	235	240
gac ggc atc aac cgc gcc act gac atg ctc atg ggc ggc aag aac gtg			883
Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met Gly Gly Lys Asn Val			
	250	255	260
ctt gtc tgc ggt tac ggc gat gtc ggc aag ggc tgc gct gag gct ttc			931
Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly Cys Ala Glu Ala Phe			
	265	270	275
gac ggc cag ggc gct cgc gtc aag gtc acc gaa gct gac cca atc aac			979
Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu Ala Asp Pro Ile Asn			
	280	285	290
gct ctt cag gct ctg atg gat ggc tac tct gtg gtc acc gtt gat gag			1027
Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val Val Thr Val Asp Glu			
	295	300	305

gcc atc gag gac gcc gac atc gtg atc acc gcg acc ggc aac aag gac 1075
 Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala Thr Gly Asn Lys Asp
 310 315 320 325

 atc att tcc ttc gag cag atg ctc aag atg aag gat cac gct ctg ctg 1123
 Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys Asp His Ala Leu Leu
 330 335 340

 ggc aac atc ggt cac ttt gat aat gag atc gat atg cat tcc ctg ttg 1171
 Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp Met His Ser Leu Leu
 345 350 355

 cac cgc gac gac gtc acc cgc acc acg atc aag cca cag gtc gac gag 1219
 His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys Pro Gln Val Asp Glu
 360 365 370

 ttc acc ttc tcc acc ggt cgc tcc atc atc gtc ctg tcc gaa ggt cgc 1267
 Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val Leu Ser Glu Gly Arg
 375 380 385

 ctg ttg aac ctt ggc aac gcc acc gga cac cca tca ttt gtc atg tcc 1315
 Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro Ser Phe Val Met Ser
 390 395 400 405

 aac tct ttc gcc gat cag acc att gcg cag atc gaa ctg ttc caa aac 1363
 Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile Glu Leu Phe Gln Asn
 410 415 420

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 Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu Pro Lys Val Leu Asp
 425 430 435

 gaa aag gtg gca cgc atc cac gtt gag gct ctc ggc ggt cag ctc acc 1459
 Glu Lys Val Ala Arg Ile His Val Glu Ala Leu Gly Gly Gln Leu Thr
 440 445 450

 gaa ctg acc aag gag cag gct gag tac atc ggc gtt gac gtt gca ggc 1507
 Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile Gly Val Asp Val Ala Gly
 455 460 465

 cca ttc aag ccg gag cac tac cgc tac taatgattgt cagcattgag 1554
 Pro Phe Lys Pro Glu His Tyr Arg Tyr
 470 475

 gga 1557

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<211> 478

<212> PRT

<213> Corynebacterium glutamicum

<400> 220

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Ala Gly Arg His Gln Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu
 20 25 30

Met Gln Leu Arg Lys Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala

35					40					45						
Arg	Ile	Ala	Gly	Ser	Ile	His	Met	Thr	Val	Gln	Thr	Ala	Val	Leu	Ile	
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Glu	Thr	Leu	Thr	Ala	Leu	Gly	Ala	Glu	Val	Arg	Trp	Ala	Ser	Cys	Asn	
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Ile	Phe	Ser	Thr	Gln	Asp	Glu	Ala	Ala	Ala	Ala	Ile	Val	Val	Gly	Ser	
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Pro	Ala	Glu	Ala	Asn	Asp	Ser	Asp	Glu	Tyr	Ile	Ala	Phe	Leu	Gly	Met	
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Ser Phe Val Met Ser Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile
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Glu Leu Phe Gln Asn Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu
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Pro Lys Val Leu Asp Glu Lys Val Ala Arg Ile His Val Glu Ala Leu
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Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile Gly
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gct gag tac atc ggc gtt gac gtt gca ggc cca ttc aag ccg gag cac 96
 Ala Glu Tyr Ile Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His
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 Tyr Arg Tyr
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Pro	Ala	Gly	Val	Pro	Val	Phe	Ala	Trp	Lys	Gly	Glu	Ser	Leu	Glu	Glu			
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His	Arg	Asp	Asp	Val	Thr	Arg	Thr	Thr	Ile	Lys	Pro	Gln	Val	Asp	Glu								
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Phe	Thr	Phe	Ser	Thr	Gly	Arg	Ser	Ile	Ile	Val	Leu	Ser	Glu	Gly	Arg								
375								380									385						
ctg	ttg	aac	ctt	ggc	aac	gcc	acc	gga	cac	cca	tca	ttt	gtc	atg	tcc	1315							
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Asn	Ser	Phe	Ala	Asp	Gln	Thr	Ile	Ala	Gln	Ile	Glu	Leu	Phe	Gln	Asn								
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1396

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<213> *Corynebacterium glutamicum*

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 35 40 45

Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr Ala Val Leu Ile
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Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn
 65 70 75 80

Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ala Ile Val Val Gly Ser
 85 90 95

Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly
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Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp
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Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr
 130 135 140

Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro
 145 150 155 160

Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met
 165 170 175

Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala
 180 185 190

Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr Gly Val His Arg
 195 200 205

Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn
 210 215 220

Val Asn Asp Ala Val Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr
 225 230 235 240

Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met
 245 250 255

Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly

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Cys	Ala	Glu	Ala	Phe	Asp	Gly	Gln	Gly	Ala	Arg	Val	Lys	Val	Thr	Glu
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Val	Thr	Val	Asp	Glu	Ala	Ile	Glu	Asp	Ala	Asp	Ile	Val	Ile	Thr	Ala
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Thr	Gly	Asn	Lys	Asp	Ile	Ile	Ser	Phe	Glu	Gln	Met	Leu	Lys	Met	Lys
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			340					345					350		
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Leu	Ser	Glu	Gly	Arg	Leu	Leu	Asn	Leu	Gly	Asn	Ala	Thr	Gly	His	Pro
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Ser	Phe	Val	Met	Ser	Asn	Ser	Phe	Ala	Asp	Gln	Thr	Ile	Ala	Gln	Ile
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<213> Corynebacterium glutamicum

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<221> CDS

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Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala	
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Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp	
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Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg	
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Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met	
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Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser	
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Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly	
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Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro	
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Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys	
185 190 195	
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Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr	
200 205 210	
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Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr	
215 220 225	
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Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly	
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Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly	
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Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly	
265 270 275	
gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc	979

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Lys	Ser	Leu	Glu	Leu	Pro	Ala	Leu	Pro	Thr	Thr	Thr	Ile	Gly	Ser	Phe		
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gac gtc gat aag cct gcc tac ctg cag tgg tcc gtg gac tcc ttc cgc Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg 600 605 610			1939
ctg gcg act gcc ggc gca ccc gac gac gtc caa atc cac acc cac atg Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met 615 620 625			1987
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gcc gat gtc acc acc atc gaa gca gca cgt tcc gac atg cag gtc ctc Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu 650 655 660			2083
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tgg gat atc cac tcc ccg cgc gtt cct tcc gcg cag aaa gtg gac ggt Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly 680 685 690			2179
ctc ctc gag gct gca ctg cag tcc gtg gat cct cgc cag ctg tgg gtc Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val 695 700 705			2227
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<213> *Corynebacterium glutamicum*

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Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
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Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
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Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
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Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg
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Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
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Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
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Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
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Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
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Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly
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Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys
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 Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg
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 Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr
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 Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met
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 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr
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 Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile
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 Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu
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 Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln
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 Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser

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Val Ile Ala Leu Asp	Ala Asp Val Thr Thr	Ile Glu Ala Ala Arg Ser				
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Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala						
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Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro						
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Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp						
	705		710		715	
Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln						
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Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala	
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Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met	
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Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser	
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Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu	
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Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys	
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Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly	
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Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg	
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Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg	
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Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr	
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Lys	Ser	Leu	Glu	Leu	Pro	Ala	Leu	Pro	Thr	Thr	Thr	Ile	Gly	Ser	Phe		
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Phe	Val	Arg	Asp	Asp	Gln	Pro	Leu	Ala	Thr	Thr	Ala	Asp	Gln	Val	Ala		
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Leu	Ala	Leu	Arg	Asp	Glu	Ile	Asn	Asp	Leu	Ile	Glu	Ala	Gly	Ala	Lys		

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<213> Corynebacterium glutamicum

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Glu	Arg	Leu	Ile	Lys	Ser	Phe	Asp	Thr	Glu	Trp	Val	Gln	Ile	Asp	Glu	
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Pro	Ala	Leu	Val	Thr	Asp	Val	Ala	Pro	Glu	Val	Leu	Glu	Gln	Val	Arg	
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Ala	Gly	Tyr	Thr	Thr	Leu	Ala	Lys	Arg	Asp	Gly	Val	Phe	Val	Asn	Thr	
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Trp		Ser	Val	Asp	Ser	Phe	Arg	Leu	Ala	Thr	Ala	Gly	Ala	Pro	Asp	Asp				
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Val		Gln	Ile	His	Thr	His	Met	Cys	Tyr	Ser	Glu	Phe	Asn	Glu	Val	Ile				
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Arg		Ser	Asp	Met	Gln	Val	Leu	Ala	Ala	Leu	Lys	Ser	Ser	Gly	Phe	Glu				
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Leu		Gly	Val	Gly	Pro	Gly	Val	Trp	Asp	Ile	His	Ser	Pro	Arg	Val	Pro				
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Ser		Ala	Gln	Lys	Val	Asp	Gly	Leu	Leu	Glu	Ala	Ala	Leu	Gln	Ser	Val				
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Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala
20 25 30
Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Glu
35 40 45
Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr
50 55 60
Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys
65 70 75 80
Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His
85 90 95
Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala
100 105 110
Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys
115 120 125
Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val
130 135 140
Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
145 150 155 160

<210> 231
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<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1303)
<223> RXN02648

<400> 231
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gagtttgata	ctttcttttcg	acttttagat	tggtatttca	atg	agc	cag	aac	cgc	115							
				Met	Ser	Gln	Asn	Arg								
				1				5								
atc	agg	acc	act	cac	gtt	ggt	tcc	ttg	ccc	cgt	acc	cca	gag	cta	ctt	163
Ile	Arg	Thr	Thr	His	Val	Gly	Ser	Leu	Pro	Arg	Thr	Pro	Glu	Leu	Leu	
				10				15						20		
gat	gca	aac	atc	aag	cgt	tct	aac	ggt	gag	att	ggg	gag	gag	gaa	ttc	211
Asp	Ala	Asn	Ile	Lys	Arg	Ser	Asn	Gly	Glu	Ile	Gly	Glu	Glu	Glu	Phe	
			25					30					35			
ttc	cag	att	ctg	cag	tct	tct	gta	gat	gac	gtg	atc	aag	cgc	cag	gtt	259
Phe	Gln	Ile	Leu	Gln	Ser	Ser	Val	Asp	Asp	Val	Ile	Lys	Arg	Gln	Val	
		40					45					50				
gac	ctg	ggt	atc	gac	atc	ctt	aac	gag	ggc	gaa	tac	ggc	cac	gtc	acc	307
Asp	Leu	Gly	Ile	Asp	Ile	Leu	Asn	Glu	Gly	Glu	Tyr	Gly	His	Val	Thr	
	55					60					65					
tcc	ggt	gca	gtt	gac	ttc	ggt	gca	tgg	tgg	aac	tac	tcc	ttc	acc	cgc	355
Ser	Gly	Ala	Val	Asp	Phe	Gly	Ala	Trp	Trp	Asn	Tyr	Ser	Phe	Thr	Arg	
	70				75					80					85	
ctg	ggc	gga	ctg	acc	atg	acc	gat	acc	gac	cgt	tgg	gca	agc	cag	gaa	403
Leu	Gly	Gly	Leu	Thr	Met	Thr	Asp	Thr	Asp	Arg	Trp	Ala	Ser	Gln	Glu	
				90					95					100		
gca	gtg	cgt	tcc	acc	cct	ggc	aac	atc	gag	ctg	acc	agc	ttc	tct	gat	451
Ala	Val	Arg	Ser	Thr	Pro	Gly	Asn	Ile	Glu	Leu	Thr	Ser	Phe	Ser	Asp	
			105					110					115			
cgt	cgc	gac	cgc	gca	ttg	ttc	agc	gaa	gca	tac	gag	gat	cca	gta	tct	499
Arg	Arg	Asp	Arg	Ala	Leu	Phe	Ser	Glu	Ala	Tyr	Glu	Asp	Pro	Val	Ser	
		120					125					130				
ggc	atc	ttc	acc	ggt	cgc	gct	tct	gtg	ggc	aac	cca	gag	ttc	acc	gga	547
Gly	Ile	Phe	Thr	Gly	Arg	Ala	Ser	Val	Gly	Asn	Pro	Glu	Phe	Thr	Gly	
	135					140					145					
cct	att	acc	tac	att	ggc	cag	gaa	gaa	act	cag	acg	gat	gtt	gat	ctg	595
Pro	Ile	Thr	Tyr	Ile	Gly	Gln	Glu	Glu	Thr	Gln	Thr	Asp	Val	Asp	Leu	
	150				155					160					165	
ctg	aag	aag	ggc	atg	aac	gca	gcg	gga	gct	acc	gac	ggc	ttc	gtt	gca	643
Leu	Lys	Lys	Gly	Met	Asn	Ala	Ala	Gly	Ala	Thr	Asp	Gly	Phe	Val	Ala	
				170				175						180		
gca	cta	tcc	cca	gga	tct	gca	gct	cga	ttg	acc	aac	aag	ttc	tac	gac	691
Ala	Leu	Ser	Pro	Gly	Ser	Ala	Ala	Arg	Leu	Thr	Asn	Lys	Phe	Tyr	Asp	
			185					190					195			
act	gat	gaa	gaa	gtc	gtc	gca	gca	tgt	gct	gat	gcg	ctt	tcc	cag	gaa	739
Thr	Asp	Glu	Glu	Val	Val	Ala	Ala	Cys	Ala	Asp	Ala	Leu	Ser	Gln	Glu	
		200				205						210				
tac	aag	atc	atc	acc	gat	gca	ggt	ctg	acc	gtt	cag	ctc	gac	gca	ccg	787
Tyr	Lys	Ile	Ile	Thr	Asp	Ala	Gly	Leu	Thr	Val	Gln	Leu	Asp	Ala	Pro	
	215					220					225					

gac ttg gca gaa gca tgg gat cag atc aac cca gag cca agc gtg aag 835
 Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro Ser Val Lys
 230 235 240 245

 gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc aac agt gca 883
 Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile Asn Ser Ala
 250 255 260

 gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc tgc tgg ggc 931
 Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile Cys Trp Gly
 265 270 275

 tct tgg cac gga cca cac gtc act gac atc cca ttc ggt gac atc att 979
 Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly Asp Ile Ile
 280 285 290

 ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc gaa ggc gca 1027
 Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe Glu Gly Ala
 295 300 305

 tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa aac aag ctt 1075
 Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu Asn Lys Leu
 310 315 320 325

 cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac tcc atc aac 1123
 Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His Ser Ile Asn
 330 335 340

 gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt cag ttc gcc 1171
 Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val Gln Phe Ala
 345 350 355

 aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac tgt ggt ctg 1219
 Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp Cys Gly Leu
 360 365 370

 ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg gag tcc cta 1267
 Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu Glu Ser Leu
 375 380 385

 gta gag ggc gct cgc att gca tca aag gaa ctg ttc taagctagac 1313
 Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
 390 395 400

 aacgagggtt gct 1326

<210> 232

<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 232

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
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Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
 20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
 35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
 50 55 60
 Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
 65 70 75 80
 Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
 85 90 95
 Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
 100 105 110
 Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
 115 120 125
 Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
 130 135 140
 Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160
 Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175
 Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190
 Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205
 Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220
 Gln Leu Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro
 225 230 235 240
 Glu Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp
 245 250 255
 Ala Ile Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu
 260 265 270
 His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro
 275 280 285
 Phe Gly Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe
 290 295 300
 Ser Phe Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp
 305 310 315 320
 Glu Glu Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val
 325 330 335
 Ser His Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg
 340 345 350
 Ile Val Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser
 355 360 365

Thr Asp Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala
370 375 380

Lys Leu Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu
385 390 395 400

Phe

<210> 233

<211> 548

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(525)

<223> FRXA02648

<400> 233

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1	5	10	15	
agc gtg aag gat	tac ttg gac tgg	atc ggt aca cgc	atc gat gcc atc	96
Ser Val Lys Asp	Tyr Leu Asp Trp	Ile Gly Thr Arg	Ile Asp Ala Ile	
	20	25	30	
aac agt gca gtg	aag ggc ctt cca	aag gaa cag acc	cgc ctg cac atc	144
Asn Ser Ala Val	Lys Gly Leu Pro	Lys Glu Gln Thr	Arg Leu His Ile	
	35	40	45	
tgc tgg ggc tct	tgg cac gga cca	cac gtc act gac	atc cca ttc ggt	192
Cys Trp Gly Ser	Trp His Gly Pro	His Val Thr Asp	Ile Pro Phe Gly	
	50	55	60	
gac atc att ggt	gag atc ctg cgc	gca gag gtc ggt	ggc ttc tcc ttc	240
Asp Ile Ile Gly	Glu Ile Leu Arg	Ala Glu Val Gly	Gly Phe Ser Phe	
	65	70	75	80
gaa ggc gca tct	cct cgt cac gca	cac gag tgg cgt	gta tgg gaa gaa	288
Glu Gly Ala Ser	Pro Arg His Ala	His Glu Trp Arg	Val Trp Glu Glu	
	85	90	95	
aac aag ctt cct	gaa ggc tct gtt	atc tac cct ggt	gtt gtg tct cac	336
Asn Lys Leu Pro	Glu Gly Ser Val	Ile Tyr Pro Gly	Val Val Ser His	
	100	105	110	
tcc atc aac gct	gtg gag cac cca	cgc ctg gtt gct	gat cgt atc gtt	384
Ser Ile Asn Ala	Val Glu His Pro	Arg Leu Val Ala	Asp Arg Ile Val	
	115	120	125	
cag ttc gcc aag	ctt gtt ggc cct	gag aac gtc att	gcg tcc act gac	432
Gln Phe Ala Lys	Leu Val Gly Pro	Glu Asn Val Ile	Ala Ser Thr Asp	
	130	135	140	
tgt ggt ctg ggc	gga cgt ctg cat	tcc cag atc gca	tgg gca aag ctg	480
Cys Gly Leu Gly	Gly Arg Leu His	Ser Gln Ile Ala	Trp Ala Lys Leu	
	145	150	155	160

gag tcc cta gta gag ggc gct cgc att gca tca aag gaa ctg ttc 525
 Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
 165 170 175

taagctagac aacgagggtt gct 548

<210> 234

<211> 175

<212> PRT

<213> Corynebacterium glutamicum

<400> 234

Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
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Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
 20 25 30

Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
 35 40 45

Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
 50 55 60

Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
 65 70 75 80

Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
 85 90 95

Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
 100 105 110

Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
 115 120 125

Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
 130 135 140

Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
 145 150 155 160

Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
 165 170 175

<210> 235

<211> 784

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(784)

<223> FRXA02658

<400> 235

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gagtttgata ctttctttcg acttttagat tggattttca atg agc cag aac cgc 115

	Met	Ser	Gln	Asn	Arg	
	1				5	
atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163						
Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu						
				10	15	20
gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211						
Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe						
			25		30	35
ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259						
Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val						
			40		45	50
gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307						
Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr						
	55			60	65	
tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355						
Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg						
	70			75	80	85
ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403						
Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu						
			90		95	100
gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451						
Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp						
			105		110	115
cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499						
Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser						
			120		125	130
ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547						
Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly						
	135			140	145	
cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595						
Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu						
	150			155	160	165
ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca 643						
Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala						
			170		175	180
gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691						
Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp						
			185		190	195
act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739						
Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu						
	200			205	210	
tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca 784						
Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala						
	215			220	225	

<211> 228

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 236

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Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
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Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
          20           25           30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
          35           40           45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
          50           55           60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
          65           70           75           80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
          85           90           95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
          100          105          110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
          115          120          125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
          130          135          140

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
          145          150          155          160

Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
          165          170          175

Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
          180          185          190

Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
          195          200          205

Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
          210          215          220

Gln Leu Asp Ala
225

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<210> 237

<211> 408

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(385)

<223> RXC02238

<400> 237

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ctcttaacac tactgtccat atacttttga aaaggtgtca gtg acc aac gtg agc 115
                               Val Thr Asn Val Ser
                               1      5

aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163
Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile
                10                15                20

acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211
Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr
                25                30                35

gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259
Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe
                40                45                50

tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307
Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val
                55                60                65

act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355
Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile
                70                75                80                85

aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca 405
Asn Ala Gly Leu Leu Asp His Glu Glu Gly
                90                95

cac 408

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<210> 238

<211> 95

<212> PRT

<213> Corynebacterium glutamicum

<400> 238

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Val Thr Asn Val Ser Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp
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Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys
 20      25      30

Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg
 35      40      45

Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe
 50      55      60

Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile
 65      70      75      80

Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly
 85      90      95

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<210> 239

<211> 1827

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1804)

<223> RXC00128

<400> 239

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cgttgatcgc tccagagaca ccgtgggaag gggagcagca gtg agt aaa att tcg 115
              Val Ser Lys Ile Ser
              1              5

acg aaa ctg aag gcc ctc acc gcg gtg ctg tct gtg acc act ctg gtg 163
Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser Val Thr Thr Leu Val
              10              15              20

gct ggg tgt tcc acg ctt ccg cag aac acg gat ccg caa gtg ctg cgc 211
Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp Pro Gln Val Leu Arg
              25              30              35

tca ttt tcc ggg tcc caa agc aca caa gag ata gca ggg ccg acc ccg 259
Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile Ala Gly Pro Thr Pro
              40              45              50

aat caa gat ccg gat ttg ttg atc cgc ggc ttc ttc agc gca ggt gcg 307
Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe Phe Ser Ala Gly Ala
              55              60              65

tat ccg act cag cag tat gaa gcg gcg aag gcg tat ctg acg gaa ggg 355
Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala Tyr Leu Thr Glu Gly
              70              75              80              85

acg cgc agc acg tgg aat ccg gct gcg tcg act cgt att ttg gat cgc 403
Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr Arg Ile Leu Asp Arg
              90              95              100

att gat ctg aac act ctg cca ggt tcg acg aat gcg gaa cga acg att 451
Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn Ala Glu Arg Thr Ile
              105              110              115

gcg atc cgt gga acg cag gtc gga acg ttg ctc agc ggt ggc gtg tat 499
Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu Ser Gly Gly Val Tyr
              120              125              130

cag ccg gag aat gcg gag ttt gaa gct gag atc acg atg cgt cgg gaa 547
Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile Thr Met Arg Arg Glu
              135              140              145

gat ggg gag tgg cgt atc gat gct ttg ccg gac ggg att tta tta gag 595
Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu
              150              155              160              165

aga aac gat ctg cgg aac cat tac act ccg cac gat gtg tat ttc ttt 643
Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Phe Phe
              170              175              180

gat cct tct ggc cag gtg ttg gtg ggg gat cgg cgt tgg ttg ttc aat 691
Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn

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185						190						195						
gag	tcg	cag	tcg	atg	tcc	acg	gtg	ctg	atg	gcc	ctt	ctg	gtt	aat	ggt			739
Glu	Ser	Gln	Ser	Met	Ser	Thr	Val	Leu	Met	Ala	Leu	Leu	Val	Asn	Gly			
		200						205					210					
cct	tcg	ccg	gca	att	tct	cct	ggt	gtg	gtc	aat	cag	ctg	tcc	acg	gat			787
Pro	Ser	Pro	Ala	Ile	Ser	Pro	Gly	Val	Val	Asn	Gln	Leu	Ser	Thr	Asp			
		215				220					225							
gcg	tcg	ttc	gtg	ggg	ttc	aat	gat	ggg	gag	tat	cag	ttc	act	ggt	ttg			835
Ala	Ser	Phe	Val	Gly	Phe	Asn	Asp	Gly	Glu	Tyr	Gln	Phe	Thr	Gly	Leu			
		230			235					240					245			
gga	aat	ttg	gat	gat	gat	gcg	cgt	ttg	cgt	ttc	gcc	gcc	cag	gcc	gtg			883
Gly	Asn	Leu	Asp	Asp	Asp	Ala	Arg	Leu	Arg	Phe	Ala	Ala	Gln	Ala	Val			
				250					255					260				
tgg	acg	ttg	gcg	cat	gct	gat	gtc	gca	ggc	ccc	tac	act	ttg	gtc	gct			931
Trp	Thr	Leu	Ala	His	Ala	Asp	Val	Ala	Gly	Pro	Tyr	Thr	Leu	Val	Ala			
			265					270						275				
gac	ggc	gcg	ccg	ttg	ctg	tcg	gag	ttc	cca	acg	ctc	acc	acc	gat	gac			979
Asp	Gly	Ala	Pro	Leu	Leu	Ser	Glu	Phe	Pro	Thr	Leu	Thr	Thr	Asp	Asp			
		280					285					290						
ctc	gcc	gaa	tac	aac	cca	gag	gct	tac	acc	aac	acg	gtg	tcc	acg	ttg			1027
Leu	Ala	Glu	Tyr	Asn	Pro	Glu	Ala	Tyr	Thr	Asn	Thr	Val	Ser	Thr	Leu			
		295				300					305							
ttt	gcg	ttg	cag	gat	gga	tcg	ttg	tcg	agg	gtc	agt	tcc	ggc	aat	gtg			1075
Phe	Ala	Leu	Gln	Asp	Gly	Ser	Leu	Ser	Arg	Val	Ser	Ser	Gly	Asn	Val			
		310			315					320					325			
agt	cca	cta	cag	ggc	att	tgg	agc	ggt	gga	gat	atc	gat	tct	gca	gcg			1123
Ser	Pro	Leu	Gln	Gly	Ile	Trp	Ser	Gly	Gly	Asp	Ile	Asp	Ser	Ala	Ala			
				330					335					340				
att	tcc	tcc	tcc	gcc	aat	gtg	gtg	gca	gcg	gta	cgc	cac	gaa	aac	aac			1171
Ile	Ser	Ser	Ser	Ala	Asn	Val	Val	Ala	Ala	Val	Arg	His	Glu	Asn	Asn			
				345				350					355					
gag	gca	gtg	ctt	act	gtt	ggc	tcc	atg	gaa	ggc	gtg	act	tca	gat	gcg			1219
Glu	Ala	Val	Leu	Thr	Val	Gly	Ser	Met	Glu	Gly	Val	Thr	Ser	Asp	Ala			
		360					365					370						
ttg	agg	agt	gaa	acg	atc	act	cgt	ccc	acc	ttt	gaa	tac	gcg	tcg	agt			1267
Leu	Arg	Ser	Glu	Thr	Ile	Thr	Arg	Pro	Thr	Phe	Glu	Tyr	Ala	Ser	Ser			
		375				380					385							
ggg	ttg	tgg	gct	gtg	gtg	gat	ggg	gag	acg	cct	gtc	cga	gtc	gca	cga			1315
Gly	Leu	Trp	Ala	Val	Val	Asp	Gly	Glu	Thr	Pro	Val	Arg	Val	Ala	Arg			
					395					400					405			
tcg	gca	aca	acc	ggg	gag	ctc	gtc	cag	acg	gag	gcg	gag	att	gtg	ctg			1363
Ser	Ala	Thr	Thr	Gly	Glu	Leu	Val	Gln	Thr	Glu	Ala	Glu	Ile	Val	Leu			
				410					415					420				
cca	agg	gat	gtg	acg	ggg	ccg	atc	tct	gaa	ttc	caa	ctg	tca	cga	act			1411
Pro	Arg	Asp	Val	Thr	Gly	Pro	Ile	Ser	Glu	Phe	Gln	Leu	Ser	Arg	Thr			
			425					430					435					

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ggg gtc cgg gcc gcc atg atc att gaa ggc aag gtg tac gtg ggc gtc 1459
Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys Val Tyr Val Gly Val
      440                      445                      450

gta acg cgt cct ggt ccg ggc gag cgg cgc gtg aca aat atc acg gag 1507
Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val Thr Asn Ile Thr Glu
      455                      460                      465

gtg gcg ccg agc ttg ggc gag gcg gcg ctg tcg atc aac tgg cgc cca 1555
Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro
      470                      475                      480                      485

gac ggc att ttg ctt gtg ggc acg tca att cca gag acg ccg ctg tgg 1603
Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp
      490                      495                      500

cgc gtc gag cag gac gga tcg gcg att tcg tcg atg ccg agc ggg aat 1651
Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn
      505                      510                      515

ctc agc gcg ccg gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac 1699
Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr
      520                      525                      530

gtc act gat tcg cat gcg atg ctt cag ctg ccg act gcc gat aat gat 1747
Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp
      535                      540                      545

att tgg cgc gag gtg ccc ggt ttg ctg ggc acg cgt gcg gcg ccg gtg 1795
Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val
      550                      555                      560                      565

gtt gcg tac tgatggagct gttcttcccg cgc 1827
Val Ala Tyr

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<210> 240

<211> 568

<212> PRT

<213> Corynebacterium glutamicum

<400> 240

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Val Ser Lys Ile Ser Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser
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Val Thr Thr Leu Val Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp
      20                      25                      30

Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile
      35                      40                      45

Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe
      50                      55                      60

Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala
      65                      70                      75                      80

Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr
      85                      90                      95

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Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn
 100 105 110
 Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu
 115 120 125
 Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile
 130 135 140
 Thr Met Arg Arg Glu Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp
 145 150 155 160
 Gly Ile Leu Leu Glu Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His
 165 170 175
 Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg
 180 185 190
 Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala
 195 200 205
 Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn
 210 215 220
 Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr
 225 230 235 240
 Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe
 245 250 255
 Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro
 260 265 270
 Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr
 275 280 285
 Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn
 290 295 300
 Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val
 305 310 315 320
 Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp
 325 330 335
 Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val
 340 345 350
 Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly
 355 360 365
 Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe
 370 375 380
 Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro
 385 390 395 400
 Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu
 405 410 415

Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe
420 425 430

Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys
435 440 445

Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val
450 455 460

Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser
465 470 475 480

Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro
485 490 495

Glu Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser
500 505 510

Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser
515 520 525

Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro
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Thr Ala Asp Asn Asp Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr
545 550 555 560

Arg Ala Ala Pro Val Val Ala Tyr
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<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1321)
<223> RXA02240

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aagactattt attctcaact tcttcgaaag aagggtattt gtg gct cag cca acc 115
Val Ala Gln Pro Thr
1 5

gcc gtc cgt ttg ttc acc agt gaa tct gta act gag gga cat cca gac 163
Ala Val Arg Leu Phe Thr Ser Glu Ser Val Thr Glu Gly His Pro Asp
10 15 20

aaa ata tgt gat gct att tcc gat acc att ttg gac gcg ctg ctc gaa 211
Lys Ile Cys Asp Ala Ile Ser Asp Thr Ile Leu Asp Ala Leu Leu Glu
25 30 35

aaa gat ccg cag tcg cgc gtc gca gtg gaa act gtg gtc acc acc gga 259
Lys Asp Pro Gln Ser Arg Val Ala Val Glu Thr Val Val Thr Thr Gly
40 45 50

atc gtc cat gtt gtt ggc gag gtc cgt acc agc gct tac gta gag atc 307

Ile	Val	His	Val	Val	Gly	Glu	Val	Arg	Thr	Ser	Ala	Tyr	Val	Glu	Ile		
	55					60					65						
cct	caa	tta	gtc	cgc	aac	aag	ctc	atc	gaa	atc	gga	ttc	aac	tcc	tct	355	
Pro	Gln	Leu	Val	Arg	Asn	Lys	Leu	Ile	Glu	Ile	Gly	Phe	Asn	Ser	Ser	85	
	70				75					80							
gag	gtt	gga	ttc	gac	gga	cgc	acc	tgt	ggc	gtc	tca	gta	tcc	atc	ggt	403	
Glu	Val	Gly	Phe	Asp	Gly	Arg	Thr	Cys	Gly	Val	Ser	Val	Ser	Ile	Gly		
				90					95					100			
gag	cag	tcc	cag	gaa	atc	gct	gac	ggc	gtg	gat	aac	tcc	gac	gaa	gcc	451	
Glu	Gln	Ser	Gln	Glu	Ile	Ala	Asp	Gly	Val	Asp	Asn	Ser	Asp	Glu	Ala		
			105					110					115				
cgc	acc	aac	ggc	gac	gtt	gaa	gaa	gac	gac	cgc	gca	ggt	gct	ggc	gac	499	
Arg	Thr	Asn	Gly	Asp	Val	Glu	Glu	Asp	Asp	Arg	Ala	Gly	Ala	Gly	Asp		
		120					125					130					
cag	ggc	ctg	atg	ttc	ggc	tac	gcc	acc	aac	gaa	acc	gaa	gag	tac	atg	547	
Gln	Gly	Leu	Met	Phe	Gly	Tyr	Ala	Thr	Asn	Glu	Thr	Glu	Glu	Tyr	Met		
	135					140					145						
cct	ctt	cct	atc	gcg	ttg	gcg	cac	cga	ctg	tca	cgt	cgt	ctg	acc	cag	595	
Pro	Leu	Pro	Ile	Ala	Leu	Ala	His	Arg	Leu	Ser	Arg	Arg	Leu	Thr	Gln		
	150				155					160					165		
gtt	cgt	aaa	gag	ggc	atc	gtt	cct	cac	ctg	cgt	cca	gac	gga	aaa	acc	643	
Val	Arg	Lys	Glu	Gly	Ile	Val	Pro	His	Leu	Arg	Pro	Asp	Gly	Lys	Thr		
				170					175					180			
cag	gtc	acc	ttc	gca	tac	gat	gcg	caa	gac	cgc	cct	agc	cac	ctg	gat	691	
Gln	Val	Thr	Phe	Ala	Tyr	Asp	Ala	Gln	Asp	Arg	Pro	Ser	His	Leu	Asp		
			185					190					195				
acc	gtt	gtc	atc	tcc	acc	cag	cac	gac	cca	gaa	gtt	gac	cgt	gca	tgg	739	
Thr	Val	Val	Ile	Ser	Thr	Gln	His	Asp	Pro	Glu	Val	Asp	Arg	Ala	Trp		
		200					205					210					
ttg	gaa	acc	caa	ctg	cgc	gaa	cac	gtc	att	gat	tgg	gta	atc	aaa	gac	787	
Leu	Glu	Thr	Gln	Leu	Arg	Glu	His	Val	Ile	Asp	Trp	Val	Ile	Lys	Asp		
	215					220					225						
gca	ggc	att	gag	gat	ctg	gca	acc	ggt	gag	atc	acc	gtg	ttg	atc	aac	835	
Ala	Gly	Ile	Glu	Asp	Leu	Ala	Thr	Gly	Glu	Ile	Thr	Val	Leu	Ile	Asn		
	230				235					240					245		
cct	tca	ggt	tcc	ttc	att	ctg	ggt	ggc	ccc	atg	ggt	gat	gcg	ggt	ctg	883	
Pro	Ser	Gly	Ser	Phe	Ile	Leu	Gly	Gly	Pro	Met	Gly	Asp	Ala	Gly	Leu		
				250					255					260			
acc	ggc	cgc	aag	atc	atc	gtg	gat	acc	tac	ggt	ggc	atg	gct	cgc	cat	931	
Thr	Gly	Arg	Lys	Ile	Ile	Val	Asp	Thr	Tyr	Gly	Gly	Met	Ala	Arg	His		
			265					270					275				
ggt	ggt	gga	gca	ttc	tcc	ggt	aag	gat	cca	agc	aag	gtg	gac	cgc	tct	979	
Gly	Gly	Gly	Ala	Phe	Ser	Gly	Lys	Asp	Pro	Ser	Lys	Val	Asp	Arg	Ser		
		280					285					290					
gct	gca	tac	gcc	atg	cgt	tgg	gta	gca	aag	aac	atc	gtg	gca	gca	ggc	1027	
Ala	Ala	Tyr	Ala	Met	Arg	Trp	Val	Ala	Lys	Asn	Ile	Val	Ala	Ala	Gly		

295	300	305	
ctt gct gat cgc gct gaa gtt cag gtt gca tac gcc att gga cgc gca			1075
Leu Ala Asp Arg Ala Glu Val Gln Val Ala Tyr Ala Ile Gly Arg Ala			
310	315	320	325
aag cca gtc gga ctt tac gtt gaa acc ttt gac acc aac aag gaa ggc			1123
Lys Pro Val Gly Leu Tyr Val Glu Thr Phe Asp Thr Asn Lys Glu Gly			
	330	335	340
ctg agc gac gag cag att cag gct gcc gtg ttg gag gtc ttt gac ctg			1171
Leu Ser Asp Glu Gln Ile Gln Ala Ala Val Leu Glu Val Phe Asp Leu			
	345	350	355
cgt cca gca gca att atc cgt gag ctt gat ctg ctt cgt ccg atc tac			1219
Arg Pro Ala Ala Ile Ile Arg Glu Leu Asp Leu Leu Arg Pro Ile Tyr			
	360	365	370
gct gac act gct gcc tac ggc cac ttt ggt cgc act gat ttg gac ctt			1267
Ala Asp Thr Ala Ala Tyr Gly His Phe Gly Arg Thr Asp Leu Asp Leu			
	375	380	385
cct tgg gag gct atc gac cgc gtt gat gaa ctt cgc gca gcc ctc aag			1315
Pro Trp Glu Ala Ile Asp Arg Val Asp Glu Leu Arg Ala Ala Leu Lys			
	390	395	400
ttg gcc taaaaatctg atgtagtattc ttc			1344
Leu Ala			

<210> 242

<211> 407

<212> PRT

<213> Corynebacterium glutamicum

<400> 242

Val Ala Gln Pro Thr Ala Val Arg Leu Phe Thr Ser Glu Ser Val Thr	
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Glu Gly His Pro Asp Lys Ile Cys Asp Ala Ile Ser Asp Thr Ile Leu	
20 25 30	
Asp Ala Leu Leu Glu Lys Asp Pro Gln Ser Arg Val Ala Val Glu Thr	
35 40 45	
Val Val Thr Thr Gly Ile Val His Val Val Gly Glu Val Arg Thr Ser	
50 55 60	
Ala Tyr Val Glu Ile Pro Gln Leu Val Arg Asn Lys Leu Ile Glu Ile	
65 70 75 80	
Gly Phe Asn Ser Ser Glu Val Gly Phe Asp Gly Arg Thr Cys Gly Val	
85 90 95	
Ser Val Ser Ile Gly Glu Gln Ser Gln Glu Ile Ala Asp Gly Val Asp	
100 105 110	
Asn Ser Asp Glu Ala Arg Thr Asn Gly Asp Val Glu Glu Asp Asp Arg	
115 120 125	

Ala Gly Ala Gly Asp Gln Gly Leu Met Phe Gly Tyr Ala Thr Asn Glu
 130 135 140
 Thr Glu Glu Tyr Met Pro Leu Pro Ile Ala Leu Ala His Arg Leu Ser
 145 150 155 160
 Arg Arg Leu Thr Gln Val Arg Lys Glu Gly Ile Val Pro His Leu Arg
 165 170 175
 Pro Asp Gly Lys Thr Gln Val Thr Phe Ala Tyr Asp Ala Gln Asp Arg
 180 185 190
 Pro Ser His Leu Asp Thr Val Val Ile Ser Thr Gln His Asp Pro Glu
 195 200 205
 Val Asp Arg Ala Trp Leu Glu Thr Gln Leu Arg Glu His Val Ile Asp
 210 215 220
 Trp Val Ile Lys Asp Ala Gly Ile Glu Asp Leu Ala Thr Gly Glu Ile
 225 230 235 240
 Thr Val Leu Ile Asn Pro Ser Gly Ser Phe Ile Leu Gly Gly Pro Met
 245 250 255
 Gly Asp Ala Gly Leu Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly
 260 265 270
 Gly Met Ala Arg His Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser
 275 280 285
 Lys Val Asp Arg Ser Ala Ala Tyr Ala Met Arg Trp Val Ala Lys Asn
 290 295 300
 Ile Val Ala Ala Gly Leu Ala Asp Arg Ala Glu Val Gln Val Ala Tyr
 305 310 315 320
 Ala Ile Gly Arg Ala Lys Pro Val Gly Leu Tyr Val Glu Thr Phe Asp
 325 330 335
 Thr Asn Lys Glu Gly Leu Ser Asp Glu Gln Ile Gln Ala Ala Val Leu
 340 345 350
 Glu Val Phe Asp Leu Arg Pro Ala Ala Ile Ile Arg Glu Leu Asp Leu
 355 360 365
 Leu Arg Pro Ile Tyr Ala Asp Thr Ala Ala Tyr Gly His Phe Gly Arg
 370 375 380
 Thr Asp Leu Asp Leu Pro Trp Glu Ala Ile Asp Arg Val Asp Glu Leu
 385 390 395 400
 Arg Ala Ala Leu Lys Leu Ala
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<210> 243

<211> 669

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

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<222> (101)..(646)

<223> RXA00780

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                                         Met Ile Arg Glu Asp
                                         1 5

ctc gca aac gct cgt gaa cac gat cca gca gcc cga ggc gat tta gaa 163
Leu Ala Asn Ala Arg Glu His Asp Pro Ala Ala Arg Gly Asp Leu Glu
                        10 15 20

aac gca gtg gtt tac tcc gga ctc cac gcc atc tgg gca cat cga gtt 211
Asn Ala Val Val Tyr Ser Gly Leu His Ala Ile Trp Ala His Arg Val
                        25 30 35

gcc aac agc tgg tgg aaa tcc ggt ttc cgc ggc ccc gcc cgc gta tta 259
Ala Asn Ser Trp Trp Lys Ser Gly Phe Arg Gly Pro Ala Arg Val Leu
                        40 45 50

gcc caa ttc acc cga ttc ctc acc ggc att gaa att cac ccc ggt gcc 307
Ala Gln Phe Thr Arg Phe Leu Thr Gly Ile Glu Ile His Pro Gly Ala
                        55 60 65

acc att ggt cgt cgc ttt ttt att gac cac gga atg gga atc gtc atc 355
Thr Ile Gly Arg Arg Phe Phe Ile Asp His Gly Met Gly Ile Val Ile
                        70 75 80 85

ggc gaa acc gct gaa atc ggc gaa ggc gtc atg ctc tac cac ggc gtc 403
Gly Glu Thr Ala Glu Ile Gly Glu Gly Val Met Leu Tyr His Gly Val
                        90 95 100

acc ctc ggc gga cag gtt ctc acc caa acc aag cgc cac ccc acg ctc 451
Thr Leu Gly Gly Gln Val Leu Thr Gln Thr Lys Arg His Pro Thr Leu
                        105 110 115

tgc gac aac gtg aca gtc ggc gcg ggc gca aaa atc tta ggt ccc atc 499
Cys Asp Asn Val Thr Val Gly Ala Gly Ala Lys Ile Leu Gly Pro Ile
                        120 125 130

acc atc ggc gaa ggc tcc gca att ggc gcc aat gca gtt gtc acc aaa 547
Thr Ile Gly Glu Gly Ser Ala Ile Gly Ala Asn Ala Val Val Thr Lys
                        135 140 145

gac gtg ccg gca gaa cac atc gca gtc gga att cct gcg gta gca cgc 595
Asp Val Pro Ala Glu His Ile Ala Val Gly Ile Pro Ala Val Ala Arg
                        150 155 160 165

cca cgt ggc aag aca gag aag atc aag ctc gtc gat ccg gac tat tac 643
Pro Arg Gly Lys Thr Glu Lys Ile Lys Leu Val Asp Pro Asp Tyr Tyr
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att taagaacagt tagcgcccta cct 669
Ile

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<210> 244

<211> 182

<212> PRT

<213> Corynebacterium glutamicum

<400> 244

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Arg Gly Asp Leu Glu Asn Ala Val Val Tyr Ser Gly Leu His Ala Ile
      20             25             30

Trp Ala His Arg Val Ala Asn Ser Trp Trp Lys Ser Gly Phe Arg Gly
      35             40             45

Pro Ala Arg Val Leu Ala Gln Phe Thr Arg Phe Leu Thr Gly Ile Glu
      50             55             60

Ile His Pro Gly Ala Thr Ile Gly Arg Arg Phe Phe Ile Asp His Gly
      65             70             75             80

Met Gly Ile Val Ile Gly Glu Thr Ala Glu Ile Gly Glu Gly Val Met
      85             90             95

Leu Tyr His Gly Val Thr Leu Gly Gly Gln Val Leu Thr Gln Thr Lys
      100            105            110

Arg His Pro Thr Leu Cys Asp Asn Val Thr Val Gly Ala Gly Ala Lys
      115            120            125

Ile Leu Gly Pro Ile Thr Ile Gly Glu Gly Ser Ala Ile Gly Ala Asn
      130            135            140

Ala Val Val Thr Lys Asp Val Pro Ala Glu His Ile Ala Val Gly Ile
      145            150            155            160

Pro Ala Val Ala Arg Pro Arg Gly Lys Thr Glu Lys Ile Lys Leu Val
      165            170            175

Asp Pro Asp Tyr Tyr Ile
      180

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<210> 245

<211> 1056

<212> DNA

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<220>

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<222> (101)..(1033)

<223> RXA00779

<400> 245

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                                   Met Gly Asn Val Tyr
                                   1             5

aac aac atc acc gaa acc atc ggc cac acc cca ctg gta aag ctg aac 163
Asn Asn Ile Thr Glu Thr Ile Gly His Thr Pro Leu Val Lys Leu Asn

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				10				15				20							
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Lys	Leu	Thr	Glu	Gly	Leu	Asp	Ala	Thr	Val	Leu	Val	Lys	Leu	Glu	Ser				
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ttc	aac	cca	gca	aac	tcc	gtc	aag	gac	cgt	atc	ggg	ctg	gcc	atc	gtt	259			
Phe	Asn	Pro	Ala	Asn	Ser	Val	Lys	Asp	Arg	Ile	Gly	Leu	Ala	Ile	Val				
40				45				50											
gaa	gat	gca	gag	aag	tcc	ggg	gca	ctg	aag	cca	ggc	ggc	acc	atc	gtt	307			
Glu	Asp	Ala	Glu	Lys	Ser	Gly	Ala	Leu	Lys	Pro	Gly	Gly	Thr	Ile	Val				
55				60				65											
gaa	gca	acc	tcc	ggc	aac	acc	ggg	atc	gca	ctg	gca	atg	gtc	ggc	gct	355			
Glu	Ala	Thr	Ser	Gly	Asn	Thr	Gly	Ile	Ala	Leu	Ala	Met	Val	Gly	Ala				
70				75				80				85							
gca	cgc	gga	tac	aac	gtt	gtt	ctc	acc	atg	cgc	gag	acc	atg	tcc	aac	403			
Ala	Arg	Gly	Tyr	Asn	Val	Val	Leu	Thr	Met	Pro	Glu	Thr	Met	Ser	Asn				
90				95				100											
gag	cgt	cgc	gtt	ctc	ctc	cgc	gct	tac	ggg	gca	gag	atc	gtt	ctt	acc	451			
Glu	Arg	Arg	Val	Leu	Leu	Arg	Ala	Tyr	Gly	Ala	Glu	Ile	Val	Leu	Thr				
105				110				115											
cca	ggg	gca	gca	ggc	atg	cag	ggg	gca	aag	gac	aag	gca	gac	gaa	atc	499			
Pro	Gly	Ala	Ala	Gly	Met	Gln	Gly	Ala	Lys	Asp	Lys	Ala	Asp	Glu	Ile				
120				125				130											
gtc	gct	gaa	cgc	gaa	aac	gca	gtc	ctt	gct	cgc	cag	ttc	gag	aac	gag	547			
Val	Ala	Glu	Arg	Glu	Asn	Ala	Val	Leu	Ala	Arg	Gln	Phe	Glu	Asn	Glu				
135				140				145											
gca	aac	cca	cgc	gtc	aac	cgc	gac	acc	acc	gcg	aag	gaa	atc	ctc	gaa	595			
Ala	Asn	Pro	Arg	Val	Asn	Arg	Asp	Thr	Thr	Ala	Lys	Glu	Ile	Leu	Glu				
150				155				160				165							
gac	acc	gac	ggc	acc	gtt	gat	atc	ttc	gtt	gca	agc	ttc	ggc	acc	ggc	643			
Asp	Thr	Asp	Gly	Thr	Val	Asp	Ile	Phe	Val	Ala	Ser	Phe	Gly	Thr	Gly				
170				175				180											
gga	acc	gtc	acc	ggc	gtt	ggc	cag	gtc	ctg	aag	gaa	aac	aac	gca	gac	691			
Gly	Thr	Val	Thr	Gly	Val	Gly	Gln	Val	Leu	Lys	Glu	Asn	Asn	Ala	Asp				
185				190				195											
gta	cag	gtc	tac	acc	gtc	gag	cca	gaa	gcg	tcc	cca	ctt	ctg	acc	gct	739			
Val	Gln	Val	Tyr	Thr	Val	Glu	Pro	Glu	Ala	Ser	Pro	Leu	Leu	Thr	Ala				
200				205				210											
ggc	aag	gct	ggg	cca	cac	aag	atc	cag	ggc	atc	ggc	gca	aac	ttc	atc	787			
Gly	Lys	Ala	Gly	Pro	His	Lys	Ile	Gln	Gly	Ile	Gly	Ala	Asn	Phe	Ile				
215				220				225											
ccc	gag	gtc	ctg	gac	cgc	aag	gtt	ctc	gac	gac	gtg	ctg	acc	gtc	tcc	835			
Pro	Glu	Val	Leu	Asp	Arg	Lys	Val	Leu	Asp	Asp	Val	Leu	Thr	Val	Ser				
230				235				240				245							
aac	gaa	gac	gca	atc	gca	ttc	tcc	cgc	aag	ctc	gct	acc	gaa	gag	ggc	883			
Asn	Glu	Asp	Ala	Ile	Ala	Phe	Ser	Arg	Lys	Leu	Ala	Thr	Glu	Glu	Gly				
250				255				260											

atc ctc ggc ggt atc tcc acc ggc gca aac atc aag gca gct ctt gac 931
 Ile Leu Gly Gly Ile Ser Thr Gly Ala Asn Ile Lys Ala Ala Leu Asp
 265 270 275

ctt gca gca aag cca gag aac gct ggc aaa acc atc gtc acc gtt gtc 979
 Leu Ala Ala Lys Pro Glu Asn Ala Gly Lys Thr Ile Val Thr Val Val
 280 285 290

acc gac ttc ggc gag cgc tac gtc tcc acc gtt ctt tac gaa gac atc 1027
 Thr Asp Phe Gly Glu Arg Tyr Val Ser Thr Val Leu Tyr Glu Asp Ile
 295 300 305

cgc gac taattcttag cgactgttaa cca 1056
 Arg Asp
 310

<210> 246

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 246

Met Gly Asn Val Tyr Asn Asn Ile Thr Glu Thr Ile Gly His Thr Pro
 1 5 10 15

Leu Val Lys Leu Asn Lys Leu Thr Glu Gly Leu Asp Ala Thr Val Leu
 20 25 30

Val Lys Leu Glu Ser Phe Asn Pro Ala Asn Ser Val Lys Asp Arg Ile
 35 40 45

Gly Leu Ala Ile Val Glu Asp Ala Glu Lys Ser Gly Ala Leu Lys Pro
 50 55 60

Gly Gly Thr Ile Val Glu Ala Thr Ser Gly Asn Thr Gly Ile Ala Leu
 65 70 75 80

Ala Met Val Gly Ala Ala Arg Gly Tyr Asn Val Val Leu Thr Met Pro
 85 90 95

Glu Thr Met Ser Asn Glu Arg Arg Val Leu Leu Arg Ala Tyr Gly Ala
 100 105 110

Glu Ile Val Leu Thr Pro Gly Ala Ala Gly Met Gln Gly Ala Lys Asp
 115 120 125

Lys Ala Asp Glu Ile Val Ala Glu Arg Glu Asn Ala Val Leu Ala Arg
 130 135 140

Gln Phe Glu Asn Glu Ala Asn Pro Arg Val Asn Arg Asp Thr Thr Ala
 145 150 155 160

Lys Glu Ile Leu Glu Asp Thr Asp Gly Thr Val Asp Ile Phe Val Ala
 165 170 175

Ser Phe Gly Thr Gly Gly Thr Val Thr Gly Val Gly Gln Val Leu Lys
 180 185 190

Glu Asn Asn Ala Asp Val Gln Val Tyr Thr Val Glu Pro Glu Ala Ser

195					200					205					
Pro	Leu	Leu	Thr	Ala	Gly	Lys	Ala	Gly	Pro	His	Lys	Ile	Gln	Gly	Ile
210						215					220				
Gly	Ala	Asn	Phe	Ile	Pro	Glu	Val	Leu	Asp	Arg	Lys	Val	Leu	Asp	Asp
225					230					235				240	
Val	Leu	Thr	Val	Ser	Asn	Glu	Asp	Ala	Ile	Ala	Phe	Ser	Arg	Lys	Leu
				245					250					255	
Ala	Thr	Glu	Glu	Gly	Ile	Leu	Gly	Gly	Ile	Ser	Thr	Gly	Ala	Asn	Ile
		260					265						270		
Lys	Ala	Ala	Leu	Asp	Leu	Ala	Ala	Lys	Pro	Glu	Asn	Ala	Gly	Lys	Thr
	275					280						285			
Ile	Val	Thr	Val	Val	Thr	Asp	Phe	Gly	Glu	Arg	Tyr	Val	Ser	Thr	Val
290					295						300				
Leu	Tyr	Glu	Asp	Ile	Arg	Asp									
305					310										

<210> 247

<211> 623

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(600)

<223> RXN00402

<400> 247

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Thr	Asp	Glu	Lys	Asp	Gly	Lys	Pro	Val	Leu	Pro	Tyr	Phe	Val	Thr	Pro	
1				5				10					15			
gat	gct	gct	tac	cac	gga	ttg	aag	tac	gca	gac	ctt	ggg	gca	cca	gcc	96
Asp	Ala	Ala	Tyr	His	Gly	Leu	Lys	Tyr	Ala	Asp	Leu	Gly	Ala	Pro	Ala	
			20				25					30				
ttc	ggc	ctc	aag	gtt	cgc	gtt	ggc	ctt	cta	cgc	gac	acc	ggc	tcc	acc	144
Phe	Gly	Leu	Lys	Val	Arg	Val	Gly	Leu	Leu	Arg	Asp	Thr	Gly	Ser	Thr	
		35				40						45				
ctc	tcc	gca	ttc	aac	gca	tgg	gct	gca	gtc	cag	ggc	atc	gac	acc	ctt	192
Leu	Ser	Ala	Phe	Asn	Ala	Trp	Ala	Ala	Val	Gln	Gly	Ile	Asp	Thr	Leu	
	50				55				60							
tcc	ctg	cgc	ctg	gag	cgc	cac	aac	gaa	aac	gcc	atc	aag	gtt	gca	gaa	240
Ser	Leu	Arg	Leu	Glu	Arg	His	Asn	Glu	Asn	Ala	Ile	Lys	Val	Ala	Glu	
65				70				75						80		
ttc	ctc	aac	aac	cac	gag	aag	gtg	gaa	aag	gtt	aac	ttc	gca	ggc	ctg	288
Phe	Leu	Asn	Asn	His	Glu	Lys	Val	Glu	Lys	Val	Asn	Phe	Ala	Gly	Leu	
				85			90							95		
aag	gat	tcc	cct	tgg	tac	gca	acc	aag	gaa	aag	ctt	ggc	ctg	aag	tac	336
Lys	Asp	Ser	Pro	Trp	Tyr	Ala	Thr	Lys	Glu	Lys	Leu	Gly	Leu	Lys	Tyr	

100					105					110					
acc ggc tcc gtt ctc acc ttc gag atc aag ggc ggc aag gat gag gct	384														
Thr Gly Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala															
115 120 125															
tgg gca ttt atc gac gcc ctg aag cta cac tcc aac ctt gca aac atc	432														
Trp Ala Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile															
130 135 140															
ggc gat gtt cgc tcc ctc gtt gtt cac cca gca acc acc acc cat tca	480														
Gly Asp Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser															
145 150 155 160															
cag tcc gac gaa gct ggc ctg gca cgc gcg ggc gtt acc cag tcc acc	528														
Gln Ser Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr															
165 170 175															
gtc cgc ctg tcc gtt ggc atc gag acc att gat gat atc atc gct gac	576														
Val Arg Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp															
180 185 190															
ctc gaa ggc ggc ttt gct gca atc tagctttaaa tagactcacc cca	623														
Leu Glu Gly Gly Phe Ala Ala Ile															
195 200															

<210> 248

<211> 200

<212> PRT

<213> Corynebacterium glutamicum

<400> 248

Thr Asp Glu Lys Asp Gly Lys Pro Val Leu Pro Tyr Phe Val Thr Pro	
1 5 10 15	
Asp Ala Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala	
20 25 30	
Phe Gly Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr	
35 40 45	
Leu Ser Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu	
50 55 60	
Ser Leu Arg Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu	
65 70 75 80	
Phe Leu Asn Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu	
85 90 95	
Lys Asp Ser Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr	
100 105 110	
Thr Gly Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala	
115 120 125	
Trp Ala Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile	
130 135 140	
Gly Asp Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser	

145 150 155 160
 Gln Ser Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr
 165 170 175
 Val Arg Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp
 180 185 190
 Leu Glu Gly Gly Phe Ala Ala Ile
 195 200

<210> 249

<211> 599

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1) .. (576)

<223> FRXA00402

<400> 249

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 Val Leu Pro Tyr Phe Val Thr Pro Asp Ala Ala Tyr His Gly Leu Lys
 1 5 10 15

tac gca gac ctt ggt gca cca gcc ttc ggc ctc aag gtt cgc gtt ggc 96
 Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu Lys Val Arg Val Gly
 20 25 30

ctt cta cgc gac acc ggc tcc acc ctc tcc gca ttc aac gca tgg gct 144
 Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala Phe Asn Ala Trp Ala
 35 40 45

gca gtc cag ggc atc gac acc ctt tcc ctg cgc ctg gag cgc cac aac 192
 Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg Leu Glu Arg His Asn
 50 55 60

gaa aac gcc atc aag gtt gca gaa ttc ctc aac aac cac gag aag gtg 240
 Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn Asn His Glu Lys Val
 65 70 75 80

gaa aag gtt aac ttc gca ggc ctg aag gat tcc cct tgg tac gca acc 288
 Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser Pro Trp Tyr Ala Thr
 85 90 95

aag gaa aag ctt ggc ctg aag tac acc ggc tcc gtt ctc acc ttc gag 336
 Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu
 100 105 110

atc aag ggc ggc aag gat gag gct tgg gca ttt atc gac gcc ctg aag 384
 Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys
 115 120 125

cta cac tcc aac ctt gca aac atc ggc gat gtt cgc tcc ctc gtt gtt 432
 Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val Arg Ser Leu Val Val
 130 135 140

cac cca gca acc acc acc cat tca cag tcc gac gaa gct ggc ctg gca 480
 His Pro Ala Thr Thr Thr His Ser Gln Ser Asp Glu Ala Gly Leu Ala

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145              150              155              160
cgc gcg ggc gtt acc cag tcc acc gtc cgc ctg tcc gtt ggc atc gag 528
Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu Ser Val Gly Ile Glu
              165              170              175

acc att gat gat atc atc gct gac ctc gaa ggc ggc ttt gct gca atc 576
Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly Gly Phe Ala Ala Ile
              180              185              190

tagctttaaa tagactcacc cca 599

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<210> 250
 <211> 192
 <212> PRT
 <213> Corynebacterium glutamicum

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<400> 250
Val Leu Pro Tyr Phe Val Thr Pro Asp Ala Ala Tyr His Gly Leu Lys
  1              5              10              15

Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu Lys Val Arg Val Gly
      20              25              30

Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala Phe Asn Ala Trp Ala
      35              40              45

Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg Leu Glu Arg His Asn
      50              55              60

Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn Asn His Glu Lys Val
      65              70              75              80

Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser Pro Trp Tyr Ala Thr
      85              90              95

Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu
      100             105             110

Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys
      115             120             125

Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val Arg Ser Leu Val Val
      130             135             140

His Pro Ala Thr Thr Thr His Ser Gln Ser Asp Glu Ala Gly Leu Ala
      145             150             155             160

Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu Ser Val Gly Ile Glu
      165             170             175

Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly Gly Phe Ala Ala Ile
      180             185             190

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<210> 251
 <211> 613

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(613)

<223> RXS00405

<400> 251

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ggagaagaat ttcttaataa aaactcttaa ggacctccaa atg cca aag tac gac 115
                                         Met Pro Lys Tyr Asp
                                         1      5

aat tcc aat gct gac cag tgg ggc ttt gaa acc cgc tcc att cac gca 163
Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu Thr Arg Ser Ile His Ala
              10              15              20

ggc cag tca gta gac gca cag acc agc gca cga aac ctt ccg atc tac 211
Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg Asn Leu Pro Ile Tyr
              25              30              35

caa tcc acc gct ttc gtg ttc gac tcc gct gag cac gcc aag cag cgt 259
Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu His Ala Lys Gln Arg
              40              45              50

ttc gca ctt gag gat cta ggc cct gtt tac tcc cgc ctc acc aac cca 307
Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser Arg Leu Thr Asn Pro
              55              60              65

acc gtt gag gct ttg gaa aac cgc atc gct tcc ctc gaa ggt ggc gtc 355
Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser Leu Glu Gly Gly Val
              70              75              80              85

cac gct gta gcg ttc tcc tcc gga cag gcc gca acc acc aac gcc att 403
His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala Thr Thr Asn Ala Ile
              90              95              100

ttg aac ctg gca gga gcg ggc gac cac atc gtc acc tcc cca cgc ctc 451
Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val Thr Ser Pro Arg Leu
              105              110              115

tac ggt ggc acc gag act cta ttc ctt atc act ctt aac cgc ctg ggt 499
Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr Leu Asn Arg Leu Gly
              120              125              130

atc gat gtt tcc ttc gtg gaa aac ccc gac gac cct gag tcc tgg cag 547
Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp Pro Glu Ser Trp Gln
              135              140              145

gca gcc gtt cag cca aac acc aaa gca ttc ttc ggc gag act ttc gcc 595
Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe Gly Glu Thr Phe Ala
              150              155              160              165

aac cca cag gca gac gtc 613
Asn Pro Gln Ala Asp Val
              170

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<210> 252

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 252

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Met Pro Lys Tyr Asp Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu Thr
  1           5           10           15

Arg Ser Ile His Ala Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg
          20           25           30

Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu
          35           40           45

His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser
  50           55           60

Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser
  65           70           75           80

Leu Glu Gly Gly Val His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala
          85           90           95

Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val
          100          105          110

Thr Ser Pro Arg Leu Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr
          115          120          125

Leu Asn Arg Leu Gly Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp
          130          135          140

Pro Glu Ser Trp Gln Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe
          145          150          155          160

Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val
          165          170

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<210> 253

<211> 1812

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1789)

<223> RXC00164

<400> 253

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ggccagcctg ccgcaagtgc ggcgcgaggt ggcccggcag gtg ggt cgt att ccg 115
                               Val Gly Arg Ile Pro
                               1           5

cgg gcg aag tgg tgg ttt tta ggc gcg ctg gtg ttg ctg agt gcg ggc 163
Arg Ala Lys Trp Trp Phe Leu Gly Ala Leu Val Leu Leu Ser Ala Gly
          10           15           20

gct tat gcg tcg gtg ctg gtg ccg cag gtg ctg ggg cgg att gtg gat 211

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Ala	Tyr	Ala	Ser	Val	Leu	Val	Pro	Gln	Val	Leu	Gly	Arg	Ile	Val	Asp		
			25					30					35				
ctg	gtg	tcc	gat	ggc	gcg	cag	atg	cgt	gat	ttt	gtt	gag	ctc	agt	gtg	259	
Leu	Val	Ser	Asp	Gly	Ala	Gln	Met	Arg	Asp	Phe	Val	Glu	Leu	Ser	Val		
		40					45					50					
att	ctc	att	gcg	gtg	gca	att	gcc	ggc	gcg	gtg	ctc	agt	gcg	tgc	ggg	307	
Ile	Leu	Ile	Ala	Val	Ala	Ile	Ala	Gly	Ala	Val	Leu	Ser	Ala	Cys	Gly		
	55					60					65						
ttc	tat	gtg	gtg	tcg	cgg	att	tct	gag	aag	att	atc	gcc	aat	ttg	agg	355	
Phe	Tyr	Val	Val	Ser	Arg	Ile	Ser	Glu	Lys	Ile	Ile	Ala	Asn	Leu	Arg		
70					75				80						85		
gaa	gat	atg	gtg	ggc	acc	gcg	ctt	ggg	ttg	ccc	acg	cac	cag	gtg	gaa	403	
Glu	Asp	Met	Val	Gly	Thr	Ala	Leu	Gly	Leu	Pro	Thr	His	Gln	Val	Glu		
				90				95					100				
gat	gcg	ggc	tct	ggc	gat	ttg	gtg	agc	cgc	tcc	acc	gat	gat	gtc	tcc	451	
Asp	Ala	Gly	Ser	Gly	Asp	Leu	Val	Ser	Arg	Ser	Thr	Asp	Asp	Val	Ser		
			105					110					115				
gag	cta	tcc	gca	gcg	gtg	aca	gag	acc	gtc	ccg	att	tta	agt	tcc	tca	499	
Glu	Leu	Ser	Ala	Ala	Val	Thr	Glu	Thr	Val	Pro	Ile	Leu	Ser	Ser	Ser		
		120					125					130					
ctg	ttt	acc	att	gcc	gcg	acg	atc	att	gcg	ctg	ttt	tct	ttg	gac	tgg	547	
Leu	Phe	Thr	Ile	Ala	Ala	Thr	Ile	Ile	Ala	Leu	Phe	Ser	Leu	Asp	Trp		
	135					140					145						
caa	ttt	gtg	ctc	att	cct	gtc	gtg	gtg	gcg	ccg	gtg	tac	tac	ttc	gcg	595	
Gln	Phe	Val	Leu	Ile	Pro	Val	Val	Val	Ala	Pro	Val	Tyr	Tyr	Phe	Ala		
150					155					160					165		
tcc	aag	cac	tat	ttg	agc	aag	gcg	ccg	gat	cgg	tat	gcg	gca	gaa	cgc	643	
Ser	Lys	His	Tyr	Leu	Ser	Lys	Ala	Pro	Asp	Arg	Tyr	Ala	Ala	Glu	Arg		
				170					175					180			
gcg	gcg	atg	gcg	gag	cgt	gcg	cga	aag	gta	ctt	gag	gct	att	cgc	ggg	691	
Ala	Ala	Met	Ala	Glu	Arg	Ala	Arg	Lys	Val	Leu	Glu	Ala	Ile	Arg	Gly		
			185					190					195				
cgt	gca	act	gtg	cgg	gcg	tat	tcc	atg	gaa	gat	gcc	atg	cat	aat	cag	739	
Arg	Ala	Thr	Val	Arg	Ala	Tyr	Ser	Met	Glu	Asp	Ala	Met	His	Asn	Gln		
		200					205					210					
att	gat	cag	gcg	tcg	tgg	tct	gtg	gtg	gtc	aag	ggg	att	cgt	gcg	cgc	787	
Ile	Asp	Gln	Ala	Ser	Trp	Ser	Val	Val	Val	Lys	Gly	Ile	Arg	Ala	Arg		
	215					220					225						
acc	acc	atg	ttg	att	ttg	aac	atg	tgg	atg	ctg	ttt	gcg	gaa	ttc	ctc	835	
Thr	Thr	Met	Leu	Ile	Leu	Asn	Met	Trp	Met	Leu	Phe	Ala	Glu	Phe	Leu		
230					235					240					245		
atg	ctc	gcg	gtc	gcg	ttg	gtg	atc	ggc	tac	aag	ctg	gtc	att	gat	aat	883	
Met	Leu	Ala	Val	Ala	Leu	Val	Ile	Gly	Tyr	Lys	Leu	Val	Ile	Asp	Asn		
			250					255						260			
gcg	ctg	acg	atc	ggc	gcg	gtt	acc	ggg	gcc	gtg	ctg	atg	att	att	cgt	931	
Ala	Leu	Thr	Ile	Gly	Ala	Val	Thr	Gly	Ala	Val	Leu	Met	Ile	Ile	Arg		

265					270					275						
ctg	cgt	ggc	ccg	atg	aat	atg	ttc	atg	cgc	gtg	ctc	gac	acc	att	caa	979
Leu	Arg	Gly	Pro	Met	Asn	Met	Phe	Met	Arg	Val	Leu	Asp	Thr	Ile	Gln	
		280					285					290				
tcc	ggc	tat	gcg	tcg	ctg	gcg	cgc	atc	gtg	gga	gtt	gtt	gcg	gat	ccg	1027
Ser	Gly	Tyr	Ala	Ser	Leu	Ala	Arg	Ile	Val	Gly	Val	Val	Ala	Asp	Pro	
	295					300					305					
ccg	att	cct	gtg	ccc	gac	agc	ggg	gtg	aaa	gca	cct	cag	ggc	aaa	gtg	1075
Pro	Ile	Pro	Val	Pro	Asp	Ser	Gly	Val	Lys	Ala	Pro	Gln	Gly	Lys	Val	
310					315					320					325	
gaa	ttg	cgc	aac	gtc	agc	ttt	agc	tat	ggc	gat	tcc	tgg	gcg	gtg	aaa	1123
Glu	Leu	Arg	Asn	Val	Ser	Phe	Ser	Tyr	Gly	Asp	Ser	Trp	Ala	Val	Lys	
			330						335					340		
gac	atc	gac	atc	acg	atc	aat	tcc	ggc	gaa	act	gtc	gcg	ctc	gtg	ggc	1171
Asp	Ile	Asp	Ile	Thr	Ile	Asn	Ser	Gly	Glu	Thr	Val	Ala	Leu	Val	Gly	
			345					350					355			
gca	tct	ggc	gca	ggg	aag	acg	acg	gtc	gcc	gcc	ttg	ctg	gcg	ggc	ttg	1219
Ala	Ser	Gly	Ala	Gly	Lys	Thr	Thr	Val	Ala	Ala	Leu	Leu	Ala	Gly	Leu	
		360					365					370				
cgg	gtg	cca	gat	caa	ggg	caa	gtg	ctt	gtc	gac	gac	ttc	ccc	gtc	tct	1267
Arg	Val	Pro	Asp	Gln	Gly	Gln	Val	Leu	Val	Asp	Asp	Phe	Pro	Val	Ser	
	375					380					385					
cac	ctc	tct	gac	cgc	gag	cgt	atc	gcc	cgc	ttg	gcc	atg	gtc	agc	cag	1315
His	Leu	Ser	Asp	Arg	Glu	Arg	Ile	Ala	Arg	Leu	Ala	Met	Val	Ser	Gln	
390					395				400						405	
gag	gtt	cat	gtt	ttc	tcc	ggc	acg	ctg	cgc	cag	gat	ctc	acc	ttg	gct	1363
Glu	Val	His	Val	Phe	Ser	Gly	Thr	Leu	Arg	Gln	Asp	Leu	Thr	Leu	Ala	
			410					415						420		
aaa	cca	gat	gcc	tcc	gat	gag	gaa	tta	gcg	cat	gct	ctt	ggg	caa	gtt	1411
Lys	Pro	Asp	Ala	Ser	Asp	Glu	Glu	Leu	Ala	His	Ala	Leu	Gly	Gln	Val	
		425					430					435				
aat	gcc	ctt	gac	tgg	ttg	gag	agt	ctt	cca	gaa	gga	ctg	gac	acg	gtc	1459
Asn	Ala	Leu	Asp	Trp	Leu	Glu	Ser	Leu	Pro	Glu	Gly	Leu	Asp	Thr	Val	
		440				445						450				
gtt	ggg	gcg	cga	gga	atc	cag	cta	gaa	cca	gtg	gtg	gct	cag	cag	ttg	1507
Val	Gly	Ala	Arg	Gly	Ile	Gln	Leu	Glu	Pro	Val	Val	Ala	Gln	Gln	Leu	
	455					460					465					
gcg	ttg	gcc	cgg	gtg	ttg	ttg	ctc	aat	ccg	gcg	atc	gtc	atc	atg	gat	1555
Ala	Leu	Ala	Arg	Val	Leu	Leu	Leu	Asn	Pro	Ala	Ile	Val	Ile	Met	Asp	
470					475				480					485		
gaa	gcc	acg	gca	gaa	gca	gga	tcg	gcg	ggg	gcc	agc	gca	ctg	gaa	gag	1603
Glu	Ala	Thr	Ala	Glu	Ala	Gly	Ser	Ala	Gly	Ala	Ser	Ala	Leu	Glu	Glu	
			490						495					500		
gct	gca	gat	gca	gtg	agc	aag	aac	cgt	tcc	gca	ttg	gtg	gtg	gcg	cac	1651
Ala	Ala	Asp	Ala	Val	Ser	Lys	Asn	Arg	Ser	Ala	Leu	Val	Val	Ala	His	
		505						510					515			

cgg ttg gat cag gca tcg cgg gct gat cag att ctg gtg atg gat aag 1699
 Arg Leu Asp Gln Ala Ser Arg Ala Asp Gln Ile Leu Val Met Asp Lys
 520 525 530

ggg gag gtt gtg gaa tcc ggt act cac cag gag tta ttg gat cac ggg 1747
 Gly Glu Val Val Glu Ser Gly Thr His Gln Glu Leu Leu Asp His Gly
 535 540 545

ggt att tat cag cgt ctg tgg act gcg tgg agt gtc gga aga 1789
 Gly Ile Tyr Gln Arg Leu Trp Thr Ala Trp Ser Val Gly Arg
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<213> *Corynebacterium glutamicum*

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Gly Arg Ile Val Asp Leu Val Ser Asp Gly Ala Gln Met Arg Asp Phe
 35 40 45

Val Glu Leu Ser Val Ile Leu Ile Ala Val Ala Ile Ala Gly Ala Val
 50 55 60

Leu Ser Ala Cys Gly Phe Tyr Val Val Ser Arg Ile Ser Glu Lys Ile
 65 70 75 80

Ile Ala Asn Leu Arg Glu Asp Met Val Gly Thr Ala Leu Gly Leu Pro
 85 90 95

Thr His Gln Val Glu Asp Ala Gly Ser Gly Asp Leu Val Ser Arg Ser
 100 105 110

Thr Asp Asp Val Ser Glu Leu Ser Ala Ala Val Thr Glu Thr Val Pro
 115 120 125

Ile Leu Ser Ser Ser Leu Phe Thr Ile Ala Ala Thr Ile Ile Ala Leu
 130 135 140

Phe Ser Leu Asp Trp Gln Phe Val Leu Ile Pro Val Val Val Ala Pro
 145 150 155 160

Val Tyr Tyr Phe Ala Ser Lys His Tyr Leu Ser Lys Ala Pro Asp Arg
 165 170 175

Tyr Ala Ala Glu Arg Ala Ala Met Ala Glu Arg Ala Arg Lys Val Leu
 180 185 190

Glu Ala Ile Arg Gly Arg Ala Thr Val Arg Ala Tyr Ser Met Glu Asp
 195 200 205

Ala	Met	His	Asn	Gln	Ile	Asp	Gln	Ala	Ser	Trp	Ser	Val	Val	Val	Lys
210						215					220				
Gly	Ile	Arg	Ala	Arg	Thr	Thr	Met	Leu	Ile	Leu	Asn	Met	Trp	Met	Leu
225					230					235					240
Phe	Ala	Glu	Phe	Leu	Met	Leu	Ala	Val	Ala	Leu	Val	Ile	Gly	Tyr	Lys
				245					250					255	
Leu	Val	Ile	Asp	Asn	Ala	Leu	Thr	Ile	Gly	Ala	Val	Thr	Gly	Ala	Val
			260					265					270		
Leu	Met	Ile	Ile	Arg	Leu	Arg	Gly	Pro	Met	Asn	Met	Phe	Met	Arg	Val
	275						280					285			
Leu	Asp	Thr	Ile	Gln	Ser	Gly	Tyr	Ala	Ser	Leu	Ala	Arg	Ile	Val	Gly
	290					295					300				
Val	Val	Ala	Asp	Pro	Pro	Ile	Pro	Val	Pro	Asp	Ser	Gly	Val	Lys	Ala
305					310					315					320
Pro	Gln	Gly	Lys	Val	Glu	Leu	Arg	Asn	Val	Ser	Phe	Ser	Tyr	Gly	Asp
				325					330					335	
Ser	Trp	Ala	Val	Lys	Asp	Ile	Asp	Ile	Thr	Ile	Asn	Ser	Gly	Glu	Thr
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Val	Ala	Leu	Val	Gly	Ala	Ser	Gly	Ala	Gly	Lys	Thr	Thr	Val	Ala	Ala
		355					360						365		
Leu	Leu	Ala	Gly	Leu	Arg	Val	Pro	Asp	Gln	Gly	Gln	Val	Leu	Val	Asp
	370					375					380				
Asp	Phe	Pro	Val	Ser	His	Leu	Ser	Asp	Arg	Glu	Arg	Ile	Ala	Arg	Leu
385					390					395					400
Ala	Met	Val	Ser	Gln	Glu	Val	His	Val	Phe	Ser	Gly	Thr	Leu	Arg	Gln
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Asp	Leu	Thr	Leu	Ala	Lys	Pro	Asp	Ala	Ser	Asp	Glu	Glu	Leu	Ala	His
			420					425					430		
Ala	Leu	Gly	Gln	Val	Asn	Ala	Leu	Asp	Trp	Leu	Glu	Ser	Leu	Pro	Glu
	435						440					445			
Gly	Leu	Asp	Thr	Val	Val	Gly	Ala	Arg	Gly	Ile	Gln	Leu	Glu	Pro	Val
	450					455					460				
Val	Ala	Gln	Gln	Leu	Ala	Leu	Ala	Arg	Val	Leu	Leu	Leu	Asn	Pro	Ala
465				470						475					480
Ile	Val	Ile	Met	Asp	Glu	Ala	Thr	Ala	Glu	Ala	Gly	Ser	Ala	Gly	Ala
				485					490					495	
Ser	Ala	Leu	Glu	Glu	Ala	Ala	Asp	Ala	Val	Ser	Lys	Asn	Arg	Ser	Ala
			500					505					510		
Leu	Val	Val	Ala	His	Arg	Leu	Asp	Gln	Ala	Ser	Arg	Ala	Asp	Gln	Ile
		515					520					525			
Leu	Val	Met	Asp	Lys	Gly	Glu	Val	Val	Glu	Ser	Gly	Thr	His	Gln	Glu

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Val Gly Arg

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<213> *Corynebacterium glutamicum*

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<223> RXC01191

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Val Gly Gly Leu Val
1 5

gat aag ctc ctt gca acc ccg agc atg cgc gac gtt gta gtg ttc gcg 163
Asp Lys Leu Leu Ala Thr Pro Ser Met Arg Asp Val Val Val Phe Ala
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ctg ctt atc gtg gct ggc ggc gtt gtt tcg agc ctg ggc acg tgg tgg 211
Leu Leu Ile Val Ala Gly Gly Val Val Ser Ser Leu Gly Thr Trp Trp
25 30 35

ggc agc gcg ctg atg gcg cgc gcg ttg gag ccg gcg atc gcg ggg ctg 259
Gly Ser Ala Leu Met Ala Arg Ala Leu Glu Pro Ala Ile Ala Gly Leu
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cgc gag gat gtg ttg cgc gcg gcg gtg agt ttg gat gcg aac acg att 307
Arg Glu Asp Val Leu Arg Ala Ala Val Ser Leu Asp Ala Asn Thr Ile
55 60 65

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Glu Thr Ala Gly Arg Gly Asp Val Ile Ser Arg Ile Ala Asp Asp Ser
70 75 80 85

cgg gag gtg tcc act gcg gcg agc acc gtg gtg ccg ctg atg gtg cag 403
Arg Glu Val Ser Thr Ala Ala Ser Thr Val Val Pro Leu Met Val Gln
90 95 100

gcg ggc ttt acc gtg gtg att tcc gcg ttt ggc atg gcg gcg gtt gat 451
Ala Gly Phe Thr Val Val Ile Ser Ala Phe Gly Met Ala Ala Val Asp
105 110 115

tgg cgc ctc ggc ctt gtc ggt ttg gtc gcg atc ccg ctg tat tgg acc 499
Trp Arg Leu Gly Leu Val Gly Leu Val Ala Ile Pro Leu Tyr Trp Thr
120 125 130

acg ttg cgc gtc tat tta ccc cgc tca ggt ccg ctt tat acg cgt gag 547
Thr Leu Arg Val Tyr Leu Pro Arg Ser Gly Pro Leu Tyr Thr Arg Glu
135 140 145

cgc gag gcc ttt ggg gtg cgc acg cag cgg ctt gtc ggc gca gtc gaa	595
Arg Glu Ala Phe Gly Val Arg Thr Gln Arg Leu Val Gly Ala Val Glu	
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ggc gcg gaa acc ttg cgc gct ttc cgc gca gaa gat aca gaa tta aag	643
Gly Ala Glu Thr Leu Arg Ala Phe Arg Ala Glu Asp Thr Glu Leu Lys	
170 175 180	
cgt atc gac gca gcc tcc ggc gaa gcc cgc gac att tcc att tct gtt	691
Arg Ile Asp Ala Ala Ser Gly Glu Ala Arg Asp Ile Ser Ile Ser Val	
185 190 195	
ttc agg ttc ctc aca tgg gca ttt tcc cgc aac aac cgc gcg gaa tgc	739
Phe Arg Phe Leu Thr Trp Ala Phe Ser Arg Asn Asn Arg Ala Glu Cys	
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Ile Thr Leu Val Leu Ile Leu Gly Thr Gly Phe Tyr Leu Val Asn Ile	
215 220 225	
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Asp Leu Val Thr Val Gly Ala Val Ser Thr Ala Ala Leu Ile Phe His	
230 235 240 245	
cga ctc ttc ggt cca atc ggc acg ctc gtg ggc atg ttc tcc gac atc	883
Arg Leu Phe Gly Pro Ile Gly Thr Leu Val Gly Met Phe Ser Asp Ile	
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Gln Ser Ala Ser Ala Ser Leu Ile Arg Met Val Gly Val Ile Asn Ala	
265 270 275	
gca tcg aac cag gtc agc ggc acc tcg ccg gcg tct gcc agc acc gct	979
Ala Ser Asn Gln Val Ser Gly Thr Ser Pro Ala Ser Ala Ser Thr Ala	
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Leu Thr Leu Phe Asp Val Ser His His Tyr His Thr Ala Pro Val Ile	
295 300 305	
aag aat gca tcc gtg cag ctg gaa cca ggg gaa cac atc gcc att gtg	1075
Lys Asn Ala Ser Val Gln Leu Glu Pro Gly Glu His Ile Ala Ile Val	
310 315 320 325	
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Gly Ala Thr Gly Ala Gly Lys Ser Thr Leu Ala Leu Ile Ala Ala Gly	
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Leu Leu Ser Pro Thr Ser Gly Gln Val Ala Leu Gly Gly Ser Ser Phe	
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Ser Asn Val Glu Pro Glu Ala Leu Arg Gln Lys Ile Ala Met Val Ser	
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Gln Glu Ile His Cys Phe Arg Gly Ser Val Leu Asp Asn Leu Arg Ile	
375 380 385	

gca cgc ccc gaa gcc acc gat gcg gac atc cac gcc gtt ctc gcc gat 1315
 Ala Arg Pro Glu Ala Thr Asp Ala Asp Ile His Ala Val Leu Ala Asp
 390 395 400 405
 att ggt gat tcc tgg ttg gag cgc tta ccg caa ggc ata gac acc atc 1363
 Ile Gly Asp Ser Trp Leu Glu Arg Leu Pro Gln Gly Ile Asp Thr Ile
 410 415 420
 gtg ggt gat ggc gct ttc cgt tta acc tct gtg gaa aac cag atc atg 1411
 Val Gly Asp Gly Ala Phe Arg Leu Thr Ser Val Glu Asn Gln Ile Met
 425 430 435
 gcg ctt gct cgc gta cat ttg gcc gac cta gca atc gtc atc ctt gat 1459
 Ala Leu Ala Arg Val His Leu Ala Asp Leu Ala Ile Val Ile Leu Asp
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 Glu Ala Thr Ala Glu Ser Gly Ser Asp His Ala Lys Gln Leu Glu Asp
 455 460 465
 gca gcc ctt aaa gtc act gaa aac aga tca gcc atc atc gtg gct cac 1555
 Ala Ala Leu Lys Val Thr Glu Asn Arg Ser Ala Ile Ile Val Ala His
 470 475 480 485
 cgc ctc aac caa gcg aaa acc gcc gat cgc atc atc gtc atg gac tcc 1603
 Arg Leu Asn Gln Ala Lys Thr Ala Asp Arg Ile Ile Val Met Asp Ser
 490 495 500
 gga gaa atc ata gaa tct gga acc cat gaa gag ctt cga gcg atc ggc 1651
 Gly Glu Ile Ile Glu Ser Gly Thr His Glu Glu Leu Arg Ala Ile Gly
 505 510 515
 ggc cga tat gaa caa ctg tgg act gcg tgg tct gcg cgc taattagcca 1700
 Gly Arg Tyr Glu Gln Leu Trp Thr Ala Trp Ser Ala Arg
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<212> PRT

<213> Corynebacterium glutamicum

<400> 256

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 35 40 45
 Ala Ile Ala Gly Leu Arg Glu Asp Val Leu Arg Ala Ala Val Ser Leu
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 Asp Ala Asn Thr Ile Glu Thr Ala Gly Arg Gly Asp Val Ile Ser Arg
 65 70 75 80
 Ile Ala Asp Asp Ser Arg Glu Val Ser Thr Ala Ala Ser Thr Val Val

85										90					95				
Pro	Leu	Met	Val	Gln	Ala	Gly	Phe	Thr	Val	Val	Val	Ile	Ser	Ala	Phe	Gly			
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Met	Ala	Ala	Val	Asp	Trp	Arg	Leu	Gly	Leu	Val	Gly	Leu	Val	Ala	Ile				
115										120					125				
Pro	Leu	Tyr	Trp	Thr	Thr	Leu	Arg	Val	Tyr	Leu	Pro	Arg	Ser	Gly	Pro				
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Leu	Tyr	Thr	Arg	Glu	Arg	Glu	Ala	Phe	Gly	Val	Arg	Thr	Gln	Arg	Leu				
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Val	Gly	Ala	Val	Glu	Gly	Ala	Glu	Thr	Leu	Arg	Ala	Phe	Arg	Ala	Glu				
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Asp	Thr	Glu	Leu	Lys	Arg	Ile	Asp	Ala	Ala	Ser	Gly	Glu	Ala	Arg	Asp				
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Ile	Ser	Ile	Ser	Val	Phe	Arg	Phe	Leu	Thr	Trp	Ala	Phe	Ser	Arg	Asn				
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Tyr	Leu	Val	Asn	Ile	Asp	Leu	Val	Thr	Val	Gly	Ala	Val	Ser	Thr	Ala				
225										230					235				
Ala	Leu	Ile	Phe	His	Arg	Leu	Phe	Gly	Pro	Ile	Gly	Thr	Leu	Val	Gly				
245										250					255				
Met	Phe	Ser	Asp	Ile	Gln	Ser	Ala	Ser	Ala	Ser	Leu	Ile	Arg	Met	Val				
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Gly	Val	Ile	Asn	Ala	Ala	Ser	Asn	Gln	Val	Ser	Gly	Thr	Ser	Pro	Ala				
275										280					285				
Ser	Ala	Ser	Thr	Ala	Leu	Thr	Leu	Phe	Asp	Val	Ser	His	His	Tyr	His				
290										295					300				
Thr	Ala	Pro	Val	Ile	Lys	Asn	Ala	Ser	Val	Gln	Leu	Glu	Pro	Gly	Glu				
305										310					315				
His	Ile	Ala	Ile	Val	Gly	Ala	Thr	Gly	Ala	Gly	Lys	Ser	Thr	Leu	Ala				
325										330					335				
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Gly	Gly	Ser	Ser	Phe	Ser	Asn	Val	Glu	Pro	Glu	Ala	Leu	Arg	Gln	Lys				
355										360					365				
Ile	Ala	Met	Val	Ser	Gln	Glu	Ile	His	Cys	Phe	Arg	Gly	Ser	Val	Leu				
370										375					380				
Asp	Asn	Leu	Arg	Ile	Ala	Arg	Pro	Glu	Ala	Thr	Asp	Ala	Asp	Ile	His				
385										390					395				
Ala	Val	Leu	Ala	Asp	Ile	Gly	Asp	Ser	Trp	Leu	Glu	Arg	Leu	Pro	Gln				
405										410					415				

Gly Ile Asp Thr Ile Val Gly Asp Gly Ala Phe Arg Leu Thr Ser Val
 420 425 430

Glu Asn Gln Ile Met Ala Leu Ala Arg Val His Leu Ala Asp Leu Ala
 435 440 445

Ile Val Ile Leu Asp Glu Ala Thr Ala Glu Ser Gly Ser Asp His Ala
 450 455 460

Lys Gln Leu Glu Asp Ala Ala Leu Lys Val Thr Glu Asn Arg Ser Ala
 465 470 475 480

Ile Ile Val Ala His Arg Leu Asn Gln Ala Lys Thr Ala Asp Arg Ile
 485 490 495

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Ala Arg
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 Met Ala Ser Gly Ala
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gag ctg att cgt gcc gcc gac att caa acg gcg cag gca cga att tcc 163
 Glu Leu Ile Arg Ala Ala Asp Ile Gln Thr Ala Gln Ala Arg Ile Ser
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tcc gtc att gca cca act cca ttg cag tat tgc cct cgt ctt tct gag 211
 Ser Val Ile Ala Pro Thr Pro Leu Gln Tyr Cys Pro Arg Leu Ser Glu
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gaa acc gga gcg gaa atc tac ctt aag cgt gag gat ctg cag gat gtt 259
 Glu Thr Gly Ala Glu Ile Tyr Leu Lys Arg Glu Asp Leu Gln Asp Val
 40 45 50

cgt tcc tac aag atc cgc ggt gcg ctg aac tct gga gcg cag ctc acc 307
 Arg Ser Tyr Lys Ile Arg Gly Ala Leu Asn Ser Gly Ala Gln Leu Thr
 55 60 65

caa gag cag cgc gat gca ggt atc gtt gcc gca tct gca ggt aac cat 355
 Gln Glu Gln Arg Asp Ala Gly Ile Val Ala Ala Ser Ala Gly Asn His

70	75	80	85	
gcc cag ggc gtg gcc tat gtg tgc aag tcc ttg ggc gtt cag gga cgc				403
Ala Gln Gly Val Ala Tyr Val Cys Lys Ser Leu Gly Val Gln Gly Arg	90	95	100	
atc tat gtt cct gtg cag act cca aag caa aag cgt gac cgc atc atg				451
Ile Tyr Val Pro Val Gln Thr Pro Lys Gln Lys Arg Asp Arg Ile Met	105	110	115	
gtt cac ggc gga gag ttt gtc tcc ttg gtg gtc act ggc aat aac ttc				499
Val His Gly Gly Glu Phe Val Ser Leu Val Val Thr Gly Asn Asn Phe	120	125	130	
gac gaa gca tcg gct gca gcg cat gaa gat gca gag cgc acc ggc gca				547
Asp Glu Ala Ser Ala Ala Ala His Glu Asp Ala Glu Arg Thr Gly Ala	135	140	145	
acg ctg atc gag cct ttc gat gct cgc aac acc gtc atc ggt cag ggc				595
Thr Leu Ile Glu Pro Phe Asp Ala Arg Asn Thr Val Ile Gly Gln Gly	150	155	160	165
acc gtg gct gct gag atc ttg tcg cag ctg act tcc atg ggc aag agt				643
Thr Val Ala Ala Glu Ile Leu Ser Gln Leu Thr Ser Met Gly Lys Ser	170	175	180	
gca gat cac gtg atg gtt cca gtc ggc ggt ggc gga ctt ctt gca ggt				691
Ala Asp His Val Met Val Pro Val Gly Gly Gly Gly Leu Leu Ala Gly	185	190	195	
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Val Val Ser Tyr Met Ala Asp Met Ala Pro Arg Thr Ala Ile Val Gly	200	205	210	
atc gaa cca gcg gga gca gca tcc atg cag gct gca ttg cac aat ggt				787
Ile Glu Pro Ala Gly Ala Ala Ser Met Gln Ala Ala Leu His Asn Gly	215	220	225	
gga cca atc act ttg gag act gtt gat ccc ttt gtg gac ggc gca gca				835
Gly Pro Ile Thr Leu Glu Thr Val Asp Pro Phe Val Asp Gly Ala Ala	230	235	240	245
gtc aaa cgt gtc gga gat ctc aac tac acc atc gtg gag aag aac cag				883
Val Lys Arg Val Gly Asp Leu Asn Tyr Thr Ile Val Glu Lys Asn Gln	250	255	260	
ggt cgc gtg cac atg atg agc gcg acc gag ggc gct gtg tgt act gag				931
Gly Arg Val His Met Met Ser Ala Thr Glu Gly Ala Val Cys Thr Glu	265	270	275	
atg ctc gat ctt tac caa aac gaa ggc atc atc gcg gag cct gct ggc				979
Met Leu Asp Leu Tyr Gln Asn Glu Gly Ile Ile Ala Glu Pro Ala Gly	280	285	290	
gcg ctg tct atc gct ggg ttg aag gaa atg tcc ttt gca gct cgc tct				1027
Ala Leu Ser Ile Ala Gly Leu Lys Glu Met Ser Phe Ala Ala Arg Ser	295	300	305	
gtc gtg gtg tgc atc atc tct ggt ggc aac aac gat gtg ctg cgt tat				1075
Val Val Val Cys Ile Ile Ser Gly Gly Asn Asn Asp Val Leu Arg Tyr	310	315	320	325

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 Ala Glu Ile Ala Glu Arg Ser Leu Val Arg Arg Gly Leu Lys His Tyr
 330 335 340

ttc ttg gtg aac ttc ccg caa aag cct ggt cag ttg cgt cac ttc ctg 1171
 Phe Leu Val Asn Phe Pro Gln Lys Pro Gly Gln Leu Arg His Phe Leu
 345 350 355

gaa gat atc ctg gga ccg gat gat gac atc acg ctg ttt gag tac ctc 1219
 Glu Asp Ile Leu Gly Pro Asp Asp Asp Ile Thr Leu Phe Glu Tyr Leu
 360 365 370

aag cgc aac aac cgt gag acc ggt act gcg ttg gtg ggt att cac ttg 1267
 Lys Arg Asn Asn Arg Glu Thr Gly Thr Ala Leu Val Gly Ile His Leu
 375 380 385

agt gaa gca tca gga ttg gat tct ttg ctg gaa cgt atg gag gaa tcg 1315
 Ser Glu Ala Ser Gly Leu Asp Ser Leu Leu Glu Arg Met Glu Glu Ser
 390 395 400 405

gca att gat tcc cgt cgc ctc gag ccg ggc acc cct gag tac gaa tac 1363
 Ala Ile Asp Ser Arg Arg Leu Glu Pro Gly Thr Pro Glu Tyr Glu Tyr
 410 415 420

ttg acc taaacatagc tgaaggccac ctc 1392
 Leu Thr

<210> 258

<211> 423

<212> PRT

<213> Corynebacterium glutamicum

<400> 258

Met Ala Ser Gly Ala Glu Leu Ile Arg Ala Ala Asp Ile Gln Thr Ala
 1 5 10 15

Gln Ala Arg Ile Ser Ser Val Ile Ala Pro Thr Pro Leu Gln Tyr Cys
 20 25 30

Pro Arg Leu Ser Glu Glu Thr Gly Ala Glu Ile Tyr Leu Lys Arg Glu
 35 40 45

Asp Leu Gln Asp Val Arg Ser Tyr Lys Ile Arg Gly Ala Leu Asn Ser
 50 55 60

Gly Ala Gln Leu Thr Gln Glu Gln Arg Asp Ala Gly Ile Val Ala Ala
 65 70 75 80

Ser Ala Gly Asn His Ala Gln Gly Val Ala Tyr Val Cys Lys Ser Leu
 85 90 95

Gly Val Gln Gly Arg Ile Tyr Val Pro Val Gln Thr Pro Lys Gln Lys
 100 105 110

Arg Asp Arg Ile Met Val His Gly Gly Glu Phe Val Ser Leu Val Val
 115 120 125

Thr Gly Asn Asn Phe Asp Glu Ala Ser Ala Ala Ala His Glu Asp Ala

130	135	140
Glu Arg Thr Gly Ala Thr	Leu Ile Glu Pro Phe Asp Ala Arg Asn Thr	
145	150	155 160
Val Ile Gly Gln Gly Thr Val Ala Ala Glu Ile Leu Ser Gln Leu Thr		
	165	170 175
Ser Met Gly Lys Ser Ala Asp His Val Met Val Pro Val Gly Gly Gly		
	180	185 190
Gly Leu Leu Ala Gly Val Val Ser Tyr Met Ala Asp Met Ala Pro Arg		
	195	200 205
Thr Ala Ile Val Gly Ile Glu Pro Ala Gly Ala Ala Ser Met Gln Ala		
	210	215 220
Ala Leu His Asn Gly Gly Pro Ile Thr Leu Glu Thr Val Asp Pro Phe		
	225	230 235 240
Val Asp Gly Ala Ala Val Lys Arg Val Gly Asp Leu Asn Tyr Thr Ile		
	245	250 255
Val Glu Lys Asn Gln Gly Arg Val His Met Met Ser Ala Thr Glu Gly		
	260	265 270
Ala Val Cys Thr Glu Met Leu Asp Leu Tyr Gln Asn Glu Gly Ile Ile		
	275	280 285
Ala Glu Pro Ala Gly Ala Leu Ser Ile Ala Gly Leu Lys Glu Met Ser		
	290	295 300
Phe Ala Ala Arg Ser Val Val Val Cys Ile Ile Ser Gly Gly Asn Asn		
	305	310 315 320
Asp Val Leu Arg Tyr Ala Glu Ile Ala Glu Arg Ser Leu Val Arg Arg		
	325	330 335
Gly Leu Lys His Tyr Phe Leu Val Asn Phe Pro Gln Lys Pro Gly Gln		
	340	345 350
Leu Arg His Phe Leu Glu Asp Ile Leu Gly Pro Asp Asp Asp Ile Thr		
	355	360 365
Leu Phe Glu Tyr Leu Lys Arg Asn Asn Arg Glu Thr Gly Thr Ala Leu		
	370	375 380
Val Gly Ile His Leu Ser Glu Ala Ser Gly Leu Asp Ser Leu Leu Glu		
	385	390 395 400
Arg Met Glu Glu Ser Ala Ile Asp Ser Arg Arg Leu Glu Pro Gly Thr		
	405	410 415
Pro Glu Tyr Glu Tyr Leu Thr		
	420	

<210> 259

<211> 966

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(943)

<223> RXA00766

<400> 259

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ctacggcgagg tccatccggc aacaaaaccc caacctacca	
atg gtt ttt tgg gac	115
Met Val Phe Trp Asp	
1 5	
gat gca gcc tta acc cga ggc gat ggc atc ttt gaa aca ctc ctc atc	163
Asp Ala Ala Leu Thr Arg Gly Asp Gly Ile Phe Glu Thr Leu Leu Ile	
10 15 20	
cgc gac gga cat gcc tgc aac gtg cgc cga cac gga gaa cgc ttc aaa	211
Arg Asp Gly His Ala Cys Asn Val Arg Arg His Gly Glu Arg Phe Lys	
25 30 35	
gca tcg gca gca cta ttg gga ctg cca gag ccg atc ctg gaa gac tgg	259
Ala Ser Ala Ala Leu Leu Gly Leu Pro Glu Pro Ile Leu Glu Asp Trp	
40 45 50	
gaa aaa gcc acc caa atg ggc atc gaa tcc tgg tac tcc cac ccc aac	307
Glu Lys Ala Thr Gln Met Gly Ile Glu Ser Trp Tyr Ser His Pro Asn	
55 60 65	
gca ggc gag gcc tca tgc acc tgg acg ctc agc cga ggt cgt tcc tcc	355
Ala Gly Glu Ala Ser Cys Thr Trp Thr Leu Ser Arg Gly Arg Ser Ser	
70 75 80 85	
acg ggg ctg gcc tca gga tgg tta acc atc acc cca gtc tcc tcc gac	403
Thr Gly Leu Ala Ser Gly Trp Leu Thr Ile Thr Pro Val Ser Ser Asp	
90 95 100	
aaa ctg gcg caa cgt gaa cac ggt gta tcg gtc atg acc agt tca aga	451
Lys Leu Ala Gln Arg Glu His Gly Val Ser Val Met Thr Ser Ser Arg	
105 110 115	
gga tat tcc atc gac acc ggc ctc ccc gga atc gga aaa gcc acc cga	499
Gly Tyr Ser Ile Asp Thr Gly Leu Pro Gly Ile Gly Lys Ala Thr Arg	
120 125 130	
ggc gag cta tct aaa gtg gaa cga acc ccc gca cca tgg ctg aca gtc	547
Gly Glu Leu Ser Lys Val Glu Arg Thr Pro Ala Pro Trp Leu Thr Val	
135 140 145	
ggc gcc aaa aca cta gcc tac gca gca aac atg gca gcc ctg cgc tac	595
Gly Ala Lys Thr Leu Ala Tyr Ala Ala Asn Met Ala Ala Leu Arg Tyr	
150 155 160 165	
gcc aaa tca aac gga ttc gac gat gtg atc ttc acc gat ggc gac cgc	643
Ala Lys Ser Asn Gly Phe Asp Asp Val Ile Phe Thr Asp Gly Asp Arg	
170 175 180	
gtt cta gaa ggc gcc acc tcc acc gta gtg agt ttc aaa ggc gac aaa	691
Val Leu Glu Gly Ala Thr Ser Thr Val Val Ser Phe Lys Gly Asp Lys	
185 190 195	

atc cgc acc cct tca ccc ggt ggc gac att ctc ccc gga acc acc caa 739
 Ile Arg Thr Pro Ser Pro Gly Gly Asp Ile Leu Pro Gly Thr Thr Gln
 200 205 210

gca gca ctc ttt gca cac gca acc gaa aaa gga tgg cga tgt aaa gaa 787
 Ala Ala Leu Phe Ala His Ala Thr Glu Lys Gly Trp Arg Cys Lys Glu
 215 220 225

aaa gac tta agc att gac gat ctt ttc gga gcc gac agc gtg tgg cta 835
 Lys Asp Leu Ser Ile Asp Asp Leu Phe Gly Ala Asp Ser Val Trp Leu
 230 235 240 245

gtg tcc tcc gtc cgc gga cca gtt cgg gtg acc agg ctc gat gga cac 883
 Val Ser Ser Val Arg Gly Pro Val Arg Val Thr Arg Leu Asp Gly His
 250 255 260

aaa tta cgg aaa cca gac aat gaa aaa gaa atc aag gcg ctg att acc 931
 Lys Leu Arg Lys Pro Asp Asn Glu Lys Glu Ile Lys Ala Leu Ile Thr
 265 270 275

aaa gct ctg ggg tagaggctgg cgctgggact tgc 966
 Lys Ala Leu Gly
 280

<210> 260

<211> 281

<212> PRT

<213> Corynebacterium glutamicum

<400> 260

Met Val Phe Trp Asp Asp Ala Ala Leu Thr Arg Gly Asp Gly Ile Phe
 1 5 10 15

Glu Thr Leu Leu Ile Arg Asp Gly His Ala Cys Asn Val Arg Arg His
 20 25 30

Gly Glu Arg Phe Lys Ala Ser Ala Ala Leu Leu Gly Leu Pro Glu Pro
 35 40 45

Ile Leu Glu Asp Trp Glu Lys Ala Thr Gln Met Gly Ile Glu Ser Trp
 50 55 60

Tyr Ser His Pro Asn Ala Gly Glu Ala Ser Cys Thr Trp Thr Leu Ser
 65 70 75 80

Arg Gly Arg Ser Ser Thr Gly Leu Ala Ser Gly Trp Leu Thr Ile Thr
 85 90 95

Pro Val Ser Ser Asp Lys Leu Ala Gln Arg Glu His Gly Val Ser Val
 100 105 110

Met Thr Ser Ser Arg Gly Tyr Ser Ile Asp Thr Gly Leu Pro Gly Ile
 115 120 125

Gly Lys Ala Thr Arg Gly Glu Leu Ser Lys Val Glu Arg Thr Pro Ala
 130 135 140

Pro Trp Leu Thr Val Gly Ala Lys Thr Leu Ala Tyr Ala Ala Asn Met
 145 150 155 160

Ala Ala Leu Arg Tyr Ala Lys Ser Asn Gly Phe Asp Asp Val Ile Phe
 165 170 175

Thr Asp Gly Asp Arg Val Leu Glu Gly Ala Thr Ser Thr Val Val Ser
 180 185 190

Phe Lys Gly Asp Lys Ile Arg Thr Pro Ser Pro Gly Gly Asp Ile Leu
 195 200 205

Pro Gly Thr Thr Gln Ala Ala Leu Phe Ala His Ala Thr Glu Lys Gly
 210 215 220

Trp Arg Cys Lys Glu Lys Asp Leu Ser Ile Asp Asp Leu Phe Gly Ala
 225 230 235 240

Asp Ser Val Trp Leu Val Ser Ser Val Arg Gly Pro Val Arg Val Thr
 245 250 255

Arg Leu Asp Gly His Lys Leu Arg Lys Pro Asp Asn Glu Lys Glu Ile
 260 265 270

Lys Ala Leu Ile Thr Lys Ala Leu Gly
 275 280

<210> 261
 <211> 1224
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1201)
 <223> RXN01690

<400> 261
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actagtgtat ctgtcaggta gcagggtgtac cttaaaatcc atg acg tca tta gag 115
 Met Thr Ser Leu Glu
 1 5

ttc aca gta acc cgt acc gaa aat ccg acg tca ccc gat cgt ctg aag 163
 Phe Thr Val Thr Arg Thr Glu Asn Pro Thr Ser Pro Asp Arg Leu Lys
 10 15 20

gaa att ctt gcc gca ccg aag ttc ggt aag ttc ttc acc gac cac atg 211
 Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe Phe Thr Asp His Met
 25 30 35

gtg acc att gac tgg aac gag tcg gaa ggc tgg cac aac gcc caa tta 259
 Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp His Asn Ala Gln Leu
 40 45 50

gtg cca tac gcg ccg att cct atg gat cct gcc acc acc gta ttc cac 307
 Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala Thr Thr Val Phe His
 55 60 65

tac gga cag gca att ttt gag gga att aag gcc tac cgc cat tcg gac 355
 Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala Tyr Arg His Ser Asp
 70 75 80 85

gaa acc atc aag act ttc cgt cct gat gaa aac gcc gag cgt atg cag	403
Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn Ala Glu Arg Met Gln	
90 95 100	
cgt tca gca gct cga atg gca atg cca cag ttg cca acc gag gac ttt	451
Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu Pro Thr Glu Asp Phe	
105 110 115	
att aaa gca ctt gaa ctg ctg gta gac gcg gat cag gat tgg gtt cct	499
Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp Gln Asp Trp Val Pro	
120 125 130	
gag tac ggc gga gaa gct tcc ctc tac ctg cgc cca ttc atg atc tcc	547
Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg Pro Phe Met Ile Ser	
135 140 145	
acc gaa att ggc ttg ggt gtc agc cca gct gat gcc tac aag ttc ctg	595
Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp Ala Tyr Lys Phe Leu	
150 155 160 165	
gtc atc gca tcc cca gtc ggc gct tac ttc acc ggt gga atc aag cct	643
Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr Gly Gly Ile Lys Pro	
170 175 180	
gtt tcc gtc tgg ctg agc gaa gat tac gtc cgc gct gca ccc ggc gga	691
Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg Ala Ala Pro Gly Gly	
185 190 195	
act ggt gac gcc aaa ttt gct ggc aac tac gcg gct tct ttg ctt gcc	739
Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala Ala Ser Leu Leu Ala	
200 205 210	
cag tcc cag gct gcg gaa aag ggc tgt gac cag gtc gta tgg ttg gat	787
Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln Val Trp Leu Asp	
215 220 225	
gcc atc gag cac aag tac atc gaa gaa atg ggt ggc atg aac ctt ggg	835
Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly Gly Met Asn Leu Gly	
230 235 240 245	
ttc atc tac cgc aac ggc gac caa gtc aag cta gtc acc cct gaa ctt	883
Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu Val Thr Pro Glu Leu	
250 255 260	
tcc ggc tca cta ctt cca ggc atc acc cgc aag tca ctt cta caa gta	931
Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys Ser Leu Leu Gln Val	
265 270 275	
gca cgc gac ttg gga tac gaa gta gaa gag cga aag atc acc acc acc	979
Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg Lys Ile Thr Thr Thr	
280 285 290	
gag tgg gaa gaa gac gca aag tct ggc gcc atg acc gag gca ttt gct	1027
Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met Thr Glu Ala Phe Ala	
295 300 305	
tgc ggt act gca gct gtt atc acc cct gtt ggc acc gtg aaa tca gct	1075
Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly Thr Val Lys Ser Ala	
310 315 320 325	

cac ggc acc ttc gaa gtg aac aac aat gaa gtc gga gaa atc acg atg 1123
 His Gly Thr Phe Glu Val Asn Asn Asn Glu Val Gly Glu Ile Thr Met
 330 335 340

aag ctt cgt gaa acc ctc acc gga att cag caa gga aac gtt gaa gac 1171
 Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln Gly Asn Val Glu Asp
 345 350 355

caa aac gga tgg ctt tac cca ctg gtt ggc taaatcaacc ggttttaaga 1221
 Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly
 360 365

ccc 1224

<210> 262

<211> 367

<212> PRT

<213> Corynebacterium glutamicum

<400> 262

Met Thr Ser Leu Glu Phe Thr Val Thr Arg Thr Glu Asn Pro Thr Ser
 1 5 10 15

Pro Asp Arg Leu Lys Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe
 20 25 30

Phe Thr Asp His Met Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp
 35 40 45

His Asn Ala Gln Leu Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala
 50 55 60

Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala
 65 70 75 80

Tyr Arg His Ser Asp Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn
 85 90 95

Ala Glu Arg Met Gln Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu
 100 105 110

Pro Thr Glu Asp Phe Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp
 115 120 125

Gln Asp Trp Val Pro Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg
 130 135 140

Pro Phe Met Ile Ser Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp
 145 150 155 160

Ala Tyr Lys Phe Leu Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr
 165 170 175

Gly Gly Ile Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg
 180 185 190

Ala Ala Pro Gly Gly Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala
 195 200 205

Ala Ser Leu Leu Ala Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln

210					215					220					
Val	Val	Trp	Leu	Asp	Ala	Ile	Glu	His	Lys	Tyr	Ile	Glu	Glu	Met	Gly
225					230					235					240
Gly	Met	Asn	Leu	Gly	Phe	Ile	Tyr	Arg	Asn	Gly	Asp	Gln	Val	Lys	Leu
				245					250					255	
Val	Thr	Pro	Glu	Leu	Ser	Gly	Ser	Leu	Leu	Pro	Gly	Ile	Thr	Arg	Lys
			260					265					270		
Ser	Leu	Leu	Gln	Val	Ala	Arg	Asp	Leu	Gly	Tyr	Glu	Val	Glu	Glu	Arg
			275				280					285			
Lys	Ile	Thr	Thr	Thr	Glu	Trp	Glu	Glu	Asp	Ala	Lys	Ser	Gly	Ala	Met
	290					295					300				
Thr	Glu	Ala	Phe	Ala	Cys	Gly	Thr	Ala	Ala	Val	Ile	Thr	Pro	Val	Gly
305					310					315					320
Thr	Val	Lys	Ser	Ala	His	Gly	Thr	Phe	Glu	Val	Asn	Asn	Asn	Glu	Val
				325					330					335	
Gly	Glu	Ile	Thr	Met	Lys	Leu	Arg	Glu	Thr	Leu	Thr	Gly	Ile	Gln	Gln
			340					345					350		
Gly	Asn	Val	Glu	Asp	Gln	Asn	Gly	Trp	Leu	Tyr	Pro	Leu	Val	Gly	
			355				360					365			

<210> 263
 <211> 1076
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1053)
 <223> FRXA01690

ccc	gat	cgt	ctg	aag	gaa	att	ctt	gcc	gca	ccg	aag	ttc	ggt	aag	ttc	48
Pro	Asp	Arg	Leu	Lys	Glu	Ile	Leu	Ala	Ala	Pro	Lys	Phe	Gly	Lys	Phe	
1				5				10					15			
ttc	acc	gac	cac	atg	gtg	acc	att	gac	tgg	aac	gag	tcg	gaa	ggc	tgg	96
Phe	Thr	Asp	His	Met	Val	Thr	Ile	Asp	Trp	Asn	Glu	Ser	Glu	Gly	Trp	
			20					25					30			
cac	aac	gcc	caa	tta	gtg	cca	tac	gcg	ccg	att	cct	atg	gat	cct	gcc	144
His	Asn	Ala	Gln	Leu	Val	Pro	Tyr	Ala	Pro	Ile	Pro	Met	Asp	Pro	Ala	
			35				40					45				
acc	acc	gta	ttc	cac	tac	gga	cag	gca	att	ttt	gag	gga	att	aag	gcc	192
Thr	Thr	Val	Phe	His	Tyr	Gly	Gln	Ala	Ile	Phe	Glu	Gly	Ile	Lys	Ala	
		50				55					60					
tac	cgc	cat	tcg	gac	gaa	acc	atc	aag	act	ttc	cgt	cct	gat	gaa	aac	240
Tyr	Arg	His	Ser	Asp	Glu	Thr	Ile	Lys	Thr	Phe	Arg	Pro	Asp	Glu	Asn	
65					70				75						80	

gcc gag cgt atg cag cgt tca gca gct cga atg gca atg cca cag ttg	288
Ala Glu Arg Met Gln Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu	
85 90 95	
cca acc gag gac ttt att aaa gca ctt gaa ctg ctg gta gac gcg gat	336
Pro Thr Glu Asp Phe Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp	
100 105 110	
cag gat tgg gtt cct gag tac ggc gga gaa gct tcc ctc tac ctg cgc	384
Gln Asp Trp Val Pro Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg	
115 120 125	
cca ttc atg atc tcc acc gaa att ggc ttg ggt gtc agc cca gct gat	432
Pro Phe Met Ile Ser Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp	
130 135 140	
gcc tac aag ttc ctg gtc atc gca tcc cca gtc ggc gct tac ttc acc	480
Ala Tyr Lys Phe Leu Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr	
145 150 155 160	
ggg gga atc aag cct gtt tcc gtc tgg ctg agc gaa gat tac gtc cgc	528
Gly Gly Ile Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg	
165 170 175	
gct gca ccc ggc gga act ggt gac gcc aaa ttt gct ggc aac tac gcg	576
Ala Ala Pro Gly Gly Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala	
180 185 190	
gct tct ttg ctt gcc cag tcc cag gct gcg gaa aag ggc tgt gac cag	624
Ala Ser Leu Leu Ala Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln	
195 200 205	
gtc gta tgg ttg gat gcc atc gag cac aag tac atc gaa gaa atg ggt	672
Val Val Trp Leu Asp Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly	
210 215 220	
ggc atg aac ctt ggg ttc atc tac cgc aac ggc gac caa gtc aag cta	720
Gly Met Asn Leu Gly Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu	
225 230 235 240	
gtc acc cct gaa ctt tcc ggc tca cta ctt cca ggc atc acc cgc aag	768
Val Thr Pro Glu Leu Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys	
245 250 255	
tca ctt cta caa gta gca cgc gac ttg gga tac gaa gta gaa gag cga	816
Ser Leu Leu Gln Val Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg	
260 265 270	
aag atc acc acc acc gag tgg gaa gaa gac gca aag tct ggc gcc atg	864
Lys Ile Thr Thr Thr Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met	
275 280 285	
acc gag gca ttt gct tgc ggt act gca gct gtt atc acc cct gtt ggc	912
Thr Glu Ala Phe Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly	
290 295 300	
acc gtg aaa tca gct cac ggc acc ttc gaa gtg aac aac aat gaa gtc	960
Thr Val Lys Ser Ala His Gly Thr Phe Glu Val Asn Asn Asn Glu Val	
305 310 315 320	
gga gaa atc acg atg aag ctt cgt gaa acc ctc acc gga att cag caa	1008

Gly Glu Ile Thr Met Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln
 325 330 335

gga aac gtt gaa gac caa aac gga tgg ctt tac cca ctg gtt ggc 1053
 Gly Asn Val Glu Asp Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly
 340 345 350

taaatacaacc gggtttaaga ccc 1076

<210> 264

<211> 351

<212> PRT

<213> Corynebacterium glutamicum

<400> 264

Pro Asp Arg Leu Lys Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe
 1 5 10 15

Phe Thr Asp His Met Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp
 20 25 30

His Asn Ala Gln Leu Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala
 35 40 45

Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala
 50 55 60

Tyr Arg His Ser Asp Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn
 65 70 75 80

Ala Glu Arg Met Gln Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu
 85 90 95

Pro Thr Glu Asp Phe Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp
 100 105 110

Gln Asp Trp Val Pro Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg
 115 120 125

Pro Phe Met Ile Ser Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp
 130 135 140

Ala Tyr Lys Phe Leu Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr
 145 150 155 160

Gly Gly Ile Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg
 165 170 175

Ala Ala Pro Gly Gly Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala
 180 185 190

Ala Ser Leu Leu Ala Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln
 195 200 205

Val Val Trp Leu Asp Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly
 210 215 220

Gly Met Asn Leu Gly Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu
 225 230 235 240

Val Thr Pro Glu Leu Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys
 245 250 255

Ser Leu Leu Gln Val Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg
 260 265 270

Lys Ile Thr Thr Thr Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met
 275 280 285

Thr Glu Ala Phe Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly
 290 295 300

Thr Val Lys Ser Ala His Gly Thr Phe Glu Val Asn Asn Asn Glu Val
 305 310 315 320

Gly Glu Ile Thr Met Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln
 325 330 335

Gly Asn Val Glu Asp Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly
 340 345 350

<210> 265
 <211> 1782
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1759)
 <223> RXN01026

<400> 265
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tatagtgaga tttacagatt tttaaaggac ggtgagttcc atg acc agc ccc gtg 115
 Met Thr Ser Pro Val
 1 5

gag aac agc acc tca act gag aag ctg acc ctg gca gag aag gtg tgg 163
 Glu Asn Ser Thr Ser Thr Glu Lys Leu Thr Leu Ala Glu Lys Val Trp
 10 15 20

cgc gac cat gtc gtg tcc aag gga gaa aac ggc gag ccc gac ctc ctc 211
 Arg Asp His Val Val Ser Lys Gly Glu Asn Gly Glu Pro Asp Leu Leu
 25 30 35

tac atc gac ctg cag ctg ctg cat gaa gtg acc tca cca cag gca ttt 259
 Tyr Ile Asp Leu Gln Leu Leu His Glu Val Thr Ser Pro Gln Ala Phe
 40 45 50

gac ggc ctg cgc atg acc ggc cgt aaa ctg cgc cac cca gaa ctg cac 307
 Asp Gly Leu Arg Met Thr Gly Arg Lys Leu Arg His Pro Glu Leu His
 55 60 65

ctg gcc acc gaa gac cac aac gtg cca acc gaa ggc atc aag act ggc 355
 Leu Ala Thr Glu Asp His Asn Val Pro Thr Glu Gly Ile Lys Thr Gly
 70 75 80 85

tca ctg ctg gaa atc aac gac aag att tcc cgc ctg cag gta tct act 403
 Ser Leu Leu Glu Ile Asn Asp Lys Ile Ser Arg Leu Gln Val Ser Thr

90								95				100					
ctg	cgc	gac	aac	tgt	gaa	gaa	ttc	ggc	gtg	cgc	ctg	cac	cca	atg	ggt	451	
Leu	Arg	Asp	Asn	Cys	Glu	Glu	Phe	Gly	Val	Arg	Leu	His	Pro	Met	Gly		
			105					110					115				
gat	gtc	cga	cag	ggc	atc	gtg	cac	acc	gtc	ggc	cca	cag	ctc	ggc	gca	499	
Asp	Val	Arg	Gln	Gly	Ile	Val	His	Thr	Val	Gly	Pro	Gln	Leu	Gly	Ala		
		120					125					130					
acc	cag	cca	ggc	atg	acc	att	gtg	tgc	ggg	gac	tcc	cac	acc	tcc	acc	547	
Thr	Gln	Pro	Gly	Met	Thr	Ile	Val	Cys	Gly	Asp	Ser	His	Thr	Ser	Thr		
	135					140				145							
cac	ggg	gct	ttt	ggc	tcc	atg	gca	ttc	ggc	atc	ggg	acc	tca	gag	gtt	595	
His	Gly	Ala	Phe	Gly	Ser	Met	Ala	Phe	Gly	Ile	Gly	Thr	Ser	Glu	Val		
150					155					160					165		
gag	cac	gtc	atg	gct	act	caa	acc	ctg	cca	ctg	aag	cct	ttc	aag	acc	643	
Glu	His	Val	Met	Ala	Thr	Gln	Thr	Leu	Pro	Leu	Lys	Pro	Phe	Lys	Thr		
				170					175					180			
atg	gcc	att	gaa	gtt	act	ggg	gaa	ctg	cag	cca	ggg	gtt	tcc	tcc	aag	691	
Met	Ala	Ile	Glu	Val	Thr	Gly	Glu	Leu	Gln	Pro	Gly	Val	Ser	Ser	Lys		
			185					190					195				
gac	ctg	att	ctg	gcg	att	atc	gcc	aag	atc	ggc	acc	ggc	ggc	gga	cag	739	
Asp	Leu	Ile	Leu	Ala	Ile	Ile	Ala	Lys	Ile	Gly	Thr	Gly	Gly	Gly	Gln		
		200					205					210					
ggc	tac	gtt	ctg	gaa	tac	cgc	ggc	gaa	gca	atc	cgt	aag	atg	tcc	atg	787	
Gly	Tyr	Val	Leu	Glu	Tyr	Arg	Gly	Glu	Ala	Ile	Arg	Lys	Met	Ser	Met		
	215					220					225						
gat	gca	cgc	atg	acc	atg	tgc	aac	atg	tcc	atc	gaa	gct	ggc	gca	cgt	835	
Asp	Ala	Arg	Met	Thr	Met	Cys	Asn	Met	Ser	Ile	Glu	Ala	Gly	Ala	Arg		
230					235					240					245		
gcc	ggc	atg	atc	gcc	cca	gac	caa	acc	acc	ttc	gac	tac	gtt	gaa	ggc	883	
Ala	Gly	Met	Ile	Ala	Pro	Asp	Gln	Thr	Thr	Phe	Asp	Tyr	Val	Glu	Gly		
				250					255					260			
cgc	gaa	atg	gca	cca	aag	ggc	gcc	gac	tgg	gac	gaa	gca	gtt	gct	tac	931	
Arg	Glu	Met	Ala	Pro	Lys	Gly	Ala	Asp	Trp	Asp	Glu	Ala	Val	Ala	Tyr		
			265					270					275				
tgg	aag	acc	ctg	cca	acc	gac	gaa	ggc	gca	acc	ttt	gac	aag	gtc	gta	979	
Trp	Lys	Thr	Leu	Pro	Thr	Asp	Glu	Gly	Ala	Thr	Phe	Asp	Lys	Val	Val		
		280					285					290					
gaa	atc	gat	ggc	tcg	gca	ctg	acc	cca	ttc	atc	acc	tgg	ggc	acc	aac	1027	
Glu	Ile	Asp	Gly	Ser	Ala	Leu	Thr	Pro	Phe	Ile	Thr	Trp	Gly	Thr	Asn		
	295					300					305						
cca	ggc	cag	ggc	ctg	cca	ctg	ggc	gaa	tcc	gta	cca	agc	cca	gaa	gac	1075	
Pro	Gly	Gln	Gly	Leu	Pro	Leu	Gly	Glu	Ser	Val	Pro	Ser	Pro	Glu	Asp		
310					315					320					325		
ttc	acc	aac	gac	aac	gac	aag	gca	gca	gcc	gaa	aag	gca	ctg	cag	tac	1123	
Phe	Thr	Asn	Asp	Asn	Asp	Lys	Ala	Ala	Ala	Glu	Lys	Ala	Leu	Gln	Tyr		
				330					335					340			

atg gac ctg gta cca gga acc cca ctg cgc gac atc aag atc gac acc	1171
Met Asp Leu Val Pro Gly Thr Pro Leu Arg Asp Ile Lys Ile Asp Thr	
345 350 355	
gtc ttc ctg gga tcc tgc acc aac gcc cgc atc gaa gac ctg cag atc	1219
Val Phe Leu Gly Ser Cys Thr Asn Ala Arg Ile Glu Asp Leu Gln Ile	
360 365 370	
gcc gct gac atc ctc aag ggc cac aaa atc gcc gac ggc atg cgc atg	1267
Ala Ala Asp Ile Leu Lys Gly His Lys Ile Ala Asp Gly Met Arg Met	
375 380 385	
atg gtc gtg cct tcc tcc acc tgg atc aag caa gag gca gaa gcg ctc	1315
Met Val Val Pro Ser Ser Thr Trp Ile Lys Gln Glu Ala Glu Ala Leu	
390 395 400 405	
gga ctg gac aaa atc ttc acc gac gct ggc gct gaa tgg cgt acc gca	1363
Gly Leu Asp Lys Ile Phe Thr Asp Ala Gly Ala Glu Trp Arg Thr Ala	
410 415 420	
ggc tgc tcc atg tgc ctg ggc atg aac cca gac caa ctg aag cca ggc	1411
Gly Cys Ser Met Cys Leu Gly Met Asn Pro Asp Gln Leu Lys Pro Gly	
425 430 435	
gag cgc tcc gca ttc acc tcc aac cga aac ttc gaa gga cgc caa gga	1459
Glu Arg Ser Ala Phe Thr Ser Asn Arg Asn Phe Glu Gly Arg Gln Gly	
440 445 450	
cca gga ggc cgc acc cac ctg gta tcc cca gca gtc gca gcc gcc acc	1507
Pro Gly Gly Arg Thr His Leu Val Ser Pro Ala Val Ala Ala Thr	
455 460 465	
gaa tcc gcg gac cct gtc ctc acc tgc aga tat cta agg aag gct aga	1555
Glu Ser Ala Asp Pro Val Leu Thr Cys Arg Tyr Leu Arg Lys Ala Arg	
470 475 480 485	
aaa caa tgg aaa aat tta cca cct aca ccg gcg ttg gcg ttc cac tgc	1603
Lys Gln Trp Lys Asn Leu Pro Pro Thr Pro Ala Leu Ala Phe His Cys	
490 495 500	
agc gat cca acg tgg aca ccg acc aga tca tcc cag ccg tct acc tca	1651
Ser Asp Pro Thr Trp Thr Pro Thr Arg Ser Ser Gln Pro Ser Thr Ser	
505 510 515	
agc gcg tca ccc gga ccg gct tgc aag acg gac tgt ttt cca act ggc	1699
Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp Cys Phe Pro Thr Gly	
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gcc aaa acg acc cca act ttg tcc tca aca ccg aca cct aca aga acg	1747
Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro Thr Pro Thr Arg Thr	
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Ala Pro Phe Ser	
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<210> 266

<211> 553

<212> PRT

<213> Corynebacterium glutamicum

<400> 266

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Glu Pro Asp Leu Leu Tyr Ile Asp Leu Gln Leu Leu His Glu Val Thr
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Ser Pro Gln Ala Phe Asp Gly Leu Arg Met Thr Gly Arg Lys Leu Arg
      50              55              60

His Pro Glu Leu His Leu Ala Thr Glu Asp His Asn Val Pro Thr Glu
      65              70              75              80

Gly Ile Lys Thr Gly Ser Leu Leu Glu Ile Asn Asp Lys Ile Ser Arg
      85              90              95

Leu Gln Val Ser Thr Leu Arg Asp Asn Cys Glu Glu Phe Gly Val Arg
      100              105              110

Leu His Pro Met Gly Asp Val Arg Gln Gly Ile Val His Thr Val Gly
      115              120              125

Pro Gln Leu Gly Ala Thr Gln Pro Gly Met Thr Ile Val Cys Gly Asp
      130              135              140

Ser His Thr Ser Thr His Gly Ala Phe Gly Ser Met Ala Phe Gly Ile
      145              150              155              160

Gly Thr Ser Glu Val Glu His Val Met Ala Thr Gln Thr Leu Pro Leu
      165              170              175

Lys Pro Phe Lys Thr Met Ala Ile Glu Val Thr Gly Glu Leu Gln Pro
      180              185              190

Gly Val Ser Ser Lys Asp Leu Ile Leu Ala Ile Ile Ala Lys Ile Gly
      195              200              205

Thr Gly Gly Gly Gln Gly Tyr Val Leu Glu Tyr Arg Gly Glu Ala Ile
      210              215              220

Arg Lys Met Ser Met Asp Ala Arg Met Thr Met Cys Asn Met Ser Ile
      225              230              235              240

Glu Ala Gly Ala Arg Ala Gly Met Ile Ala Pro Asp Gln Thr Thr Phe
      245              250              255

Asp Tyr Val Glu Gly Arg Glu Met Ala Pro Lys Gly Ala Asp Trp Asp
      260              265              270

Glu Ala Val Ala Tyr Trp Lys Thr Leu Pro Thr Asp Glu Gly Ala Thr
      275              280              285

Phe Asp Lys Val Val Glu Ile Asp Gly Ser Ala Leu Thr Pro Phe Ile
      290              295              300

Thr Trp Gly Thr Asn Pro Gly Gln Gly Leu Pro Leu Gly Glu Ser Val

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305 310 315 320
 Pro Ser Pro Glu Asp Phe Thr Asn Asp Asn Asp Lys Ala Ala Ala Glu
 325 330 335
 Lys Ala Leu Gln Tyr Met Asp Leu Val Pro Gly Thr Pro Leu Arg Asp
 340 345 350
 Ile Lys Ile Asp Thr Val Phe Leu Gly Ser Cys Thr Asn Ala Arg Ile
 355 360 365
 Glu Asp Leu Gln Ile Ala Ala Asp Ile Leu Lys Gly His Lys Ile Ala
 370 375 380
 Asp Gly Met Arg Met Met Val Val Pro Ser Ser Thr Trp Ile Lys Gln
 385 390 395 400
 Glu Ala Glu Ala Leu Gly Leu Asp Lys Ile Phe Thr Asp Ala Gly Ala
 405 410 415
 Glu Trp Arg Thr Ala Gly Cys Ser Met Cys Leu Gly Met Asn Pro Asp
 420 425 430
 Gln Leu Lys Pro Gly Glu Arg Ser Ala Phe Thr Ser Asn Arg Asn Phe
 435 440 445
 Glu Gly Arg Gln Gly Pro Gly Gly Arg Thr His Leu Val Ser Pro Ala
 450 455 460
 Val Ala Ala Ala Thr Glu Ser Ala Asp Pro Val Leu Thr Cys Arg Tyr
 465 470 475 480
 Leu Arg Lys Ala Arg Lys Gln Trp Lys Asn Leu Pro Pro Thr Pro Ala
 485 490 495
 Leu Ala Phe His Cys Ser Asp Pro Thr Trp Thr Pro Thr Arg Ser Ser
 500 505 510
 Gln Pro Ser Thr Ser Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp
 515 520 525
 Cys Phe Pro Thr Gly Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro
 530 535 540
 Thr Pro Thr Arg Thr Ala Pro Phe Ser
 545 550

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<211> 1625

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(1602)

<223> FRXA01026

<400> 267

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ctc ctc tac atc gac ctg cag ctg ctg cat gaa gtg acc tca cca cag	Leu Leu Tyr Ile Asp Leu Gln Leu Leu His Glu Val Thr Ser Pro Gln				20 25				30								96
gca ttt gac ggc ctg cgc atg acc ggc cgt aaa ctg cgc cac cca gaa	Ala Phe Asp Gly Leu Arg Met Thr Gly Arg Lys Leu Arg His Pro Glu				35 40				45								144
ctg cac ctg gcc acc gaa gac cac aac gtg cca acc gaa ggc atc aag	Leu His Leu Ala Thr Glu Asp His Asn Val Pro Thr Glu Gly Ile Lys				50 55				60								192
act ggc tca ctg ctg gaa atc aac gac aag att tcc cgc ctg cag gta	Thr Gly Ser Leu Leu Glu Ile Asn Asp Lys Ile Ser Arg Leu Gln Val				65 70				75 80								240
tct act ctg cgc gac aac tgt gaa gaa ttc ggc gtg cgc ctg cac cca	Ser Thr Leu Arg Asp Asn Cys Glu Glu Phe Gly Val Arg Leu His Pro				85 90				95								288
atg ggt gat gtc cga cag ggc atc gtg cac acc gtc ggc cca cag ctc	Met Gly Asp Val Arg Gln Gly Ile Val His Thr Val Gly Pro Gln Leu				100 105				110								336
ggc gca acc cag cca ggc atg acc att gtg tgc ggt gac tcc cac acc	Gly Ala Thr Gln Pro Gly Met Thr Ile Val Cys Gly Asp Ser His Thr				115 120				125								384
tcc acc cac ggt gct ttt ggc tcc atg gca ttc ggc atc ggt acc tca	Ser Thr His Gly Ala Phe Gly Ser Met Ala Phe Gly Ile Gly Thr Ser				130 135				140								432
gag gtt gag cac gtc atg gct act caa acc ctg cca ctg aag cct ttc	Glu Val Glu His Val Met Ala Thr Gln Thr Leu Pro Leu Lys Pro Phe				145 150				155 160								480
aag acc atg gcc att gaa gtt act ggt gaa ctg cag cca ggt gtt tcc	Lys Thr Met Ala Ile Glu Val Thr Gly Glu Leu Gln Pro Gly Val Ser				165 170				175								528
tcc aag gac ctg att ctg gcg att atc gcc aag atc ggc acc ggc ggc	Ser Lys Asp Leu Ile Leu Ala Ile Ile Ala Lys Ile Gly Thr Gly Gly				180 185				190								576
gga cag ggc tac gtt ctg gaa tac cgc ggc gaa gca atc cgt aag atg	Gly Gln Gly Tyr Val Leu Glu Tyr Arg Gly Glu Ala Ile Arg Lys Met				195 200				205								624
tcc atg gat gca cgc atg acc atg tgc aac atg tcc atc gaa gct ggc	Ser Met Asp Ala Arg Met Thr Met Cys Asn Met Ser Ile Glu Ala Gly				210 215				220								672
gca cgt gcc ggc atg atc gcc cca gac caa acc acc ttc gac tac gtt	Ala Arg Ala Gly Met Ile Ala Pro Asp Gln Thr Thr Phe Asp Tyr Val				225 230				235 240								720
gaa ggc cgc gaa atg gca cca aag ggc gcc gac tgg gac gaa gca gtt	Glu Gly Arg Glu Met Ala Pro Lys Gly Ala Asp Trp Asp Glu Ala Val				245 250				255								768

gct tac tgg aag acc ctg cca acc gac gaa ggc gca acc ttt gac aag	816
Ala Tyr Trp Lys Thr Leu Pro Thr Asp Glu Gly Ala Thr Phe Asp Lys	
260 265 270	
gtc gta gaa atc gat ggc tcg gca ctg acc cca ttc atc acc tgg ggc	864
Val Val Glu Ile Asp Gly Ser Ala Leu Thr Pro Phe Ile Thr Trp Gly	
275 280 285	
acc aac cca ggc cag ggc ctg cca ctg ggc gaa tcc gta cca agc cca	912
Thr Asn Pro Gly Gln Gly Leu Pro Leu Gly Glu Ser Val Pro Ser Pro	
290 295 300	
gaa gac ttc acc aac gac aac gac aag gca gca gcc gaa aag gca ctg	960
Glu Asp Phe Thr Asn Asp Asn Asp Lys Ala Ala Ala Glu Lys Ala Leu	
305 310 315 320	
cag tac atg gac ctg gta cca gga acc cca ctg cgc gac atc aag atc	1008
Gln Tyr Met Asp Leu Val Pro Gly Thr Pro Leu Arg Asp Ile Lys Ile	
325 330 335	
gac acc gtc ttc ctg gga tcc tgc acc aac gcc cgc atc gaa gac ctg	1056
Asp Thr Val Phe Leu Gly Ser Cys Thr Asn Ala Arg Ile Glu Asp Leu	
340 345 350	
cag atc gcc gct gac atc ctc aag ggc cac aaa atc gcc gac ggc atg	1104
Gln Ile Ala Ala Asp Ile Leu Lys Gly His Lys Ile Ala Asp Gly Met	
355 360 365	
cgc atg atg gtc gtg cct tcc tcc acc tgg atc aag caa gag gca gaa	1152
Arg Met Met Val Val Pro Ser Ser Thr Trp Ile Lys Gln Glu Ala Glu	
370 375 380	
gcg ctc gga ctg gac aaa atc ttc acc gac gct ggc gct gaa tgg cgt	1200
Ala Leu Gly Leu Asp Lys Ile Phe Thr Asp Ala Gly Ala Glu Trp Arg	
385 390 395 400	
acc gca ggc tgc tcc atg tgc ctg ggc atg aac cca gac caa ctg aag	1248
Thr Ala Gly Cys Ser Met Cys Leu Gly Met Asn Pro Asp Gln Leu Lys	
405 410 415	
cca ggc gag cgc tcc gca ttc acc tcc aac cga aac ttc gaa gga cgc	1296
Pro Gly Glu Arg Ser Ala Phe Thr Ser Asn Arg Asn Phe Glu Gly Arg	
420 425 430	
caa gga cca gga ggc cgc acc cac ctg gta tcc cca gca gtc gca gcc	1344
Gln Gly Pro Gly Gly Arg Thr His Leu Val Ser Pro Ala Val Ala Ala	
435 440 445	
gcc acc gaa tcc gcg gac cct gtc ctc acc tgc aga tat cta agg aag	1392
Ala Thr Glu Ser Ala Asp Pro Val Leu Thr Cys Arg Tyr Leu Arg Lys	
450 455 460	
gct aga aaa caa tgg aaa aat tta cca cct aca ccg gcg ttg gcg ttc	1440
Ala Arg Lys Gln Trp Lys Asn Leu Pro Pro Thr Pro Ala Leu Ala Phe	
465 470 475 480	
cac tgc agc gat cca acg tgg aca ccg acc aga tca tcc cag ccg tct	1488
His Cys Ser Asp Pro Thr Trp Thr Pro Thr Arg Ser Ser Gln Pro Ser	
485 490 495	

acc tca agc gcg tca ccc gga ccg gct tcg aag acg gac tgt ttt cca 1536
 Thr Ser Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp Cys Phe Pro
 500 505 510

act ggc gcc aaa acg acc cca act ttg tcc tca aca ccg aca cct aca 1584
 Thr Gly Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro Thr Pro Thr
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aga acg gct ccg ttc tcg tagcaggccc tgactttggc acc 1625
 Arg Thr Ala Pro Phe Ser
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<210> 268

<211> 534

<212> PRT

<213> Corynebacterium glutamicum

<400> 268

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Ala Phe Asp Gly Leu Arg Met Thr Gly Arg Lys Leu Arg His Pro Glu
 35 40 45

Leu His Leu Ala Thr Glu Asp His Asn Val Pro Thr Glu Gly Ile Lys
 50 55 60

Thr Gly Ser Leu Leu Glu Ile Asn Asp Lys Ile Ser Arg Leu Gln Val
 65 70 75 80

Ser Thr Leu Arg Asp Asn Cys Glu Glu Phe Gly Val Arg Leu His Pro
 85 90 95

Met Gly Asp Val Arg Gln Gly Ile Val His Thr Val Gly Pro Gln Leu
 100 105 110

Gly Ala Thr Gln Pro Gly Met Thr Ile Val Cys Gly Asp Ser His Thr
 115 120 125

Ser Thr His Gly Ala Phe Gly Ser Met Ala Phe Gly Ile Gly Thr Ser
 130 135 140

Glu Val Glu His Val Met Ala Thr Gln Thr Leu Pro Leu Lys Pro Phe
 145 150 155 160

Lys Thr Met Ala Ile Glu Val Thr Gly Glu Leu Gln Pro Gly Val Ser
 165 170 175

Ser Lys Asp Leu Ile Leu Ala Ile Ile Ala Lys Ile Gly Thr Gly Gly
 180 185 190

Gly Gln Gly Tyr Val Leu Glu Tyr Arg Gly Glu Ala Ile Arg Lys Met
 195 200 205

Ser Met Asp Ala Arg Met Thr Met Cys Asn Met Ser Ile Glu Ala Gly
 210 215 220

Ala Arg Ala Gly Met Ile Ala Pro Asp Gln Thr Thr Phe Asp Tyr Val
 225 230 235 240
 Glu Gly Arg Glu Met Ala Pro Lys Gly Ala Asp Trp Asp Glu Ala Val
 245 250 255
 Ala Tyr Trp Lys Thr Leu Pro Thr Asp Glu Gly Ala Thr Phe Asp Lys
 260 265 270
 Val Val Glu Ile Asp Gly Ser Ala Leu Thr Pro Phe Ile Thr Trp Gly
 275 280 285
 Thr Asn Pro Gly Gln Gly Leu Pro Leu Gly Glu Ser Val Pro Ser Pro
 290 295 300
 Glu Asp Phe Thr Asn Asp Asn Asp Lys Ala Ala Ala Glu Lys Ala Leu
 305 310 315 320
 Gln Tyr Met Asp Leu Val Pro Gly Thr Pro Leu Arg Asp Ile Lys Ile
 325 330 335
 Asp Thr Val Phe Leu Gly Ser Cys Thr Asn Ala Arg Ile Glu Asp Leu
 340 345 350
 Gln Ile Ala Ala Asp Ile Leu Lys Gly His Lys Ile Ala Asp Gly Met
 355 360 365
 Arg Met Met Val Val Pro Ser Ser Thr Trp Ile Lys Gln Glu Ala Glu
 370 375 380
 Ala Leu Gly Leu Asp Lys Ile Phe Thr Asp Ala Gly Ala Glu Trp Arg
 385 390 395 400
 Thr Ala Gly Cys Ser Met Cys Leu Gly Met Asn Pro Asp Gln Leu Lys
 405 410 415
 Pro Gly Glu Arg Ser Ala Phe Thr Ser Asn Arg Asn Phe Glu Gly Arg
 420 425 430
 Gln Gly Pro Gly Gly Arg Thr His Leu Val Ser Pro Ala Val Ala Ala
 435 440 445
 Ala Thr Glu Ser Ala Asp Pro Val Leu Thr Cys Arg Tyr Leu Arg Lys
 450 455 460
 Ala Arg Lys Gln Trp Lys Asn Leu Pro Pro Thr Pro Ala Leu Ala Phe
 465 470 475 480
 His Cys Ser Asp Pro Thr Trp Thr Pro Thr Arg Ser Ser Gln Pro Ser
 485 490 495
 Thr Ser Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp Cys Phe Pro
 500 505 510
 Thr Gly Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro Thr Pro Thr
 515 520 525
 Arg Thr Ala Pro Phe Ser
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<222> (101) .. (1120)
<223> RXN01127
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Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr Ala Glu Ala Leu Lys
10 15 20

ggc gca cgc cgt tac ctc aaa aat ggc gag ctg ctc acc gac gag gat 259
Gly Ala Arg Arg Tyr Leu Lys Asn Gly Glu Leu Leu Thr Asp Glu Asp
40 45 50

gca cca ggt tcc gtc cct cca gga att ctc gag cgt ggt ttg ctg ctg 355
Ala Pro Gly Ser Val Pro Pro Gly Ile Leu Glu Arg Gly Leu Leu Leu
70 75 80 85

ctg tac gac ggc gtg gag tcc cca ctg cgt aac cca ggc aag att gat 451
Leu Tyr Asp Gly Val Glu Ser Pro Leu Arg Asn Pro Gly Lys Ile Asp
105 110 115

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 Phe Val Val Val Arg Glu Gly Thr Glu Gly Ala Tyr Thr Gly Asn Gly
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gga gca atc cgc gtg gga acc cct cac gag att gcc aat gaa acc tcc 547
Gly Ala Ile Arg Val Gly Thr Pro His Glu Ile Ala Asn Glu Thr Ser
135 140 145

gtg aac act cgc tac ggc gct gag cgc gtt att cgc tac gca ttc gag 595
Val Asn Thr Arg Tyr Gly Ala Glu Arg Val Ile Arg Tyr Ala Phe Glu
150 155 160 165

ctg gca cag agc cgc cgc aag aag ctc acc ctc gtg cac aag acc aac 643
Leu Ala Gln Ser Arg Arg Lys Lys Leu Thr Leu Val His Lys Thr Asn
170 175 180

gtc ctg gtt cac ggt ggt ggc ctg tgg cag cgc acc gta gat gag gtt 691
 Val Leu Val His Gly Gly Gly Leu Trp Gln Arg Thr Val Asp Glu Val
 185 190 195

gca aag gaa tac cca gag gta gcc gtc gat tac aac cac atc gat gca 739
 Ala Lys Glu Tyr Pro Glu Val Ala Val Asp Tyr Asn His Ile Asp Ala
 200 205 210

gca acc atc tat ctg gtc act gat cct tcc cgc ttc gat gtg att gtt 787
 Ala Thr Ile Tyr Leu Val Thr Asp Pro Ser Arg Phe Asp Val Ile Val
 215 220 225

acc gat aac ctc ttc ggc gac atc ctc acc gat gag gca ggc gca gtc 835
 Thr Asp Asn Leu Phe Gly Asp Ile Leu Thr Asp Glu Ala Gly Ala Val
 230 235 240 245

tct ggc gga att ggc ctc gca gca tcc ggc aac atc gat gcc acg ggc 883
 Ser Gly Gly Ile Gly Leu Ala Ala Ser Gly Asn Ile Asp Ala Thr Gly
 250 255 260

acc aac cct tcc atg ttc gag cca gtc cac ggc tct gca cca gat atc 931
 Thr Asn Pro Ser Met Phe Glu Pro Val His Gly Ser Ala Pro Asp Ile
 265 270 275

gca ggc cag gga atc gca gac cca acg gca gca atc cta tcc gct gcg 979
 Ala Gly Gln Gly Ile Ala Asp Pro Thr Ala Ala Ile Leu Ser Ala Ala
 280 285 290

atg ctg ctg cgt cac tta ggt gat gaa gac aac gca gta cgt att gaa 1027
 Met Leu Leu Arg His Leu Gly Asp Glu Asp Asn Ala Val Arg Ile Glu
 295 300 305

aca gcc atc gca gct gat gtg gct ggc cga gat aac tct cag ccg att 1075
 Thr Ala Ile Ala Ala Asp Val Ala Gly Arg Asp Asn Ser Gln Pro Ile
 310 315 320 325

tct acc act gag gtg gga gac cgc atc gtc aag gcg ctg caa agc 1120
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<211> 340

<212> PRT

<213> Corynebacterium glutamicum

<400> 270

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 35 40 45

Leu Thr Asp Glu Asp Leu Ala Ser Leu Arg Glu His Asp Ala Ile Leu
 50 55 60

Leu Gly Ala Ile Gly Ala Pro Gly Ser Val Pro Pro Gly Ile Leu Glu
 65 70 75 80
 Arg Gly Leu Leu Leu Lys Met Arg Phe Ala Leu Asp His His Val Asn
 85 90 95
 Leu Arg Pro Ser Lys Leu Tyr Asp Gly Val Glu Ser Pro Leu Arg Asn
 100 105 110
 Pro Gly Lys Ile Asp Phe Val Val Val Arg Glu Gly Thr Glu Gly Ala
 115 120 125
 Tyr Thr Gly Asn Gly Gly Ala Ile Arg Val Gly Thr Pro His Glu Ile
 130 135 140
 Ala Asn Glu Thr Ser Val Asn Thr Arg Tyr Gly Ala Glu Arg Val Ile
 145 150 155 160
 Arg Tyr Ala Phe Glu Leu Ala Gln Ser Arg Arg Lys Lys Leu Thr Leu
 165 170 175
 Val His Lys Thr Asn Val Leu Val His Gly Gly Gly Leu Trp Gln Arg
 180 185 190
 Thr Val Asp Glu Val Ala Lys Glu Tyr Pro Glu Val Ala Val Asp Tyr
 195 200 205
 Asn His Ile Asp Ala Ala Thr Ile Tyr Leu Val Thr Asp Pro Ser Arg
 210 215 220
 Phe Asp Val Ile Val Thr Asp Asn Leu Phe Gly Asp Ile Leu Thr Asp
 225 230 235 240
 Glu Ala Gly Ala Val Ser Gly Gly Ile Gly Leu Ala Ala Ser Gly Asn
 245 250 255
 Ile Asp Ala Thr Gly Thr Asn Pro Ser Met Phe Glu Pro Val His Gly
 260 265 270
 Ser Ala Pro Asp Ile Ala Gly Gln Gly Ile Ala Asp Pro Thr Ala Ala
 275 280 285
 Ile Leu Ser Ala Ala Met Leu Leu Arg His Leu Gly Asp Glu Asp Asn
 290 295 300
 Ala Val Arg Ile Glu Thr Ala Ile Ala Ala Asp Val Ala Gly Arg Asp
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 Ala Leu Gln Ser
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<212> DNA

<213> *Corynebacterium glutamicum*

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<212> PRT

<213> Corynebacterium glutamicum

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<210> 273
<211> 1494
<212> DNA
<213> Corynebacterium glutamicum
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<400> 273																
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tcgtggaccc	acccaaaact	ttttaagaag	gttgaacaca	atg	tct	cct	aac	gat	115							
				Met	Ser	Pro	Asn	Asp								
				1				5								
gca	ttc	atc	tcc	gca	cct	gcc	aag	atc	gaa	acc	cca	gtt	ggg	cct	cgc	163
Ala	Phe	Ile	Ser	Ala	Pro	Ala	Lys	Ile	Glu	Thr	Pro	Val	Gly	Pro	Arg	
			10						15					20		
aac	gaa	ggc	cag	cca	gca	tgg	aat	aag	cag	cgt	ggc	tcc	tca	atg	cca	211
Asn	Glu	Gly	Gln	Pro	Ala	Trp	Asn	Lys	Gln	Arg	Gly	Ser	Ser	Met	Pro	
			25					30					35			
gtt	aac	cgc	tac	atg	cct	ttc	gag	gtt	gag	gta	gaa	gat	att	tct	ctg	259
Val	Asn	Arg	Tyr	Met	Pro	Phe	Glu	Val	Glu	Val	Glu	Asp	Ile	Ser	Leu	
		40					45					50				
ccg	gac	cgc	act	tgg	cca	gat	aaa	aaa	atc	acc	gtt	gca	cct	cag	tgg	307
Pro	Asp	Arg	Thr	Trp	Pro	Asp	Lys	Lys	Ile	Thr	Val	Ala	Pro	Gln	Trp	
	55					60					65					
tgt	gct	gtt	gac	ctg	cgt	gac	ggc	aac	cag	gct	ctg	att	gat	ccg	atg	355
Cys	Ala	Val	Asp	Leu	Arg	Asp	Gly	Asn	Gln	Ala	Leu	Ile	Asp	Pro	Met	
	70				75				80						85	
tct	cct	gag	cgt	aag	cgc	cgc	atg	ttt	gag	ctg	ctg	gtt	cag	atg	ggc	403
Ser	Pro	Glu	Arg	Lys	Arg	Arg	Met	Phe	Glu	Leu	Leu	Val	Gln	Met	Gly	
				90					95					100		
ttc	aaa	gaa	atc	gag	gtc	ggg	ttc	cct	tca	gct	tcc	cag	act	gat	ttt	451
Phe	Lys	Glu	Ile	Glu	Val	Gly	Phe	Pro	Ser	Ala	Ser	Gln	Thr	Asp	Phe	
			105					110					115			
gat	ttc	gtt	cgt	gag	atc	atc	gaa	aag	ggc	atg	atc	cct	gac	gat	gtc	499
Asp	Phe	Val	Arg	Glu	Ile	Ile	Glu	Lys	Gly	Met	Ile	Pro	Asp	Asp	Val	
		120					125					130				
acc	att	cag	gtt	ctg	gtt	cag	gct	cgt	gag	cac	ctg	att	cgc	cgt	act	547
Thr	Ile	Gln	Val	Leu	Val	Gln	Ala	Arg	Glu	His	Leu	Ile	Arg	Arg	Thr	
	135					140					145					
ttt	gaa	gct	tgc	gaa	ggc	gca	aaa	aac	gtt	atc	gtg	cac	ttc	tac	aac	595
Phe	Glu	Ala	Cys	Glu	Gly	Ala	Lys	Asn	Val	Ile	Val	His	Phe	Tyr	Asn	
	150				155					160					165	
tcc	acc	tcc	atc	ctg	cag	cgc	aac	gtg	gtg	ttc	cgc	atg	gac	aaq	qtg	643

Ser	Thr	Ser	Ile	Leu	Gln	Arg	Asn	Val	Val	Phe	Arg	Met	Asp	Lys	Val		
				170					175					180			
cag	gtg	aag	aag	ctg	gct	acc	gat	gcc	gct	gaa	cta	atc	aag	acc	atc		691
Gln	Val	Lys	Lys	Leu	Ala	Thr	Asp	Ala	Ala	Glu	Leu	Ile	Lys	Thr	Ile		
			185					190					195				
gct	cag	gat	tac	cca	gac	acc	aac	tgg	cgc	tgg	cag	tac	tcc	cct	gag		739
Ala	Gln	Asp	Tyr	Pro	Asp	Thr	Asn	Trp	Arg	Trp	Gln	Tyr	Ser	Pro	Glu		
		200					205					210					
tcc	ttc	acc	ggc	act	gag	gtt	gag	tac	gcc	aag	gaa	gtt	gtg	gac	gca		787
Ser	Phe	Thr	Gly	Thr	Glu	Val	Glu	Tyr	Ala	Lys	Glu	Val	Val	Asp	Ala		
	215					220					225						
gtt	gtt	gag	gtc	atg	gat	cca	act	cct	gag	aac	cca	atg	atc	atc	aac		835
Val	Val	Glu	Val	Met	Asp	Pro	Thr	Pro	Glu	Asn	Pro	Met	Ile	Ile	Asn		
230					235					240					245		
ctg	cct	tcc	acc	gtt	gag	atg	atc	acc	cct	aac	gtt	tac	gca	gac	tcc		883
Leu	Pro	Ser	Thr	Val	Glu	Met	Ile	Thr	Pro	Asn	Val	Tyr	Ala	Asp	Ser		
				250					255					260			
att	gaa	tgg	atg	cac	cgc	aat	cta	aac	cgt	cgt	gat	tcc	att	atc	ctg		931
Ile	Glu	Trp	Met	His	Arg	Asn	Leu	Asn	Arg	Arg	Asp	Ser	Ile	Ile	Leu		
			265			270						275					
tcc	ctg	cac	ccg	cac	aat	gac	cgt	ggc	acc	ggc	gtt	ggc	gca	gct	gag		979
Ser	Leu	His	Pro	His	Asn	Asp	Arg	Gly	Thr	Gly	Val	Gly	Ala	Ala	Glu		
		280				285						290					
ctg	ggc	tac	atg	gct	ggc	gct	gac	cgc	atc	gaa	ggc	tgc	ctg	ttc	ggc		1027
Leu	Gly	Tyr	Met	Ala	Gly	Ala	Asp	Arg	Ile	Glu	Gly	Cys	Leu	Phe	Gly		
	295					300					305						
aac	ggc	gag	cgc	acc	ggc	aac	gtc	tgc	ctg	gtc	acc	ctg	gca	ctg	aac		1075
Asn	Gly	Glu	Arg	Thr	Gly	Asn	Val	Cys	Leu	Val	Thr	Leu	Ala	Leu	Asn		
310					315					320					325		
atg	ctg	acc	cag	ggc	gtt	gac	cct	cag	ctg	gac	ttc	acc	gat	ata	cgc		1123
Met	Leu	Thr	Gln	Gly	Val	Asp	Pro	Gln	Leu	Asp	Phe	Thr	Asp	Ile	Arg		
				330					335					340			
cag	atc	cgc	agc	acc	gtt	gaa	tac	tgc	aac	cag	ctg	cgc	gtt	cct	gag		1171
Gln	Ile	Arg	Ser	Thr	Val	Glu	Tyr	Cys	Asn	Gln	Leu	Arg	Val	Pro	Glu		
			345					350					355				
cgc	cac	cca	tac	ggc	ggt	gac	ctg	gtc	ttc	acc	gct	ttc	tcc	ggt	tcc		1219
Arg	His	Pro	Tyr	Gly	Gly	Asp	Leu	Val	Phe	Thr	Ala	Phe	Ser	Gly	Ser		
		360				365						370					
cac	cag	gac	gct	gtg	aac	aag	ggt	ctg	gac	gcc	atg	gct	gcc	aag	gtt		1267
His	Gln	Asp	Ala	Val	Asn	Lys	Gly	Leu	Asp	Ala	Met	Ala	Ala	Lys	Val		
	375					380					385						
cag	cca	ggt	gct	agc	tcc	act	gaa	gtt	tct	tgg	gag	cag	ctg	cgc	gac		1315
Gln	Pro	Gly	Ala	Ser	Ser	Thr	Glu	Val	Ser	Trp	Glu	Gln	Leu	Arg	Asp		
390					395					400					405		
acc	cga	atg	gga	ggt	tcc	tta	cct	gcc	tat	cga	tcc	aaa	gga	tgt	cgg		1363
Thr	Arg	Met	Gly	Gly	Ser	Leu	Pro	Ala	Tyr	Arg	Ser	Lys	Gly	Cys	Arg		

410

415

420

tcg cga cta cga ggc tgt tat ccg cgt gaa ctc cca gtc cgg caa ggg 1411
 Ser Arg Leu Arg Gly Cys Tyr Pro Arg Glu Leu Pro Val Arg Gln Gly
 425 430 435

cgg cgt tgc tta cat cat gaa gac cga tca cgg tct gca gat ccc tcg 1459
 Arg Arg Cys Leu His His Glu Asp Arg Ser Arg Ser Ala Asp Pro Ser
 440 445 450

ctc cat gca ggt tgagttctcc accgttgtcc aga 1494
 Leu His Ala Gly
 455

<210> 274

<211> 457

<212> PRT

<213> Corynebacterium glutamicum

<400> 274

Met Ser Pro Asn Asp Ala Phe Ile Ser Ala Pro Ala Lys Ile Glu Thr
 1 5 10 15

Pro Val Gly Pro Arg Asn Glu Gly Gln Pro Ala Trp Asn Lys Gln Arg
 20 25 30

Gly Ser Ser Met Pro Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val
 35 40 45

Glu Asp Ile Ser Leu Pro Asp Arg Thr Trp Pro Asp Lys Lys Ile Thr
 50 55 60

Val Ala Pro Gln Trp Cys Ala Val Asp Leu Arg Asp Gly Asn Gln Ala
 65 70 75 80

Leu Ile Asp Pro Met Ser Pro Glu Arg Lys Arg Arg Met Phe Glu Leu
 85 90 95

Leu Val Gln Met Gly Phe Lys Glu Ile Glu Val Gly Phe Pro Ser Ala
 100 105 110

Ser Gln Thr Asp Phe Asp Phe Val Arg Glu Ile Ile Glu Lys Gly Met
 115 120 125

Ile Pro Asp Asp Val Thr Ile Gln Val Leu Val Gln Ala Arg Glu His
 130 135 140

Leu Ile Arg Arg Thr Phe Glu Ala Cys Glu Gly Ala Lys Asn Val Ile
 145 150 155 160

Val His Phe Tyr Asn Ser Thr Ser Ile Leu Gln Arg Asn Val Val Phe
 165 170 175

Arg Met Asp Lys Val Gln Val Lys Lys Leu Ala Thr Asp Ala Ala Glu
 180 185 190

Leu Ile Lys Thr Ile Ala Gln Asp Tyr Pro Asp Thr Asn Trp Arg Trp
 195 200 205

Gln Tyr Ser Pro Glu Ser Phe Thr Gly Thr Glu Val Glu Tyr Ala Lys

1411 1459 1494 274 457 274 1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205

210	215	220
Glu Val Val Asp Ala Val Val Glu Val Met Asp Pro Thr Pro Glu Asn 225 230 235 240		
Pro Met Ile Ile Asn Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn 245 250 255		
Val Tyr Ala Asp Ser Ile Glu Trp Met His Arg Asn Leu Asn Arg Arg 260 265 270		
Asp Ser Ile Ile Leu Ser Leu His Pro His Asn Asp Arg Gly Thr Gly 275 280 285		
Val Gly Ala Ala Glu Leu Gly Tyr Met Ala Gly Ala Asp Arg Ile Glu 290 295 300		
Gly Cys Leu Phe Gly Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val 305 310 315 320		
Thr Leu Ala Leu Asn Met Leu Thr Gln Gly Val Asp Pro Gln Leu Asp 325 330 335		
Phe Thr Asp Ile Arg Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln 340 345 350		
Leu Arg Val Pro Glu Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr 355 360 365		
Ala Phe Ser Gly Ser His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala 370 375 380		
Met Ala Ala Lys Val Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp 385 390 395 400		
Glu Gln Leu Arg Asp Thr Arg Met Gly Gly Ser Leu Pro Ala Tyr Arg 405 410 415		
Ser Lys Gly Cys Arg Ser Arg Leu Arg Gly Cys Tyr Pro Arg Glu Leu 420 425 430		
Pro Val Arg Gln Gly Arg Arg Cys Leu His His Glu Asp Arg Ser Arg 435 440 445		
Ser Ala Asp Pro Ser Leu His Ala Gly 450 455		

<210> 275

<211> 1333

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1333)

<223> FRXA00536

<400> 275

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tcgtggaccc	acccaaaact	ttttaagaag	gttgaacaca	atg	tct	cct	aac	gat	115
				Met	Ser	Pro	Asn	Asp	
				1				5	
gca ttc atc tcc	gca cct gcc aag	atc gaa acc cca	gtt ggg cct cgc	163					
Ala Phe Ile Ser	Ala Pro Ala Lys	Ile Glu Thr Pro	Val Gly Pro Arg						
	10	15	20						
aac gaa ggc cag	cca gca tgg aat	aag cag cgt ggc	tcc tca atg cca	211					
Asn Glu Gly Gln	Pro Ala Trp Asn	Lys Gln Arg Gly	Ser Ser Met Pro						
	25	30	35						
gtt aac cgc tac	atg cct ttc gag	gtt gag gta gaa	gat att tct ctg	259					
Val Asn Arg Tyr	Met Pro Phe Glu	Val Glu Val Glu	Asp Ile Ser Leu						
	40	45	50						
ccg gac cgc act	tgg cca gat aaa	aaa atc acc gtt	gca cct cag tgg	307					
Pro Asp Arg Thr	Trp Pro Asp Lys	Lys Ile Thr Val	Ala Pro Gln Trp						
	55	60	65						
tgt gct gtt gac	ctg cgt gac ggc	aac cag gct ctg	att gat ccg atg	355					
Cys Ala Val Asp	Leu Arg Asp Gly	Asn Gln Ala Leu	Ile Asp Pro Met						
	70	75	80	85					
tct cct gag cgt	aag cgc cgc atg	ttt gag ctg ctg	gtt cag atg ggc	403					
Ser Pro Glu Arg	Lys Arg Arg Met	Phe Glu Leu Leu	Val Gln Met Gly						
	90	95	100						
ttc aaa gaa atc	gag gtc ggt ttc	cct tca gct tcc	cag act gat ttt	451					
Phe Lys Glu Ile	Glu Val Gly Phe	Pro Ser Ala Ser	Gln Thr Asp Phe						
	105	110	115						
gat ttc gtt cgt	gag atc atc gaa	aag ggc atg atc	cct gac gat gtc	499					
Asp Phe Val Arg	Glu Ile Ile Glu	Lys Gly Met Ile	Pro Asp Asp Val						
	120	125	130						
acc att cag gtt	ctg gtt cag gct	cgt gag cac ctg	att cgc cgt act	547					
Thr Ile Gln Val	Leu Val Gln Ala	Arg Glu His Leu	Ile Arg Arg Thr						
	135	140	145						
ttt gaa gct tgc	gaa ggc gca aaa	aac gtt atc gtg	cac ttc tac aac	595					
Phe Glu Ala Cys	Glu Gly Ala Lys	Asn Val Ile Val	His Phe Tyr Asn						
	150	155	160	165					
tcc acc tcc atc	ctg cag cgc aac	gtg gtg ttc cgc	atg gac aag gtg	643					
Ser Thr Ser Ile	Leu Gln Arg Asn	Val Val Phe Arg	Met Asp Lys Val						
	170	175	180						
cag gtg aag aag	ctg gct acc gat	gcc gct gaa cta	atc aag acc atc	691					
Gln Val Lys Lys	Leu Ala Thr Asp	Ala Ala Glu Leu	Ile Lys Thr Ile						
	185	190	195						
gct cag gat tac	cca gac acc aac	tgg cgc tgg cag	tac tcc cct gag	739					
Ala Gln Asp Tyr	Pro Asp Thr Asn	Trp Arg Trp Gln	Tyr Ser Pro Glu						
	200	205	210						
tcc ttc acc ggc	act gag gtt gag	tac gcc aag gaa	gtt gtg gac gca	787					
Ser Phe Thr Gly	Thr Glu Val Glu	Tyr Ala Lys Glu	Val Val Asp Ala						
	215	220	225						
gtt gtt gag gtc	atg gat cca act	cct gag aac cca	atg atc atc aac	835					

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Val Val Glu Val Met Asp Pro Thr Pro Glu Asn Pro Met Ile Ile Asn
230          235          240          245

ctg cct tcc acc gtt gag atg atc acc cct aac gtt tac gca gac tcc      883
Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn Val Tyr Ala Asp Ser
          250          255          260

att gaa tgg atg cac cgc aat cta aac cgt cgt gat tcc att atc ctg      931
Ile Glu Trp Met His Arg Asn Leu Asn Arg Arg Asp Ser Ile Ile Leu
          265          270          275

tcc ctg cac ccg cac aat gac cgt ggc acc ggc gtt ggc gca gct gag      979
Ser Leu His Pro His Asn Asp Arg Gly Thr Gly Val Gly Ala Ala Glu
          280          285          290

ctg ggc tac atg gct ggc gct gac cgc atc gaa ggc tgc ctg ttc ggc      1027
Leu Gly Tyr Met Ala Gly Ala Asp Arg Ile Glu Gly Cys Leu Phe Gly
          295          300          305

aac ggc gag cgc acc ggc aac gtc tgc ctg gtc acc ctg gca ctg aac      1075
Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val Thr Leu Ala Leu Asn
310          315          320          325

atg ctg acc cag ggc gtt gac cct cag ctg gac ttc acc gat ata cgc      1123
Met Leu Thr Gln Gly Val Asp Pro Gln Leu Asp Phe Thr Asp Ile Arg
          330          335          340

cag atc cgc agc acc gtt gaa tac tgc aac cag ctg cgc gtt cct gag      1171
Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln Leu Arg Val Pro Glu
          345          350          355

cgc cac cca tac ggc ggt gac ctg gtc ttc acc gct ttc tcc ggt tcc      1219
Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr Ala Phe Ser Gly Ser
          360          365          370

cac cag gac gct gtg aac aag ggt ctg gac gcc atg gct gcc aag gtt      1267
His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala Met Ala Ala Lys Val
          375          380          385

cag cca ggt gct agc tcc act gaa gtt tct tgg gag cag ctg cgc gac      1315
Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp Glu Gln Leu Arg Asp
390          395          400          405

acc gaa tgg gag gtt cct
Thr Glu Trp Glu Val Pro
          410

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<210> 276

<211> 411

<212> PRT

<213> Corynebacterium glutamicum

<400> 276

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Met Ser Pro Asn Asp Ala Phe Ile Ser Ala Pro Ala Lys Ile Glu Thr
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Pro Val Gly Pro Arg Asn Glu Gly Gln Pro Ala Trp Asn Lys Gln Arg
  20          25          30

Gly Ser Ser Met Pro Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val

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35					40					45						
Glu	Asp	Ile	Ser	Leu	Pro	Asp	Arg	Thr	Trp	Pro	Asp	Lys	Lys	Ile	Thr	
50					55					60						
Val	Ala	Pro	Gln	Trp	Cys	Ala	Val	Asp	Leu	Arg	Asp	Gly	Asn	Gln	Ala	
65					70					75					80	
Leu	Ile	Asp	Pro	Met	Ser	Pro	Glu	Arg	Lys	Arg	Arg	Met	Phe	Glu	Leu	
85					90					95						
Leu	Val	Gln	Met	Gly	Phe	Lys	Glu	Ile	Glu	Val	Gly	Phe	Pro	Ser	Ala	
100					105					110						
Ser	Gln	Thr	Asp	Phe	Asp	Phe	Val	Arg	Glu	Ile	Ile	Glu	Lys	Gly	Met	
115					120					125						
Ile	Pro	Asp	Asp	Val	Thr	Ile	Gln	Val	Leu	Val	Gln	Ala	Arg	Glu	His	
130					135					140						
Leu	Ile	Arg	Arg	Thr	Phe	Glu	Ala	Cys	Glu	Gly	Ala	Lys	Asn	Val	Ile	
145					150					155					160	
Val	His	Phe	Tyr	Asn	Ser	Thr	Ser	Ile	Leu	Gln	Arg	Asn	Val	Val	Phe	
165					170					175						
Arg	Met	Asp	Lys	Val	Gln	Val	Lys	Lys	Leu	Ala	Thr	Asp	Ala	Ala	Glu	
180					185					190						
Leu	Ile	Lys	Thr	Ile	Ala	Gln	Asp	Tyr	Pro	Asp	Thr	Asn	Trp	Arg	Trp	
195					200					205						
Gln	Tyr	Ser	Pro	Glu	Ser	Phe	Thr	Gly	Thr	Glu	Val	Glu	Tyr	Ala	Lys	
210					215					220						
Glu	Val	Val	Asp	Ala	Val	Val	Glu	Val	Met	Asp	Pro	Thr	Pro	Glu	Asn	
225					230					235					240	
Pro	Met	Ile	Ile	Asn	Leu	Pro	Ser	Thr	Val	Glu	Met	Ile	Thr	Pro	Asn	
245					250					255						
Val	Tyr	Ala	Asp	Ser	Ile	Glu	Trp	Met	His	Arg	Asn	Leu	Asn	Arg	Arg	
260					265					270						
Asp	Ser	Ile	Ile	Leu	Ser	Leu	His	Pro	His	Asn	Asp	Arg	Gly	Thr	Gly	
275					280					285						
Val	Gly	Ala	Ala	Glu	Leu	Gly	Tyr	Met	Ala	Gly	Ala	Asp	Arg	Ile	Glu	
290					295					300						
Gly	Cys	Leu	Phe	Gly	Asn	Gly	Glu	Arg	Thr	Gly	Asn	Val	Cys	Leu	Val	
305					310					315					320	
Thr	Leu	Ala	Leu	Asn	Met	Leu	Thr	Gln	Gly	Val	Asp	Pro	Gln	Leu	Asp	
325					330					335						
Phe	Thr	Asp	Ile	Arg	Gln	Ile	Arg	Ser	Thr	Val	Glu	Tyr	Cys	Asn	Gln	
340					345					350						
Leu	Arg	Val	Pro	Glu	Arg	His	Pro	Tyr	Gly	Gly	Asp	Leu	Val	Phe	Thr	
355					360					365						

Ala Phe Ser Gly Ser His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala
370 375 380

Met Ala Ala Lys Val Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp
385 390 395 400

Glu Gln Leu Arg Asp Thr Glu Trp Glu Val Pro
405 410

<210> 277

<211> 714

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(691)

<223> RXN02965

<400> 277

caggaggccg caccacactg gtatccccag cagtcgcagc cgccaccgaa tccgcggacc 60

ctgtcctcac ctgcagatat ctaaggaagg ctagaaaaca atg gaa aaa ttt acc 115
Met Glu Lys Phe Thr
1 5

acc tac acc ggc gtt ggc gtt cca ctg cag cga tcc aac gtg gac acc 163
Thr Tyr Thr Gly Val Gly Val Pro Leu Gln Arg Ser Asn Val Asp Thr
10 15 20

gac cag atc atc cca gcc gtc tac ctc aag cgc gtc acc cgg acc ggc 211
Asp Gln Ile Ile Pro Ala Val Tyr Leu Lys Arg Val Thr Arg Thr Gly
25 30 35

ttc gaa gac gga ctg ttt tcc aac tgg cgc caa aac gac ccc aac ttt 259
Phe Glu Asp Gly Leu Phe Ser Asn Trp Arg Gln Asn Asp Pro Asn Phe
40 45 50

gtc ctc aac acc gac acc tac aag aac ggc tcc gtt ctc gta gca ggc 307
Val Leu Asn Thr Asp Thr Tyr Lys Asn Gly Ser Val Leu Val Ala Gly
55 60 65

cct gac ttt ggc acc ggc tcc tcc cgc gag cac gcc gtc tgg gca ctc 355
Pro Asp Phe Gly Thr Gly Ser Ser Arg Glu His Ala Val Trp Ala Leu
70 75 80 85

atg gac tac ggc ttc cgc gct gtc ttc tcc tca cga ttc gcc gac atc 403
Met Asp Tyr Gly Phe Arg Ala Val Phe Ser Ser Arg Phe Ala Asp Ile
90 95 100

ttc cgc ggc aac tcc gga aaa gcg ggc atg ctc acc ggc atc atg gaa 451
Phe Arg Gly Asn Ser Gly Lys Ala Gly Met Leu Thr Gly Ile Met Glu
105 110 115

cag tcc gac atc gaa ctt ctg tgg aag ctc atg gaa caa acc cca ggc 499
Gln Ser Asp Ile Glu Leu Leu Trp Lys Leu Met Glu Gln Thr Pro Gly
120 125 130

ctc gaa ctg acc gtg aac ctg gaa aag cag atc gtc acc gca ggc gac 547

Leu Glu Leu Thr Val Asn Leu Glu Lys Gln Ile Val Thr Ala Gly Asp
 135 140 145
 gta gtg atc agc ttc gaa gtt gac ccc tac atc cgc tgg cgt ttg atg 595
 Val Val Ile Ser Phe Glu Val Asp Pro Tyr Ile Arg Trp Arg Leu Met
 150 155 160 165
 gaa ggc ctc gac gac gct ggc ctg acc ctg cgc aag ctc gat gaa att 643
 Glu Gly Leu Asp Asp Ala Gly Leu Thr Leu Arg Lys Leu Asp Glu Ile
 170 175 180
 gaa gac tac gag gct aag cgc cct gcg ttt aag cca cgc act aac gct 691
 Glu Asp Tyr Glu Ala Lys Arg Pro Ala Phe Lys Pro Arg Thr Asn Ala
 185 190 195
 taagtttcag tctgatagcg aaa 714

<210> 278

<211> 197

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 278

Met Glu Lys Phe Thr Thr Tyr Thr Gly Val Gly Val Pro Leu Gln Arg
 1 5 10 15
 Ser Asn Val Asp Thr Asp Gln Ile Ile Pro Ala Val Tyr Leu Lys Arg
 20 25 30
 Val Thr Arg Thr Gly Phe Glu Asp Gly Leu Phe Ser Asn Trp Arg Gln
 35 40 45
 Asn Asp Pro Asn Phe Val Leu Asn Thr Asp Thr Tyr Lys Asn Gly Ser
 50 55 60
 Val Leu Val Ala Gly Pro Asp Phe Gly Thr Gly Ser Ser Arg Glu His
 65 70 75 80
 Ala Val Trp Ala Leu Met Asp Tyr Gly Phe Arg Ala Val Phe Ser Ser
 85 90 95
 Arg Phe Ala Asp Ile Phe Arg Gly Asn Ser Gly Lys Ala Gly Met Leu
 100 105 110
 Thr Gly Ile Met Glu Gln Ser Asp Ile Glu Leu Leu Trp Lys Leu Met
 115 120 125
 Glu Gln Thr Pro Gly Leu Glu Leu Thr Val Asn Leu Glu Lys Gln Ile
 130 135 140
 Val Thr Ala Gly Asp Val Val Ile Ser Phe Glu Val Asp Pro Tyr Ile
 145 150 155 160
 Arg Trp Arg Leu Met Glu Gly Leu Asp Asp Ala Gly Leu Thr Leu Arg
 165 170 175
 Lys Leu Asp Glu Ile Glu Asp Tyr Glu Ala Lys Arg Pro Ala Phe Lys
 180 185 190
 Pro Arg Thr Asn Ala

195

<210> 279

<211> 936

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(913)

<223> RXN01929

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ggaatttatt tattctgagc tggatcatcac atctataactc atg ccc atg tca ggc 115
                      Met Pro Met Ser Gly
                      1           5

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att gat gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta 163
Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val
                      10           15           20

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aac ggc cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg 211
Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala
                      25           30           35

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cgc att ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc 259
Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser
                      40           45           50

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gct gcc aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg 307
Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu
                      55           60           65

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gat gag atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt 355
Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg
                      70           75           80           85

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gcg ctt gtg gtg gtt gat ctg ccg ttt ggt acc tat gag gtg agc cca 403
Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu Val Ser Pro
                      90           95           100

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aat cag gcg gtg gag tcc gcg atc cgg gtc atg cgt gaa acg ggt gcg 451
Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu Thr Gly Ala
                      105           110           115

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gct gcg gtg aag atc gag ggt ggc gtg gag atc gcg cag acg att cga 499
Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln Thr Ile Arg
                      120           125           130

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cgc att gtt gat gct gga att ccg gtt gtc ggc cac atc ggg tac acc 547
Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr
                      135           140           145

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ccg cag tcc gag cat tcc ttg ggc ggc cac gtg gtt cag ggt cgt ggc 595
Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly
                      150           155           160           165

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gcg agt tct gga aag ctc atc gcc gat gcc cgc gcg ttg gag cag gcg 643

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Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu Glu Gln Ala
 170 175 180

ggt gcg ttt gcg gtt gtg ttg gag atg gtt cca gca gag gca gcg cgc 691
 Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg
 185 190 195

gag gtt acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc 739
 Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly
 200 205 210

aat ggc aca gat ggg cag gtt ttg gtg tgg cag gat gcc ttc ggc ctc 787
 Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu
 215 220 225

aac cgc ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc 835
 Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala Thr Leu Gly
 230 235 240 245

gat tcc ttg cac gac gcc gcg cag gcc tac atc gcc gat atc cac gcg 883
 Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala
 250 255 260

ggt acc ttc cca ggc gaa gcg gag tcc ttt taatgcaggt agcaaccaca 933
 Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe
 265 270

aag 936

<210> 280
 <211> 271
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 280
 Met Pro Met Ser Gly Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe
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Arg Glu Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr
 20 25 30

Asp Ala Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu
 35 40 45

Leu Val Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr
 50 55 60

Leu Ser Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr
 65 70 75 80

Ile Ala Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr
 85 90 95

Tyr Glu Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met
 100 105 110

Arg Glu Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile
 115 120 125

Ala Gln Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly

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<210> 281
<211> 930
<212> DNA
<213> Corynebacterium glutamicum
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tattttattct gagctgggtca tcacatctat actcatgccc															115
Met Ser Gly Ile Asp															5
gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta aac ggc															163
Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val Asn Gly															20
cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg cgc att															211
Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala Arg Ile															35
ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc gct gcc															259
Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser Ala Ala															50
aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg gat gag															307
Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu Asp Glu															65
atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt gcg ctt															355

Met	Ile	Val	Leu	Ala	Lys	Ala	Val	Thr	Ile	Ala	Thr	Lys	Arg	Ala	Leu	
70					75					80					85	
gtg	gtg	gtt	gat	ctg	ccg	ttt	ggt	acc	tat	gag	gtg	agc	cca	aat	cag	403
Val	Val	Val	Asp	Leu	Pro	Phe	Gly	Thr	Tyr	Glu	Val	Ser	Pro	Asn	Gln	
				90					95					100		
gcg	gtg	gag	tcc	gcg	atc	cgg	gtc	atg	cgt	gaa	acg	ggt	gcg	gct	gcg	451
Ala	Val	Glu	Ser	Ala	Ile	Arg	Val	Met	Arg	Glu	Thr	Gly	Ala	Ala	Ala	
			105					110					115			
gtg	aag	atc	gag	ggt	ggc	gtg	gag	atc	gcg	cag	acg	att	cga	cgc	att	499
Val	Lys	Ile	Glu	Gly	Gly	Val	Glu	Ile	Ala	Gln	Thr	Ile	Arg	Arg	Ile	
	120						125					130				
gtt	gat	gct	gga	att	ccg	gtt	gtc	ggc	cac	atc	ggg	tac	acc	ccg	cag	547
Val	Asp	Ala	Gly	Ile	Pro	Val	Val	Gly	His	Ile	Gly	Tyr	Thr	Pro	Gln	
	135					140					145					
tcc	gag	cat	tcc	ttg	ggc	ggc	cac	gtg	gtt	cag	ggt	cgt	ggc	gcg	agt	595
Ser	Glu	His	Ser	Leu	Gly	Gly	His	Val	Val	Gln	Gly	Arg	Gly	Ala	Ser	
150					155					160					165	
tct	gga	aag	ctc	atc	gcc	gat	gcc	cgc	gcg	ttg	gag	cag	gcg	ggt	gcg	643
Ser	Gly	Lys	Leu	Ile	Ala	Asp	Ala	Arg	Ala	Leu	Glu	Gln	Ala	Gly	Ala	
			170					175						180		
ttt	gcg	gtt	gtg	ttg	gag	atg	gtt	cca	gca	gag	gca	gcg	cgc	gag	gtt	691
Phe	Ala	Val	Val	Leu	Glu	Met	Val	Pro	Ala	Glu	Ala	Ala	Arg	Glu	Val	
			185					190					195			
acc	gag	gat	ctt	tcc	atc	acc	act	atc	gga	atc	ggt	gcc	ggc	aat	ggc	739
Thr	Glu	Asp	Leu	Ser	Ile	Thr	Thr	Ile	Gly	Ile	Gly	Ala	Gly	Asn	Gly	
		200					205					210				
aca	gat	ggg	cag	gtt	ttg	gtg	tgg	cag	gat	gcc	ttc	ggc	ctc	aac	cgc	787
Thr	Asp	Gly	Gln	Val	Leu	Val	Trp	Gln	Asp	Ala	Phe	Gly	Leu	Asn	Arg	
	215					220					225					
ggc	aag	aag	cca	cgc	ttc	gtc	cgc	gag	tac	gcc	acc	ttg	ggc	gat	tcc	835
Gly	Lys	Lys	Pro	Arg	Phe	Val	Arg	Glu	Tyr	Ala	Thr	Leu	Gly	Asp	Ser	
230					235					240					245	
ttg	cac	gac	gcc	gcg	cag	gcc	tac	atc	gcc	gat	atc	cac	gcg	ggt	acc	883
Leu	His	Asp	Ala	Ala	Gln	Ala	Tyr	Ile	Ala	Asp	Ile	His	Ala	Gly	Thr	
			250					255						260		
ttc	cca	ggc	gaa	gcg	gag	tcc	ttt	taatgcaggt	agcaaccaca	aag						930
Phe	Pro	Gly	Glu	Ala	Glu	Ser	Phe									
			265													

<210> 282

<211> 269

<212> PRT

<213> Corynebacterium glutamicum

<400> 282

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gcggaatgcg	ctgctcatcc	acacgtggaa	tcctgattgg	gtg	acg	ctg	ggg	gga	115							
				Val	Thr	Leu	Gly	Gly								
				1				5								
ttg	aat	gta	cca	tcg	tgg	tcg	ctg	ggc	gcg	gaa	atg	ctg	ttc	tac	ctg	163
Leu	Asn	Val	Pro	Ser	Trp	Ser	Leu	Gly	Ala	Glu	Met	Leu	Phe	Tyr	Leu	
				10				15						20		
acg	ttc	ccg	ctg	ttt	att	ccg	tta	gtg	cgc	aaa	gtg	aag	ggc	gtg	ggc	211
Thr	Phe	Pro	Leu	Phe	Ile	Pro	Leu	Val	Arg	Lys	Val	Lys	Gly	Val	Gly	
			25					30					35			
aac	tgg	tgg	gca	ttt	ggc	atc	acc	ttt	gcc	gtg	agc	ctg	gcg	ctg	att	259
Asn	Trp	Trp	Ala	Phe	Gly	Ile	Thr	Phe	Ala	Val	Ser	Leu	Ala	Leu	Ile	
			40				45					50				
aca	gtg	att	cac	ttt	tat	gcg	gac	gga	cca	aag	ggg	att	gag	aac	ttc	307
Thr	Val	Ile	His	Phe	Tyr	Ala	Asp	Gly	Pro	Lys	Gly	Ile	Glu	Asn	Phe	
	55					60					65					
ttt	gtt	cct	cgc	ctg	tgg	gac	acc	aat	gtg	tca	ccg	gtc	gcg	gaa	gtt	355
Phe	Val	Pro	Arg	Leu	Trp	Asp	Thr	Asn	Val	Ser	Pro	Val	Ala	Glu	Val	
	70				75				80						85	
cac	gcc	gat	cca	gtg	tgg	ttt	atg	cag	gaa	gaa	att	ccc	gtg	ctg	gaa	403
His	Ala	Asp	Pro	Val	Trp	Phe	Met	Gln	Glu	Glu	Ile	Pro	Val	Leu	Glu	
			90					95						100		
tct	tac	tgg	ctg	tct	tac	tac	ttc	ccg	ctg	acc	aga	ctc	atc	gag	ttc	451
Ser	Tyr	Trp	Leu	Ser	Tyr	Tyr	Phe	Pro	Leu	Thr	Arg	Leu	Ile	Glu	Phe	
			105					110					115			
tac	ctc	ggg	gtg	ttt	ggc	gcg	aag	ctg	gtt	gct	gaa	ggc	atg	ttt	aaa	499
Tyr	Leu	Gly	Val	Phe	Gly	Ala	Lys	Leu	Val	Ala	Glu	Gly	Met	Phe	Lys	
	120					125						130				
aac	acc	aac	atc	acc	atc	ccg	ctg	atc	gca	ctg	gct	gtt	tct	ttt	gtt	547
Asn	Thr	Asn	Ile	Thr	Ile	Pro	Leu	Ile	Ala	Leu	Ala	Val	Ser	Phe	Val	
	135					140					145					
gct	act	tgg	ttt	gtg	cca	ctg	gca	ttc	aag	atg	tct	gtc	atc	atg	tcc	595
Ala	Thr	Trp	Phe	Val	Pro	Leu	Ala	Phe	Lys	Met	Ser	Val	Ile	Met	Ser	
	150				155				160						165	
ctg	cca	atg	gct	ttt	gtt	gtg	gca	acg	ctt	gcg	gtg	aga	gac	att	gaa	643
Leu	Pro	Met	Ala	Phe	Val	Val	Ala	Thr	Leu	Ala	Val	Arg	Asp	Ile	Glu	
				170					175					180		
ggc	aag	agt	ggg	gaa	atc	gcc	tcg	cct	cgc	gca	gtt	ttg	ttg	ggg	aat	691
Gly	Lys	Ser	Gly	Glu	Ile	Ala	Ser	Pro	Arg	Ala	Val	Leu	Leu	Gly	Asn	
			185				190						195			
att	tcc	ttt	gcc	ttc	tac	atg	gtg	caa	ttc	ccc	gtc	atg	gtg	ttt	gtg	739
Ile	Ser	Phe	Ala	Phe	Tyr	Met	Val	Gln	Phe	Pro	Val	Met	Val	Phe	Val	
		200					205					210				
cag	cgc	tat	ttc	att	gct	ggc	aaa	gaa	tac	ggc	ttc	ctt	ggc	tgg	gca	787
Gln	Arg	Tyr	Phe	Ile	Ala	Gly	Lys	Glu	Tyr	Gly	Phe	Leu	Gly	Trp	Ala	
	215					220					225					

ttc tat gca gtg gtg tgt ttc atc gtg tcg gtc att ctc gcg tgg gtg 835
 Phe Tyr Ala Val Val Cys Phe Ile Val Ser Val Ile Leu Ala Trp Val
 230 235 240 245

ctg ttt acc ttc gtt gat gat cct ttg atg aag gcc acg gcg cgc aag 883
 Leu Phe Thr Phe Val Asp Asp Pro Leu Met Lys Ala Thr Ala Arg Lys
 250 255 260

aag ggg agt agg cgc ttg aag cag tcc aat att ttg gtc cgt gac ctg 931
 Lys Gly Ser Arg Arg Leu Lys Gln Ser Asn Ile Leu Val Arg Asp Leu
 265 270 275

aaa gtt ctc ttc ggc aaa agc ccc gaa aag ccg tta aaa gtt gag act 979
 Lys Val Leu Phe Gly Lys Ser Pro Glu Lys Pro Leu Lys Val Glu Thr
 280 285 290

cgc gct gag aat ctc aca gaa aac tcc gaa gct ccc gct aag gta gct 1027
 Arg Ala Glu Asn Leu Thr Glu Asn Ser Glu Ala Pro Ala Lys Val Ala
 295 300 305

acc gga atc aaa tct tagggaagga aaacatatgg cta 1065
 Thr Gly Ile Lys Ser
 310

<210> 284
 <211> 314
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 284
 Val Thr Leu Gly Gly Leu Asn Val Pro Ser Trp Ser Leu Gly Ala Glu
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 Met Leu Phe Tyr Leu Thr Phe Pro Leu Phe Ile Pro Leu Val Arg Lys
 20 25 30
 Val Lys Gly Val Gly Asn Trp Trp Ala Phe Gly Ile Thr Phe Ala Val
 35 40 45
 Ser Leu Ala Leu Ile Thr Val Ile His Phe Tyr Ala Asp Gly Pro Lys
 50 55 60
 Gly Ile Glu Asn Phe Phe Val Pro Arg Leu Trp Asp Thr Asn Val Ser
 65 70 75 80
 Pro Val Ala Glu Val His Ala Asp Pro Val Trp Phe Met Gln Glu Glu
 85 90 95
 Ile Pro Val Leu Glu Ser Tyr Trp Leu Ser Tyr Tyr Phe Pro Leu Thr
 100 105 110
 Arg Leu Ile Glu Phe Tyr Leu Gly Val Phe Gly Ala Lys Leu Val Ala
 115 120 125
 Glu Gly Met Phe Lys Asn Thr Asn Ile Thr Ile Pro Leu Ile Ala Leu
 130 135 140
 Ala Val Ser Phe Val Ala Thr Trp Phe Val Pro Leu Ala Phe Lys Met
 145 150 155 160

Ser Val Ile Met Ser Leu Pro Met Ala Phe Val Val Ala Thr Leu Ala
 165 170 175
 Val Arg Asp Ile Glu Gly Lys Ser Gly Glu Ile Ala Ser Pro Arg Ala
 180 185 190
 Val Leu Leu Gly Asn Ile Ser Phe Ala Phe Tyr Met Val Gln Phe Pro
 195 200 205
 Val Met Val Phe Val Gln Arg Tyr Phe Ile Ala Gly Lys Glu Tyr Gly
 210 215 220
 Phe Leu Gly Trp Ala Phe Tyr Ala Val Val Cys Phe Ile Val Ser Val
 225 230 235 240
 Ile Leu Ala Trp Val Leu Phe Thr Phe Val Asp Asp Pro Leu Met Lys
 245 250 255
 Ala Thr Ala Arg Lys Lys Gly Ser Arg Arg Leu Lys Gln Ser Asn Ile
 260 265 270
 Leu Val Arg Asp Leu Lys Val Leu Phe Gly Lys Ser Pro Glu Lys Pro
 275 280 285
 Leu Lys Val Glu Thr Arg Ala Glu Asn Leu Thr Glu Asn Ser Glu Ala
 290 295 300
 Pro Ala Lys Val Ala Thr Gly Ile Lys Ser
 305 310

<210> 285

<211> 1137

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1114)

<223> RXS01145

<400> 285

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 cttttcacca aaattttttac gaaaggcgag attttctccc atg gct att gaa ctg 115
 Met Ala Ile Glu Leu
 1 5

 ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163
 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val
 10 15 20

 gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu
 25 30 35

 cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259
 Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys
 40 45 50

tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct 307

Ser	Ala	Glu	Lys	Ala	Lys	Glu	Ala	Gly	Phe	Glu	Val	Lys	Thr	Thr	Ala		
55						60					65						
gag	gct	gca	gct	tgg	gct	gac	gtc	atc	atg	ctc	ctg	gct	cca	gac	acc	355	
Glu	Ala	Ala	Ala	Trp	Ala	Asp	Val	Ile	Met	Leu	Leu	Ala	Pro	Asp	Thr	85	
70					75					80							
tcc	cag	gca	gaa	atc	ttc	acc	aac	gac	atc	gag	cca	aac	ctg	aac	gca	403	
Ser	Gln	Ala	Glu	Ile	Phe	Thr	Asn	Asp	Ile	Glu	Pro	Asn	Leu	Asn	Ala	100	
				90					95								
ggc	gac	gca	ctg	ctg	ttc	ggc	cac	ggc	ctg	aac	att	cac	ttc	gac	ctg	451	
Gly	Asp	Ala	Leu	Leu	Phe	Gly	His	Gly	Leu	Asn	Ile	His	Phe	Asp	Leu	115	
			105					110									
atc	aag	cca	gct	gac	gac	atc	atc	gtt	ggc	atg	gtt	gcg	cca	aag	ggc	499	
Ile	Lys	Pro	Ala	Asp	Asp	Ile	Ile	Val	Gly	Met	Val	Ala	Pro	Lys	Gly	130	
		120					125										
cca	ggc	cac	ttg	gtt	cgc	cgt	cag	ttc	gtt	gat	ggc	aag	ggt	gtt	cct	547	
Pro	Gly	His	Leu	Val	Arg	Arg	Gln	Phe	Val	Asp	Gly	Lys	Gly	Val	Pro	145	
	135					140											
tgc	ctc	atc	gca	gtc	gac	cag	gac	cca	acc	gga	acc	gca	cag	gct	ctg	595	
Cys	Leu	Ile	Ala	Val	Asp	Gln	Asp	Pro	Thr	Gly	Thr	Ala	Gln	Ala	Leu	165	
	150				155					160							
acc	ctg	tcc	tac	gca	gca	gca	atc	ggc	ggc	gca	cgc	gca	ggc	gtt	atc	643	
Thr	Leu	Ser	Tyr	Ala	Ala	Ala	Ile	Gly	Gly	Ala	Arg	Ala	Gly	Val	Ile	180	
				170					175								
cca	acc	acc	ttc	gaa	gct	gag	acc	gtc	acc	gac	ctc	ttc	ggc	gag	cag	691	
Pro	Thr	Thr	Phe	Glu	Ala	Glu	Thr	Val	Thr	Asp	Leu	Phe	Gly	Glu	Gln	195	
			185					190									
gct	gtt	ctc	tgc	ggc	ggc	acc	gag	gaa	ctg	gtc	aag	gtt	ggc	ttc	gag	739	
Ala	Val	Leu	Cys	Gly	Gly	Thr	Glu	Glu	Leu	Val	Lys	Val	Gly	Phe	Glu	210	
		200					205										
gtt	ctc	acc	gaa	gct	ggc	tac	gag	cca	gag	atg	gca	tac	ttc	gag	gtt	787	
Val	Leu	Thr	Glu	Ala	Gly	Tyr	Glu	Pro	Glu	Met	Ala	Tyr	Phe	Glu	Val	225	
	215					220					225						
ctt	cac	gag	ctc	aag	ctc	atc	gtt	gac	ctc	atg	ttc	gaa	ggt	ggc	atc	835	
Leu	His	Glu	Leu	Lys	Leu	Ile	Val	Asp	Leu	Met	Phe	Glu	Gly	Gly	Ile	245	
	230				235					240							
agc	aac	atg	aac	tac	tct	gtt	tct	gac	acc	gct	gag	ttc	ggt	ggc	tac	883	
Ser	Asn	Met	Asn	Tyr	Ser	Val	Ser	Asp	Thr	Ala	Glu	Phe	Gly	Gly	Tyr	260	
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ctc	tcc	ggc	cca	cgc	gtc	atc	gat	gca	gac	acc	aag	tcc	cgc	atg	aag	931	
Leu	Ser	Gly	Pro	Arg	Val	Ile	Asp	Ala	Asp	Thr	Lys	Ser	Arg	Met	Lys	275	
			265					270									
gac	atc	ctg	acc	gat	atc	cag	gac	ggc	acc	ttc	acc	aag	cgc	ctc	atc	979	
Asp	Ile	Leu	Thr	Asp	Ile	Gln	Asp	Gly	Thr	Phe	Thr	Lys	Arg	Leu	Ile	290	
		280					285										
gca	aac	gtt	gag	aac	ggc	aac	acc	gag	ctt	gag	ggc	ctt	cgt	gct	tcc	1027	
Ala	Asn	Val	Glu	Asn	Gly	Asn	Thr	Glu	Leu	Glu	Gly	Leu	Arg	Ala	Ser		

295 300 305
 tac aac aac cac cca atc gag gag acc ggc gct aag ctc cgc gac ctc 1075
 Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala Lys Leu Arg Asp Leu
 310 315 320 325

 atg agc tgg gtc aag gtt gac gct cgc gca gaa acc gct taagtttcac 1124
 Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu Thr Ala
 330 335

 ccctttgacg gct 1137

 <210> 286
 <211> 338
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 286
 Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile
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 Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala
 20 25 30

 His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu
 35 40 45

 Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu
 50 55 60

 Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu
 65 70 75 80

 Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu
 85 90 95

 Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn
 100 105 110

 Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met
 115 120 125

 Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp
 130 135 140

 Gly Lys Gly Val Pro Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly
 145 150 155 160

 Thr Ala Gln Ala Leu Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala
 165 170 175

 Arg Ala Gly Val Ile Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp
 180 185 190

 Leu Phe Gly Glu Gln Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val
 195 200 205

 Lys Val Gly Phe Glu Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met
 210 215 220

Ala Tyr Phe Glu Val Leu His Glu Leu Lys Leu Ile Val Asp Leu Met
 225 230 235 240

Phe Glu Gly Gly Ile Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala
 245 250 255

Glu Phe Gly Gly Tyr Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr
 260 265 270

Lys Ser Arg Met Lys Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe
 275 280 285

Thr Lys Arg Leu Ile Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu
 290 295 300

Gly Leu Arg Ala Ser Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala
 305 310 315 320

Lys Leu Arg Asp Leu Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu
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Thr Ala

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 <213> Corynebacterium glutamicum

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 <223> FRXA01145

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 Met Ala Ile Glu Leu
 1 5

ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163
 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val
 10 15 20

gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu
 25 30 35

cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259
 Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys
 40 45 50

tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct 307
 Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala
 55 60 65

gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc 355
 Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr
 70 75 80 85

tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca 403
 Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala
 90 95 100

ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg 451
 Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu
 105 110 115

atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc 499
 Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly
 120 125 130

cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct 547
 Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro
 135 140 145

tgc ctc atc 556
 Cys Leu Ile
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<210> 288

<211> 152

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 288

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Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala
 20 25 30

His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu
 35 40 45

Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu
 50 55 60

Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu
 65 70 75 80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu
 85 90 95

Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn
 100 105 110

Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met
 115 120 125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp
 130 135 140

Gly Lys Gly Val Pro Cys Leu Ile
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<210> 289

<211> 1350

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1327)

<223> RXA02375

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aagcggttcga ttacgggata atctcccaac gccaacccaa atg gcg ccg gtg aca 115
Met Ala Pro Val Thr
1 5

ggg ctt cct gtc acc ccc tac agc cag gaa gca agc atc ggt gcg agc 163
Gly Leu Pro Val Thr Pro Tyr Ser Gln Glu Ala Ser Ile Gly Ala Ser
10 15 20

ttc ccg gca gtg gat ccg gac acc aaa gac agc gcc gca tac gga cat 211
Phe Pro Ala Val Asp Pro Asp Thr Lys Asp Ser Ala Ala Tyr Gly His
25 30 35

gaa tcc gga atg cgt gag cgc atc tcc aac gct aag cga gtg gtg gtg 259
Glu Ser Gly Met Arg Glu Arg Ile Ser Asn Ala Lys Arg Val Val Val
40 45 50

aaa att ggt tcg tcc tca ttg act aac gat gag gac gga cac acc gtc 307
Lys Ile Gly Ser Ser Ser Leu Thr Asn Asp Glu Asp Gly His Thr Val
55 60 65

gat ccc aac cgc atc aac act att gtc aat gcc ttg caa gca cgc atg 355
Asp Pro Asn Arg Ile Asn Thr Ile Val Asn Ala Leu Gln Ala Arg Met
70 75 80 85

gaa gct ggc tcg gac ctc atc gtt gtg tcc tct ggc gca gtg gcc gcg 403
Glu Ala Gly Ser Asp Leu Ile Val Val Ser Ser Gly Ala Val Ala Ala
90 95 100

gga atg gcc ccg ctt gga ttg agc acc cgg ccc acg gaa ttg gca gtc 451
Gly Met Ala Pro Leu Gly Leu Ser Thr Arg Pro Thr Glu Leu Ala Val
105 110 115

aag cag gct gca gca gca gtg ggg caa gtt cac ctc atg cac cag tgg 499
Lys Gln Ala Ala Ala Val Gly Gln Val His Leu Met His Gln Trp
120 125 130

gga cgt tct ttt gcc cgg tat ggt cgc ccc atc ggc cag gtg ctt ctt 547
Gly Arg Ser Phe Ala Arg Tyr Gly Arg Pro Ile Gly Gln Val Leu Leu
135 140 145

acc gca gct gat gca gga aag cgt gat cgt gcg agg aat gcg cag cgt 595
Thr Ala Ala Asp Ala Gly Lys Arg Asp Arg Ala Arg Asn Ala Gln Arg
150 155 160 165

acc atc gac aag ctg cgc att ttg ggc gcg gtt cct atc gtc aat gaa 643
Thr Ile Asp Lys Leu Arg Ile Leu Gly Ala Val Pro Ile Val Asn Glu
170 175 180

aat gac acc gtg gca acc acc ggt gtg aat ttt ggt gac aac gac cga 691
Asn Asp Thr Val Ala Thr Thr Gly Val Asn Phe Gly Asp Asn Asp Arg

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185					190					195					
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Leu Ala Ala Ile Val Ala His Leu Val Ser Ala Asp Ala Leu Val Leu															
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ctc agt gac gtg gat gga ctt ttt gat aaa aac cct act gat ccc acc	787														
Leu Ser Asp Val Asp Gly Leu Phe Asp Lys Asn Pro Thr Asp Pro Thr															
215 220 225															
gcg aag ttt att tcc gag gtt cgt gac ggc aat gat ttg aaa ggt gtc	835														
Ala Lys Phe Ile Ser Glu Val Arg Asp Gly Asn Asp Leu Lys Gly Val															
230 235 240 245															
att gcc ggc gac ggc gga aaa gtg ggc acc ggt ggc atg gca tca aag	883														
Ile Ala Gly Asp Gly Gly Lys Val Gly Thr Gly Gly Met Ala Ser Lys															
250 255 260															
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Val Ser Ala Ala Arg Leu Ala Ser Arg Ser Gly Val Pro Val Leu Leu															
265 270 275															
acc tct gcg gca aac att ggc cca gca ctg gaa gac gcc cag gtg ggc	979														
Thr Ser Ala Ala Asn Ile Gly Pro Ala Leu Glu Asp Ala Gln Val Gly															
280 285 290															
act gta ttc cac ccc aag gac aac cgc ctc tcc gcg tgg aag ttc tgg	1027														
Thr Val Phe His Pro Lys Asp Asn Arg Leu Ser Ala Trp Lys Phe Trp															
295 300 305															
gct ttg tat gcc gca gat act gca gga aag atc cga ctc gat gac ggc	1075														
Ala Leu Tyr Ala Ala Asp Thr Ala Gly Lys Ile Arg Leu Asp Asp Gly															
310 315 320 325															
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Ala Val Glu Ala Val Thr Ser Gly Gly Lys Ser Leu Leu Ala Val Gly															
330 335 340															
att act gaa atc att ggt gat ttc cag cag ggt gag atc gtg gag atc	1171														
Ile Thr Glu Ile Ile Gly Asp Phe Gln Gln Gly Glu Ile Val Glu Ile															
345 350 355															
ttg gga cct gcc ggc caa atc atc ggg cga ggc gag gtg tcc tac gat	1219														
Leu Gly Pro Ala Gly Gln Ile Ile Gly Arg Gly Glu Val Ser Tyr Asp															
360 365 370															
tct gat acc ttg caa tca atg gtt ggt atg caa acg cag gac ctt cca	1267														
Ser Asp Thr Leu Gln Ser Met Val Gly Met Gln Thr Gln Asp Leu Pro															
375 380 385															
gat ggc atg cag cgc ccg gta gtg cat gca gat tat ctg tcc aac tac	1315														
Asp Gly Met Gln Arg Pro Val Val His Ala Asp Tyr Leu Ser Asn Tyr															
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Ala Ser Arg Ala															

<210> 290

<211> 409

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 290

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Ser Ile Gly Ala Ser Phe Pro Ala Val Asp Pro Asp Thr Lys Asp Ser
          20              25              30

Ala Ala Tyr Gly His Glu Ser Gly Met Arg Glu Arg Ile Ser Asn Ala
          35              40              45

Lys Arg Val Val Val Lys Ile Gly Ser Ser Ser Leu Thr Asn Asp Glu
          50              55              60

Asp Gly His Thr Val Asp Pro Asn Arg Ile Asn Thr Ile Val Asn Ala
          65              70              75              80

Leu Gln Ala Arg Met Glu Ala Gly Ser Asp Leu Ile Val Val Ser Ser
          85              90              95

Gly Ala Val Ala Ala Gly Met Ala Pro Leu Gly Leu Ser Thr Arg Pro
          100              105              110

Thr Glu Leu Ala Val Lys Gln Ala Ala Ala Val Gly Gln Val His
          115              120              125

Leu Met His Gln Trp Gly Arg Ser Phe Ala Arg Tyr Gly Arg Pro Ile
          130              135              140

Gly Gln Val Leu Leu Thr Ala Ala Asp Ala Gly Lys Arg Asp Arg Ala
          145              150              155              160

Arg Asn Ala Gln Arg Thr Ile Asp Lys Leu Arg Ile Leu Gly Ala Val
          165              170              175

Pro Ile Val Asn Glu Asn Asp Thr Val Ala Thr Thr Gly Val Asn Phe
          180              185              190

Gly Asp Asn Asp Arg Leu Ala Ala Ile Val Ala His Leu Val Ser Ala
          195              200              205

Asp Ala Leu Val Leu Leu Ser Asp Val Asp Gly Leu Phe Asp Lys Asn
          210              215              220

Pro Thr Asp Pro Thr Ala Lys Phe Ile Ser Glu Val Arg Asp Gly Asn
          225              230              235              240

Asp Leu Lys Gly Val Ile Ala Gly Asp Gly Gly Lys Val Gly Thr Gly
          245              250              255

Gly Met Ala Ser Lys Val Ser Ala Ala Arg Leu Ala Ser Arg Ser Gly
          260              265              270

Val Pro Val Leu Leu Thr Ser Ala Ala Asn Ile Gly Pro Ala Leu Glu
          275              280              285

Asp Ala Gln Val Gly Thr Val Phe His Pro Lys Asp Asn Arg Leu Ser
          290              295              300

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Ala Trp Lys Phe Trp Ala Leu Tyr Ala Ala Asp Thr Ala Gly Lys Ile
 305 310 315 320

Arg Leu Asp Asp Gly Ala Val Glu Ala Val Thr Ser Gly Gly Lys Ser
 325 330 335

Leu Leu Ala Val Gly Ile Thr Glu Ile Ile Gly Asp Phe Gln Gln Gly
 340 345 350

Glu Ile Val Glu Ile Leu Gly Pro Ala Gly Gln Ile Ile Gly Arg Gly
 355 360 365

Glu Val Ser Tyr Asp Ser Asp Thr Leu Gln Ser Met Val Gly Met Gln
 370 375 380

Thr Gln Asp Leu Pro Asp Gly Met Gln Arg Pro Val Val His Ala Asp
 385 390 395 400

Tyr Leu Ser Asn Tyr Ala Ser Arg Ala
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> RXN02382

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 Met Ser Ser Thr Thr
 1 5

cta act gat gac caa att cgc gac aat gag cgg acc gaa gtt cta gct 163
 Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg Thr Glu Val Leu Ala
 10 15 20

aaa gca act gca gct aag aac atc gtc ccg gat att gca gtg ttg ggc 211
 Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp Ile Ala Val Leu Gly
 25 30 35

acc gga ccg aag aac gca atc ctg cgt gcg gcg gca gat gaa ctc gtt 259
 Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala Ala Asp Glu Leu Val
 40 45 50

gca cgc agc gca gaa atc atc gaa gcc aac gct tcc gat atc gaa gcg 307
 Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala Ser Asp Ile Glu Ala
 55 60 65

ggt cgc gca aac ggc atg gaa gaa tcc atg att gat cgc ctt gcc ctt 355
 Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile Asp Arg Leu Ala Leu
 70 75 80 85

gat gaa tct cgc att gag ggc atc gct ggc ggt ttg cgc cag gtt gct 403
 Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly Leu Arg Gln Val Ala

90								95				100					
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Gly	Leu	Thr	Asp	Pro	Val	Gly	Glu	Val	Leu	Arg	Gly	His	Val	Met	Glu		
105				110				115									
aac	ggc	att	cag	atg	aag	cag	gtc	cgt	gtg	cct	ttg	ggc	gtg	atg	ggc	499	
Asn	Gly	Ile	Gln	Met	Lys	Gln	Val	Arg	Val	Pro	Leu	Gly	Val	Met	Gly		
120				125				130									
atg	gtc	tat	gaa	gcc	cgc	cct	aac	gtc	acc	gtc	gac	gcc	ttc	ggc	ctg	547	
Met	Val	Tyr	Glu	Ala	Arg	Pro	Asn	Val	Thr	Val	Asp	Ala	Phe	Gly	Leu		
135				140				145									
gca	ctc	aag	tcc	gga	aac	gta	gct	ttg	ctg	cgc	ggt	tcc	tcc	aca	gct	595	
Ala	Leu	Lys	Ser	Gly	Asn	Val	Ala	Leu	Leu	Arg	Gly	Ser	Ser	Thr	Ala		
150				155				160				165					
gtg	cat	tcc	aac	acc	aag	ctc	gtg	gaa	atc	ctg	cag	gac	gtc	ctc	gag	643	
Val	His	Ser	Asn	Thr	Lys	Leu	Val	Glu	Ile	Leu	Gln	Asp	Val	Leu	Glu		
170				175				180									
cgt	ttc	gag	ctg	cca	cgc	gaa	acc	gtg	cag	ttg	ctg	cct	tgc	caa	acc	691	
Arg	Phe	Glu	Leu	Pro	Arg	Glu	Thr	Val	Gln	Leu	Leu	Pro	Cys	Gln	Thr		
185				190				195									
cgc	gga	tcc	gtc	caa	gat	ttg	atc	acc	gca	cgc	ggc	ctc	gtt	gac	gtg	739	
Arg	Gly	Ser	Val	Gln	Asp	Leu	Ile	Thr	Ala	Arg	Gly	Leu	Val	Asp	Val		
200				205				210									
gtc	atc	cca	cgc	ggc	ggc	gca	gga	cta	atc	aac	gca	gtg	gtc	acc	ggt	787	
Val	Ile	Pro	Arg	Gly	Gly	Ala	Gly	Leu	Ile	Asn	Ala	Val	Val	Thr	Gly		
215				220				225									
gcg	acc	gtg	ccc	acc	att	gaa	acc	ggc	acc	ggc	aac	tgc	cac	ttc	tac	835	
Ala	Thr	Val	Pro	Thr	Ile	Glu	Thr	Gly	Thr	Gly	Asn	Cys	His	Phe	Tyr		
230				235				240				245					
atc	gat	gcc	gaa	gcc	aag	ctt	gat	cag	gca	atc	gcc	atg	gtc	atc	aac	883	
Ile	Asp	Ala	Glu	Ala	Lys	Leu	Asp	Gln	Ala	Ile	Ala	Met	Val	Ile	Asn		
250				255				260									
ggc	aag	acc	cgc	cgc	tgc	agc	gtg	tgc	aac	gct	act	gaa	acc	gcg	ctt	931	
Gly	Lys	Thr	Arg	Arg	Cys	Ser	Val	Cys	Asn	Ala	Thr	Glu	Thr	Ala	Leu		
265				270				275									
ctc	gac	gcc	gcc	ctc	agc	gac	tca	gac	aag	ctt	gca	gtc	gtc	cag	gcg	979	
Leu	Asp	Ala	Ala	Leu	Ser	Asp	Ser	Asp	Lys	Leu	Ala	Val	Val	Gln	Ala		
280				285				290									
ctc	cag	gaa	gca	gga	gtc	aca	att	cat	gga	cgg	gtg	gcc	gaa	ttg	gaa	1027	
Leu	Gln	Glu	Ala	Gly	Val	Thr	Ile	His	Gly	Arg	Val	Ala	Glu	Leu	Glu		
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Ala	Phe	Gly	Ala	Thr	Asp	Val	Val	Glu	Ala	Thr	Glu	Thr	Asp	Trp	Asp		
310				315				320				325					
tct	gag	tac	ctg	tcc	ttc	gat	atc	gct	gtc	gct	gtg	gtt	gac	ggt	gtg	1123	
Ser	Glu	Tyr	Leu	Ser	Phe	Asp	Ile	Ala	Val	Ala	Val	Val	Asp	Gly	Val		
330				335				340									

gat gga gct ctg gca cac atc gct aag tac agc acc aag cac acc gaa 1171
 Asp Gly Ala Leu Ala His Ile Ala Lys Tyr Ser Thr Lys His Thr Glu
 345 350 355

gcg atc gcc acc caa aac att gaa acc gct cag cgc ttt gca gat cgc 1219
 Ala Ile Ala Thr Gln Asn Ile Glu Thr Ala Gln Arg Phe Ala Asp Arg
 360 365 370

gtc gat gca gca gcg gtg atg ata aac gca tcc acc gcc tac acc gat 1267
 Val Asp Ala Ala Ala Val Met Ile Asn Ala Ser Thr Ala Tyr Thr Asp
 375 380 385

ggg gag cag tac ggc atg ggc gcg gag atc ggc att tcc acc cag aaa 1315
 Gly Glu Gln Tyr Gly Met Gly Ala Glu Ile Gly Ile Ser Thr Gln Lys
 390 395 400 405

ctg cat gca cgt gga cca atg gcc ctg cca gag ctg acc tcc acc aag 1363
 Leu His Ala Arg Gly Pro Met Ala Leu Pro Glu Leu Thr Ser Thr Lys
 410 415 420

tgg att ctg cag ggc aca gga caa att agg cct taagtttgaa gaagtaatca 1416
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agc 1419

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<211> 432

<212> PRT

<213> Corynebacterium glutamicum

<400> 292

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 20 25 30

Ile Ala Val Leu Gly Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala
 35 40 45

Ala Asp Glu Leu Val Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala
 50 55 60

Ser Asp Ile Glu Ala Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile
 65 70 75 80

Asp Arg Leu Ala Leu Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly
 85 90 95

Leu Arg Gln Val Ala Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg
 100 105 110

Gly His Val Met Glu Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro
 115 120 125

Leu Gly Val Met Gly Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val
 130 135 140

Asp Ala Phe Gly Leu Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg
 145 150 155 160
 Gly Ser Ser Thr Ala Val His Ser Asn Thr Lys Leu Val Glu Ile Leu
 165 170 175
 Gln Asp Val Leu Glu Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu
 180 185 190
 Leu Pro Cys Gln Thr Arg Gly Ser Val Gln Asp Leu Ile Thr Ala Arg
 195 200 205
 Gly Leu Val Asp Val Val Ile Pro Arg Gly Gly Ala Gly Leu Ile Asn
 210 215 220
 Ala Val Val Thr Gly Ala Thr Val Pro Thr Ile Glu Thr Gly Thr Gly
 225 230 235 240
 Asn Cys His Phe Tyr Ile Asp Ala Glu Ala Lys Leu Asp Gln Ala Ile
 245 250 255
 Ala Met Val Ile Asn Gly Lys Thr Arg Arg Cys Ser Val Cys Asn Ala
 260 265 270
 Thr Glu Thr Ala Leu Leu Asp Ala Ala Leu Ser Asp Ser Asp Lys Leu
 275 280 285
 Ala Val Val Gln Ala Leu Gln Glu Ala Gly Val Thr Ile His Gly Arg
 290 295 300
 Val Ala Glu Leu Glu Ala Phe Gly Ala Thr Asp Val Val Glu Ala Thr
 305 310 315 320
 Glu Thr Asp Trp Asp Ser Glu Tyr Leu Ser Phe Asp Ile Ala Val Ala
 325 330 335
 Val Val Asp Gly Val Asp Gly Ala Leu Ala His Ile Ala Lys Tyr Ser
 340 345 350
 Thr Lys His Thr Glu Ala Ile Ala Thr Gln Asn Ile Glu Thr Ala Gln
 355 360 365
 Arg Phe Ala Asp Arg Val Asp Ala Ala Ala Val Met Ile Asn Ala Ser
 370 375 380
 Thr Ala Tyr Thr Asp Gly Glu Gln Tyr Gly Met Gly Ala Glu Ile Gly
 385 390 395 400
 Ile Ser Thr Gln Lys Leu His Ala Arg Gly Pro Met Ala Leu Pro Glu
 405 410 415
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 420 425 430

<210> 293

<211> 724

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(709)

<223> FRXA02378

<400> 293

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Met Ser Ser Thr Thr
1 5

cta act gat gac caa att cgc gac aat gag cgg acc gaa gtt cta gct 163
Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg Thr Glu Val Leu Ala
10 15 20

aaa gca act gca gct aag aac atc gtc ccg gat att gca gtg ttg ggc 211
Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp Ile Ala Val Leu Gly
25 30 35

acc gga ccg aag aac gca atc ctg cgt gcg gcg gca gat gaa ctc gtt 259
Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala Ala Asp Glu Leu Val
40 45 50

gca cgc agc gca gaa atc atc gaa gcc aac gct tcc gat atc gaa gcg 307
Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala Ser Asp Ile Glu Ala
55 60 65

ggc cgc gca aac ggc atg gaa gaa tcc atg att gat cgc ctt gcc ctt 355
Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile Asp Arg Leu Ala Leu
70 75 80 85

gat gaa tct cgc att gag ggc atc gct ggc ggt ttg cgc cag gtt gct 403
Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly Leu Arg Gln Val Ala
90 95 100

ggc ctg acc gac cca gtg ggt gaa gta ctg cgc gga cat gtc atg gaa 451
Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg Gly His Val Met Glu
105 110 115

aac ggc att cag atg aag cag gtc cgt gtg cct ttg ggc gtg atg ggc 499
Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro Leu Gly Val Met Gly
120 125 130

atg gtc tat gaa gcc cgc cct aac gtc acc gtc gac gcc ttc ggc ctg 547
Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val Asp Ala Phe Gly Leu
135 140 145

gca ctc aag tcc gga aac gta gct ttg ctg cgc ggt tcc tcc aca gct 595
Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg Gly Ser Ser Thr Ala
150 155 160 165

gtg cat tcc aac acc aag ctc gtg gaa atc ctg cag gac gta ctc gag 643
Val His Ser Asn Thr Lys Leu Val Glu Ile Leu Gln Asp Val Leu Glu
170 175 180

cgt ttc gag ctg cca cgc gaa acc gtg cag ttg ctg ctt gcc aaa ccc 691
Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu Leu Leu Ala Lys Pro
185 190 195

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gcg gat ccg tcc aag att tgatcacgg acgcg
 Ala Asp Pro Ser Lys Ile
 200

724

<210> 294

<211> 203

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 294

Met Ser Ser Thr Thr Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg
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Thr Glu Val Leu Ala Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp
 20 25 30

Ile Ala Val Leu Gly Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala
 35 40 45

Ala Asp Glu Leu Val Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala
 50 55 60

Ser Asp Ile Glu Ala Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile
 65 70 75 80

Asp Arg Leu Ala Leu Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly
 85 90 95

Leu Arg Gln Val Ala Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg
 100 105 110

Gly His Val Met Glu Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro
 115 120 125

Leu Gly Val Met Gly Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val
 130 135 140

Asp Ala Phe Gly Leu Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg
 145 150 155 160

Gly Ser Ser Thr Ala Val His Ser Asn Thr Lys Leu Val Glu Ile Leu
 165 170 175

Gln Asp Val Leu Glu Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu
 180 185 190

Leu Leu Ala Lys Pro Ala Asp Pro Ser Lys Ile
 195 200

<210> 295

<211> 623

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(600)

<223> FRXA02382

<400> 295

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Pro Thr Ile Glu Thr Gly Thr Gly Asn Cys His Phe Tyr Ile Asp Ala
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gaa gcc aag ctt gat cag gca atc gcc atg gtc atc aac ggc aag acc 96
Glu Ala Lys Leu Asp Gln Ala Ile Ala Met Val Ile Asn Gly Lys Thr
             20             25             30

cgc cgc tgc agc gtg tgc aac gct act gaa acc gcg ctt ctc gac gcc 144
Arg Arg Cys Ser Val Cys Asn Ala Thr Glu Thr Ala Leu Leu Asp Ala
             35             40             45

gcc ctc agc gac tca gac aag ctt gca gtc gtc cag gcg ctc cag gaa 192
Ala Leu Ser Asp Ser Asp Lys Leu Ala Val Val Gln Ala Leu Gln Glu
             50             55             60

gca gga gtc aca att cat gga cgg gtg gcc gaa ttg gaa gca ttc ggt 240
Ala Gly Val Thr Ile His Gly Arg Val Ala Glu Leu Glu Ala Phe Gly
             65             70             75             80

gca acc gac gtg gtg gaa gca act gaa act gac tgg gat tct gag tac 288
Ala Thr Asp Val Val Glu Ala Thr Glu Thr Asp Trp Asp Ser Glu Tyr
             85             90             95

ctg tcc ttc gat atc gct gtc gct gtg gtt gac ggt gtg gat gga gct 336
Leu Ser Phe Asp Ile Ala Val Ala Val Val Asp Gly Val Asp Gly Ala
             100             105             110

ctg gca cac atc gct aag tac agc acc aag cac acc gaa gcg atc gcc 384
Leu Ala His Ile Ala Lys Tyr Ser Thr Lys His Thr Glu Ala Ile Ala
             115             120             125

acc caa aac att gaa acc gct cag cgc ttt gca gat cgc gtc gat gca 432
Thr Gln Asn Ile Glu Thr Ala Gln Arg Phe Ala Asp Arg Val Asp Ala
             130             135             140

gca gcg gtg atg ata aac gca tcc acc gcc tac acc gat ggg gag cag 480
Ala Ala Val Met Ile Asn Ala Ser Thr Ala Tyr Thr Asp Gly Glu Gln
             145             150             155             160

tac ggc atg ggc gcg gag atc ggc att tcc acc cag aaa ctg cat gca 528
Tyr Gly Met Gly Ala Glu Ile Gly Ile Ser Thr Gln Lys Leu His Ala
             165             170             175

cgt gga cca atg gcc ctg cca gag ctg acc tcc acc aag tgg att ctg 576
Arg Gly Pro Met Ala Leu Pro Glu Leu Thr Ser Thr Lys Trp Ile Leu
             180             185             190

cag ggc aca gga caa att agg cct taagtttgaa gaagtaatca agc 623
Gln Gly Thr Gly Gln Ile Arg Pro
             195             200

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<210> 296

<211> 200

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 296

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 Glu Ala Lys Leu Asp Gln Ala Ile Ala Met Val Ile Asn Gly Lys Thr
 20 25 30
 Arg Arg Cys Ser Val Cys Asn Ala Thr Glu Thr Ala Leu Leu Asp Ala
 35 40 45
 Ala Leu Ser Asp Ser Asp Lys Leu Ala Val Val Gln Ala Leu Gln Glu
 50 55 60
 Ala Gly Val Thr Ile His Gly Arg Val Ala Glu Leu Glu Ala Phe Gly
 65 70 75 80
 Ala Thr Asp Val Val Glu Ala Thr Glu Thr Asp Trp Asp Ser Glu Tyr
 85 90 95
 Leu Ser Phe Asp Ile Ala Val Ala Val Val Asp Gly Val Asp Gly Ala
 100 105 110
 Leu Ala His Ile Ala Lys Tyr Ser Thr Lys His Thr Glu Ala Ile Ala
 115 120 125
 Thr Gln Asn Ile Glu Thr Ala Gln Arg Phe Ala Asp Arg Val Asp Ala
 130 135 140
 Ala Ala Val Met Ile Asn Ala Ser Thr Ala Tyr Thr Asp Gly Glu Gln
 145 150 155 160
 Tyr Gly Met Gly Ala Glu Ile Gly Ile Ser Thr Gln Lys Leu His Ala
 165 170 175
 Arg Gly Pro Met Ala Leu Pro Glu Leu Thr Ser Thr Lys Trp Ile Leu
 180 185 190
 Gln Gly Thr Gly Gln Ile Arg Pro
 195 200

<210> 297

<211> 933

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(910)

<223> RXA02499

<400> 297

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ctgctgcaaa acaggggtgg ttagtggcag tgtgggaacc atg aca aca att gct 115
 Met Thr Thr Ile Ala
 1 5

gta atc ggc ggc gga caa atc ggc gag gct tta gtc tca ggt ttg atc 163
 Val Ile Gly Gly Gly Gln Ile Gly Glu Ala Leu Val Ser Gly Leu Ile
 10 15 20

gcg gcc aac atg aat cca caa aat att cgc gtc acc aac cgt tcg gaa	211
Ala Ala Asn Met Asn Pro Gln Asn Ile Arg Val Thr Asn Arg Ser Glu	
25 30 35	
gag cgc ggc caa gag ctg cgt gac cgc tac ggc atc ctc aac atg acg	259
Glu Arg Gly Gln Glu Leu Arg Asp Arg Tyr Gly Ile Leu Asn Met Thr	
40 45 50	
gat aat tcc caa gcc gca gac gaa gcc gac gtg gtg ttc ctg tgc gtg	307
Asp Asn Ser Gln Ala Ala Asp Glu Ala Asp Val Val Phe Leu Cys Val	
55 60 65	
aag ccg aaa ttt atc gtc gaa gtg ctc tcc gaa atc acc ggc act ttg	355
Lys Pro Lys Phe Ile Val Glu Val Leu Ser Glu Ile Thr Gly Thr Leu	
70 75 80 85	
gat aac aac tcc gca caa agt gtt gtg gtc agc atg gcc gca ggc atc	403
Asp Asn Asn Ser Ala Gln Ser Val Val Ser Met Ala Ala Gly Ile	
90 95 100	
agc atc gct gcc atg gaa gaa agc gcc tct gcg ggg ctc ccc gtc gtg	451
Ser Ile Ala Ala Met Glu Glu Ser Ala Ser Ala Gly Leu Pro Val Val	
105 110 115	
cgc gtc atg ccg aac act cca atg ctc gtg ggc aag ggc atg tcg act	499
Arg Val Met Pro Asn Thr Pro Met Leu Val Gly Lys Gly Met Ser Thr	
120 125 130	
gtc acc aaa ggc cgc tac gtt gac gcg gaa cag ttg gaa caa gtc aag	547
Val Thr Lys Gly Arg Tyr Val Asp Ala Glu Gln Leu Glu Gln Val Lys	
135 140 145	
gac ttg ttg agc acc gtt gga gac gtc ctc gaa gtc gcg gaa tca gac	595
Asp Leu Leu Ser Thr Val Gly Asp Val Leu Glu Val Ala Glu Ser Asp	
150 155 160 165	
atc gac gca gtc acc gcg atg tcc gga tcc tcc cct gca tac ctg ttc	643
Ile Asp Ala Val Thr Ala Met Ser Gly Ser Ser Pro Ala Tyr Leu Phe	
170 175 180	
ctt gtg acc gaa gcg ctc att gag gca gga gtt aat cta ggc ctg ccc	691
Leu Val Thr Glu Ala Leu Ile Glu Ala Gly Val Asn Leu Gly Leu Pro	
185 190 195	
cgc gcg acc gct aaa aag ctc gct gtg gcc tca ttc gaa ggt gct gca	739
Arg Ala Thr Ala Lys Lys Leu Ala Val Ala Ser Phe Glu Gly Ala Ala	
200 205 210	
acc atg atg aag gaa acc ggc aaa gaa ccc tca gaa ttg cgc gca ggc	787
Thr Met Met Lys Glu Thr Gly Lys Glu Pro Ser Glu Leu Arg Ala Gly	
215 220 225	
gtt tcc tca ccc gca ggc acc acc gtc gca gcc atc cga gaa ctc gaa	835
Val Ser Ser Pro Ala Gly Thr Thr Val Ala Ala Ile Arg Glu Leu Glu	
230 235 240 245	
gaa agc gga atc cga ggc gct ttc tac cgc gca gcc caa gct tgc gcc	883
Glu Ser Gly Ile Arg Gly Ala Phe Tyr Arg Ala Ala Gln Ala Cys Ala	
250 255 260	
gac cga tct gaa gaa ctc gga aag cgc tagaaaccgt tatttccccg	930

Asp Arg Ser Glu Glu Leu Gly Lys Arg
265 270

tta

933

<210> 298

<211> 270

<212> PRT

<213> Corynebacterium glutamicum

<400> 298

Met Thr Thr Ile Ala Val Ile Gly Gly Gly Gln Ile Gly Glu Ala Leu
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Val Ser Gly Leu Ile Ala Ala Asn Met Asn Pro Gln Asn Ile Arg Val
20 25 30

Thr Asn Arg Ser Glu Glu Arg Gly Gln Glu Leu Arg Asp Arg Tyr Gly
35 40 45

Ile Leu Asn Met Thr Asp Asn Ser Gln Ala Ala Asp Glu Ala Asp Val
50 55 60

Val Phe Leu Cys Val Lys Pro Lys Phe Ile Val Glu Val Leu Ser Glu
65 70 75 80

Ile Thr Gly Thr Leu Asp Asn Asn Ser Ala Gln Ser Val Val Val Ser
85 90 95

Met Ala Ala Gly Ile Ser Ile Ala Ala Met Glu Glu Ser Ala Ser Ala
100 105 110

Gly Leu Pro Val Val Arg Val Met Pro Asn Thr Pro Met Leu Val Gly
115 120 125

Lys Gly Met Ser Thr Val Thr Lys Gly Arg Tyr Val Asp Ala Glu Gln
130 135 140

Leu Glu Gln Val Lys Asp Leu Leu Ser Thr Val Gly Asp Val Leu Glu
145 150 155 160

Val Ala Glu Ser Asp Ile Asp Ala Val Thr Ala Met Ser Gly Ser Ser
165 170 175

Pro Ala Tyr Leu Phe Leu Val Thr Glu Ala Leu Ile Glu Ala Gly Val
180 185 190

Asn Leu Gly Leu Pro Arg Ala Thr Ala Lys Lys Leu Ala Val Ala Ser
195 200 205

Phe Glu Gly Ala Ala Thr Met Met Lys Glu Thr Gly Lys Glu Pro Ser
210 215 220

Glu Leu Arg Ala Gly Val Ser Ser Pro Ala Gly Thr Thr Val Ala Ala
225 230 235 240

Ile Arg Glu Leu Glu Glu Ser Gly Ile Arg Gly Ala Phe Tyr Arg Ala
245 250 255

Ala Gln Ala Cys Ala Asp Arg Ser Glu Glu Leu Gly Lys Arg

270

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<222> (101)..(1273)  
<223> RXS02157
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caccgttttt agaaaagacg acaaggatgg ggaactgtaa atg agc acg ctg gaa 115																
Met Ser Thr Leu Glu 5																
act tgg cca cag gtc att att aat acg tac ggc acc cca cca gtt gag 163																
Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly Thr Pro Pro Val Glu 20																
ctg gtg tcc ggc aag ggc gca acc gtc act gat gac cag ggc aat gtc 211																
Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp Asp Gln Gly Asn Val 35																
tac atc gac ttg ctc gcg ggc atc gca gtc aac gcg ttg ggc cac gcc 259																
Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn Ala Leu Gly His Ala 50																
cac ccg gcg atc atc gag gcg gtc acc aac cag atc ggc caa ctt ggt 307																
His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln Ile Gly Gln Leu Gly 65																
cac gtc tca aac ttg ttc gca tcc agg ccc gtc gtc gag gtc gcc gag 355																
His Val Ser Asn Leu Phe Ala Ser Arg Pro Val Val Glu Val Ala Glu 85																
gag ctc atc aag cgt ttt tcg ctt gac gac gcc acc ctc gcc gcg caa 403																
Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala Thr Leu Ala Ala Gln 100																
acc cgg gtt ttc ttc tgc aac tcg ggc gcc gaa gca aac gag gct gct 451																
Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu Ala Asn Glu Ala Ala 115																
ttc aag att gca cgc ttg act ggt cgt tcc cgg att ctg gct gca gtt 499																
Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg Ile Leu Ala Ala Val 130																
cat ggt ttc cac ggc cgc acc atg ggt tcc ctc gcg ctg act ggc cag 547																
His Gly Phe His Gly Arg Thr Met Gly Ser Leu Ala Leu Thr Gly Gln 145																
cca gac aag cgt gaa gcg ttc ctg cca atg cca agc ggt gtg gag ttc 595																
Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro Ser Gly Val Glu Phe 165																
tac cct tac ggc gac acc gat tac ttg cgc aaa atg gta gaa acc aac 643																

Tyr	Pro	Tyr	Gly	Asp	Thr	Asp	Tyr	Leu	Arg	Lys	Met	Val	Glu	Thr	Asn	
				170					175					180		
cca	acg	gat	gtg	gct	gct	atc	ttc	ctc	gag	cca	atc	cag	ggt	gaa	acg	691
Pro	Thr	Asp	Val	Ala	Ala	Ile	Phe	Leu	Glu	Pro	Ile	Gln	Gly	Glu	Thr	
			185					190					195			
ggc	gtt	gtt	cca	gca	cct	gaa	gga	ttc	ctc	aag	gca	gtg	cgc	gag	ctg	739
Gly	Val	Val	Pro	Ala	Pro	Glu	Gly	Phe	Leu	Lys	Ala	Val	Arg	Glu	Leu	
			200				205					210				
tgc	gat	gag	tac	ggc	atc	ttg	atg	atc	acc	gat	gaa	gtc	cag	act	ggc	787
Cys	Asp	Glu	Tyr	Gly	Ile	Leu	Met	Ile	Thr	Asp	Glu	Val	Gln	Thr	Gly	
	215					220					225					
gtt	ggc	cgt	acc	ggc	gat	ttc	ttt	gca	cat	cag	cac	gat	ggc	gtt	gtt	835
Val	Gly	Arg	Thr	Gly	Asp	Phe	Phe	Ala	His	Gln	His	Asp	Gly	Val	Val	
	230				235					240					245	
ccc	gat	gtg	gtg	acc	atg	gcc	aag	gga	ctt	ggc	ggc	ggt	ctt	ccc	atc	883
Pro	Asp	Val	Val	Thr	Met	Ala	Lys	Gly	Leu	Gly	Gly	Gly	Leu	Pro	Ile	
				250				255						260		
ggt	gct	tgt	ttg	gcc	act	ggc	cgt	gca	gct	gaa	ttg	atg	acc	cca	ggc	931
Gly	Ala	Cys	Leu	Ala	Thr	Gly	Arg	Ala	Ala	Glu	Leu	Met	Thr	Pro	Gly	
			265					270					275			
aag	cac	ggc	acc	act	ttc	ggt	ggc	aac	cca	gtt	gct	tgt	gca	gct	gcc	979
Lys	His	Gly	Thr	Thr	Phe	Gly	Gly	Asn	Pro	Val	Ala	Cys	Ala	Ala	Ala	
		280					285					290				
aag	gca	gtg	ctg	tct	gtt	gtc	gat	gac	gct	ttc	tgc	gca	gaa	gtt	gcc	1027
Lys	Ala	Val	Leu	Ser	Val	Val	Asp	Asp	Ala	Phe	Cys	Ala	Glu	Val	Ala	
		295				300					305					
cgc	aag	ggc	gag	ctg	ttc	aag	gaa	ctt	ctt	gcc	aag	gtt	gac	ggc	gtt	1075
Arg	Lys	Gly	Glu	Leu	Phe	Lys	Glu	Leu	Leu	Ala	Lys	Val	Asp	Gly	Val	
	310				315					320					325	
gta	gac	gtc	cgt	ggc	agg	ggc	ttg	atg	ttg	ggc	gtg	gtg	ctg	gag	cgc	1123
Val	Asp	Val	Arg	Gly	Arg	Gly	Leu	Met	Leu	Gly	Val	Val	Leu	Glu	Arg	
				330					335					340		
gac	gtc	gca	aag	caa	gct	gtt	ctt	gat	ggc	ttt	aag	cac	ggc	gtt	att	1171
Asp	Val	Ala	Lys	Gln	Ala	Val	Leu	Asp	Gly	Phe	Lys	His	Gly	Val	Ile	
			345					350					355			
ttg	aat	gca	ccg	gcg	gac	aac	att	atc	cgt	ttg	acc	ccg	ccg	ctg	gtg	1219
Leu	Asn	Ala	Pro	Ala	Asp	Asn	Ile	Ile	Arg	Leu	Thr	Pro	Pro	Leu	Val	
		360				365						370				
atc	acc	gac	gaa	gaa	atc	gca	gac	gca	gtc	aag	gct	att	gcc	gag	aca	1267
Ile	Thr	Asp	Glu	Glu	Ile	Ala	Asp	Ala	Val	Lys	Ala	Ile	Ala	Glu	Thr	
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atc	gca	taaaggactc	aaacttatga	ctt												1296
Ile	Ala															
	390															

<210> 300

<211> 391

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 300

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Met Ser Thr Leu Glu Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly
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Thr Pro Pro Val Glu Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp
          20           25           30

Asp Gln Gly Asn Val Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn
          35           40           45

Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln
  50           55           60

Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val
  65           70           75           80

Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala
          85           90           95

Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu
          100          105          110

Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg
          115          120          125

Ile Leu Ala Ala Val His Gly Phe His Gly Arg Thr Met Gly Ser Leu
          130          135          140

Ala Leu Thr Gly Gln Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro
          145          150          155          160

Ser Gly Val Glu Phe Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys
          165          170          175

Met Val Glu Thr Asn Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro
          180          185          190

Ile Gln Gly Glu Thr Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys
          195          200          205

Ala Val Arg Glu Leu Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp
          210          215          220

Glu Val Gln Thr Gly Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln
          225          230          235          240

His Asp Gly Val Val Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly
          245          250          255

Gly Gly Leu Pro Ile Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu
          260          265          270

Leu Met Thr Pro Gly Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val
          275          280          285

Ala Cys Ala Ala Ala Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe
          290          295          300

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Cys Ala Glu Val Ala Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala
 305 310 315 320
 Lys Val Asp Gly Val Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly
 325 330 335
 Val Val Leu Glu Arg Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe
 340 345 350
 Lys His Gly Val Ile Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu
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 Thr Pro Pro Leu Val Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys
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 Ala Ile Ala Glu Thr Ile Ala
 385 390

<210> 301
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 <213> Corynebacterium glutamicum

<220>
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 <223> RXS02262

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 Met Thr Ala Thr Tyr
 1 5
 acc act gaa acc gcc atc aat ttc ttg ttc ttg agc gaa ccg gac atg 163
 Thr Thr Glu Thr Ala Ile Asn Phe Leu Phe Leu Ser Glu Pro Asp Met
 10 15 20
 atc gcg gcc gga gtc aaa gac gtc gcg caa tgc gtc gat gtc atg gag 211
 Ile Ala Ala Gly Val Lys Asp Val Ala Gln Cys Val Asp Val Met Glu
 25 30 35
 gaa acg ctc gtg ctc ttg gcg cag ggc gac tac aaa atg gcc ggt ttg 259
 Glu Thr Leu Val Leu Leu Ala Gln Gly Asp Tyr Lys Met Ala Gly Leu
 40 45 50
 aac tcc aac tcg cat ggc gcg atg atc acc ttc ccg gaa aac cca gaa 307
 Asn Ser Asn Ser His Gly Ala Met Ile Thr Phe Pro Glu Asn Pro Glu
 55 60 65
 ttt gaa ggc atg ccc aag gac ggc ccc gac cgc cga ttc atg gcg atg 355
 Phe Glu Gly Met Pro Lys Asp Gly Pro Asp Arg Arg Phe Met Ala Met
 70 75 80 85
 ccc gca tac ctc ggc ggg cga ttc aaa aac acc ggc gtg aag tgg tac 403
 Pro Ala Tyr Leu Gly Gly Arg Phe Lys Asn Thr Gly Val Lys Trp Tyr
 90 95 100

gga tcc aac gcg gaa aac aag gcc tca ggc ttg cct cgc tcg atc cac	451
Gly Ser Asn Ala Glu Asn Lys Ala Ser Gly Leu Pro Arg Ser Ile His	
105 110 115	
acc ttc gtc ctc aac gac acg gtc acc ggt gca ccg aag gcc atc atg	499
Thr Phe Val Leu Asn Asp Thr Val Thr Gly Ala Pro Lys Ala Ile Met	
120 125 130	
tcc gcg aac ctg ctg tcc gcc tac cgc acc ggc gcg gtt ccc ggc gtg	547
Ser Ala Asn Leu Leu Ser Ala Tyr Arg Thr Gly Ala Val Pro Gly Val	
135 140 145	
ggc gtg aag cac tta gcg gtc gcc gac gcg aca acc ttg gct gtc gtc	595
Gly Val Lys His Leu Ala Val Ala Asp Ala Thr Thr Leu Ala Val Val	
150 155 160 165	
gga cct ggt gtc atg gcg aaa acc atc acc gaa gcg tgc atc gca gag	643
Gly Pro Gly Val Met Ala Lys Thr Ile Thr Glu Ala Cys Ile Ala Glu	
170 175 180	
cgc cca gga atc acc acc atc aag atc aag gga cgc agc gaa cgc ggc	691
Arg Pro Gly Ile Thr Thr Ile Lys Ile Lys Gly Arg Ser Glu Arg Gly	
185 190 195	
atc aac gcc ttt gca aca tgg gcg ttg gaa aaa ttc ccc gag atc gaa	739
Ile Asn Ala Phe Ala Thr Trp Ala Leu Glu Lys Phe Pro Glu Ile Glu	
200 205 210	
gtg gtc gcc gtc gga tct gaa gaa gac gtg gtc aaa gac gcc gac atc	787
Val Val Ala Val Gly Ser Glu Glu Asp Val Val Lys Asp Ala Asp Ile	
215 220 225	
gtc atc gcc gcc acc acc acg gac gcc gcc ggc tcc tcc gcc ttc cca	835
Val Ile Ala Ala Thr Thr Thr Asp Ala Ala Gly Ser Ser Ala Phe Pro	
230 235 240 245	
tac ttc aaa aaa gaa tgg ctc aag ccg ggc gca ttg ctg ctg ctt cca	883
Tyr Phe Lys Lys Glu Trp Leu Lys Pro Gly Ala Leu Leu Leu Leu Pro	
250 255 260	
gcc gcc ggt cgc ttc gac gac gct tat ttg ctt gac gac gcc cgc ctc	931
Ala Ala Gly Arg Phe Asp Asp Ala Tyr Leu Leu Asp Asp Ala Arg Leu	
265 270 275	
gtt gtt gac tac atg ggg ctc tac gaa gcc tgg gca gaa gaa tac ggc	979
Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp Ala Glu Glu Tyr Gly	
280 285 290	
cca cag gcc tac caa cta ctc ggc att cca gga acc cac tgg tac gac	1027
Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly Thr His Trp Tyr Asp	
295 300 305	
ctg gcg ctg caa gga aaa ctc gac ctt gca aag att tcc cag att ggc	1075
Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys Ile Ser Gln Ile Gly	
310 315 320 325	
gat atc tgc tcc ggc aag cta ccc gga cgc acc aac gat gag gaa atc	1123
Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr Asn Asp Glu Glu Ile	
330 335 340	
atc ctc tat tcc gtc ggc ggc atg cca gta gaa gac gtc gcc tgg gca	1171

Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu Asp Val Ala Trp Ala
 345 350 355

acc caa gtg tat gaa aac gcc ctg gaa aaa ggc gtc ggc acc aca ttg 1219
 Thr Gln Val Tyr Glu Asn Ala Leu Glu Lys Gly Val Gly Thr Thr Leu
 360 365 370

aac ctg tgg gaa tca ccc gca ctg gct tgagagaaga aacaacaatg 1266
 Asn Leu Trp Glu Ser Pro Ala Leu Ala
 375 380

aaa 1269

<210> 302

<211> 382

<212> PRT

<213> Corynebacterium glutamicum

<400> 302

Met Thr Ala Thr Tyr Thr Thr Glu Thr Ala Ile Asn Phe Leu Phe Leu
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Ser Glu Pro Asp Met Ile Ala Ala Gly Val Lys Asp Val Ala Gln Cys
 20 25 30

Val Asp Val Met Glu Glu Thr Leu Val Leu Leu Ala Gln Gly Asp Tyr
 35 40 45

Lys Met Ala Gly Leu Asn Ser Asn Ser His Gly Ala Met Ile Thr Phe
 50 55 60

Pro Glu Asn Pro Glu Phe Glu Gly Met Pro Lys Asp Gly Pro Asp Arg
 65 70 75 80

Arg Phe Met Ala Met Pro Ala Tyr Leu Gly Gly Arg Phe Lys Asn Thr
 85 90 95

Gly Val Lys Trp Tyr Gly Ser Asn Ala Glu Asn Lys Ala Ser Gly Leu
 100 105 110

Pro Arg Ser Ile His Thr Phe Val Leu Asn Asp Thr Val Thr Gly Ala
 115 120 125

Pro Lys Ala Ile Met Ser Ala Asn Leu Leu Ser Ala Tyr Arg Thr Gly
 130 135 140

Ala Val Pro Gly Val Gly Val Lys His Leu Ala Val Ala Asp Ala Thr
 145 150 155 160

Thr Leu Ala Val Val Gly Pro Gly Val Met Ala Lys Thr Ile Thr Glu
 165 170 175

Ala Cys Ile Ala Glu Arg Pro Gly Ile Thr Thr Ile Lys Ile Lys Gly
 180 185 190

Arg Ser Glu Arg Gly Ile Asn Ala Phe Ala Thr Trp Ala Leu Glu Lys
 195 200 205

Phe Pro Glu Ile Glu Val Val Ala Val Gly Ser Glu Glu Asp Val Val
 210 215 220

Lys Asp Ala Asp Ile Val Ile Ala Ala Thr Thr Thr Asp Ala Ala Gly
 225 230 235 240
 Ser Ser Ala Phe Pro Tyr Phe Lys Lys Glu Trp Leu Lys Pro Gly Ala
 245 250 255
 Leu Leu Leu Leu Pro Ala Ala Gly Arg Phe Asp Asp Ala Tyr Leu Leu
 260 265 270
 Asp Asp Ala Arg Leu Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp
 275 280 285
 Ala Glu Glu Tyr Gly Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly
 290 295 300
 Thr His Trp Tyr Asp Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys
 305 310 315 320
 Ile Ser Gln Ile Gly Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr
 325 330 335
 Asn Asp Glu Glu Ile Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu
 340 345 350
 Asp Val Ala Trp Ala Thr Gln Val Tyr Glu Asn Ala Leu Glu Lys Gly
 355 360 365
 Val Gly Thr Thr Leu Asn Leu Trp Glu Ser Pro Ala Leu Ala
 370 375 380

<210> 303

<211> 1491

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1468)

<223> RXS02970

<400> 303

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ttatttaaag acttcataat attttgggga gtgaactggt ttg gca ttg aag ggt 115
 Leu Ala Leu Lys Gly
 1 5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
 Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
 10 15 20

aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
 Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
 25 30 35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
 His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
 40 45 50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac	307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp	
55 60 65	
atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga	355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg	
70 75 80 85	
tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac	403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn	
90 95 100	
ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg	451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val	
105 110 115	
tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc	499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly	
120 125 130	
gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga	547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly	
135 140 145	
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga	595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly	
150 155 160 165	
tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc	643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr	
170 175 180	
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc	691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
185 190 195	
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys	
200 205 210	
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
215 220 225	
atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca	835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
230 235 240 245	
gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc	883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile	
250 255 260	
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa	931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys	
265 270 275	
ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc	979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile	
280 285 290	
acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc	1027

Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile
 295 300 305
 gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc 1075
 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser
 310 315 320 325
 ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag 1123
 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys
 330 335 340
 gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct 1171
 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala
 345 350 355
 cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa 1219
 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu
 360 365 370
 gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca 1267
 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala
 375 380 385
 gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa 1315
 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu
 390 395 400 405
 ttc aag gaa cgc ggc gtg tgg ccg atg atc tcc ggc aac cga ttc cac 1363
 Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His
 410 415 420
 atc gcg ccg ccg ctg acc acc act gat gac gaa ttg gta gca ctg ctg 1411
 Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu
 425 430 435
 gac gcg gtg gaa gct gca gcc caa gct gtc gag ctg acc ttc gct ggg 1459
 Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu Leu Thr Phe Ala Gly
 440 445 450
 gcg ttg ttc taagttttct agataacaag gcc 1491
 Ala Leu Phe
 455

<210> 304

<211> 456

<212> PRT

<213> Corynebacterium glutamicum

<400> 304

Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe
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Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp
 20 25 30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
 35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
 50 55 60

Asn	Ala	Phe	Ile	Asp	Met	Gly	Ser	Gln	Leu	Val	Ser	Ala	Asn	Leu	Gly	65	70	75	80
His	Asn	Asn	Pro	Arg	Leu	Val	Glu	Ala	Ile	Gln	Arg	Gln	Ala	Ala	Arg	85	90		95
Leu	Thr	Asn	Ile	Asn	Pro	Ala	Phe	Gly	Asn	Asp	Val	Arg	Ser	Asp	Val	100	105		110
Ala	Ala	Lys	Ile	Val	Ser	Met	Ala	Arg	Gly	Glu	Phe	Ser	His	Val	Phe	115	120		125
Phe	Thr	Asn	Gly	Gly	Ala	Asp	Ala	Ile	Glu	His	Ser	Ile	Arg	Met	Ala	130	135		140
Arg	Leu	His	Thr	Gly	Arg	Asn	Lys	Ile	Leu	Ser	Ala	Tyr	Arg	Ser	Tyr	145	150	155	160
His	Gly	Ala	Thr	Gly	Ser	Ala	Met	Met	Leu	Thr	Gly	Glu	His	Arg	Arg	165	170		175
Leu	Gly	Asn	Pro	Thr	Thr	Asp	Pro	Asp	Ile	Tyr	His	Phe	Trp	Ala	Pro	180	185		190
Phe	Leu	His	His	Ser	Ser	Phe	Phe	Ala	Thr	Thr	Gln	Glu	Glu	Glu	Cys	195	200		205
Glu	Arg	Ala	Leu	Lys	His	Leu	Glu	Asp	Val	Ile	Ala	Phe	Glu	Gly	Ala	210	215		220
Gly	Met	Ile	Ala	Ala	Ile	Val	Leu	Glu	Pro	Val	Val	Gly	Ser	Ser	Gly	225	230	235	240
Ile	Ile	Leu	Pro	Pro	Ala	Gly	Tyr	Leu	Asn	Gly	Val	Arg	Glu	Leu	Cys	245	250		255
Asn	Lys	His	Gly	Ile	Leu	Phe	Ile	Ala	Asp	Glu	Val	Met	Val	Gly	Phe	260	265		270
Gly	Arg	Thr	Gly	Lys	Leu	Phe	Ala	Tyr	Glu	His	Ala	Gly	Asp	Asp	Phe	275	280		285
Gln	Pro	Asp	Met	Ile	Thr	Phe	Ala	Lys	Gly	Val	Asn	Ala	Gly	Tyr	Ala	290	295	300	
Pro	Leu	Gly	Gly	Ile	Val	Met	Thr	Gln	Ser	Ile	Arg	Asp	Thr	Phe	Gly	305	310	315	320
Ser	Glu	Ala	Tyr	Ser	Gly	Gly	Leu	Thr	Tyr	Ser	Gly	His	Pro	Leu	Ala	325	330		335
Val	Ala	Pro	Ala	Lys	Ala	Ala	Leu	Glu	Ile	Tyr	Ala	Glu	Gly	Glu	Ile	340	345		350
Ile	Pro	Arg	Val	Ala	Arg	Leu	Gly	Ala	Glu	Leu	Ile	Glu	Pro	Arg	Leu	355	360		365
Arg	Glu	Leu	Ala	Glu	Glu	Asn	Val	Ala	Ile	Ala	Asp	Val	Arg	Gly	Ile	370	375	380	

Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala
 385 390 395 400

Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser
 405 410 415

Gly Asn Arg Phe His Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu
 420 425 430

Leu Val Ala Leu Leu Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu
 435 440 445

Leu Thr Phe Ala Gly Ala Leu Phe
 450 455

<210> 305

<211> 1330

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1330)

<223> FRXA01009

<400> 305

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ttatttaaag acttcataat attttgggga gtgaactggg ttg gca ttg aag ggt 115
 Leu Ala Leu Lys Gly
 1 5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
 Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
 10 15 20

aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
 Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
 25 30 35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
 His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
 40 45 50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
 Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
 55 60 65

atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355
 Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
 70 75 80 85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
 Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
 90 95 100

ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
 Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
 105 110 115

tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc	499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly	
120 125 130	
gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga	547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly	
135 140 145	
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga	595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly	
150 155 160 165	
tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc	643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr	
170 175 180	
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc	691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
185 190 195	
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys	
200 205 210	
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
215 220 225	
atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca	835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
230 235 240 245	
gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc	883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile	
250 255 260	
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa	931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys	
265 270 275	
ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc	979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile	
280 285 290	
acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc	1027
Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile	
295 300 305	
gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc	1075
Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser	
310 315 320 325	
ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag	1123
Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys	
330 335 340	
gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct	1171
Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala	
345 350 355	
cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa	1219

Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu
 360 365 370

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca 1267
 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala
 375 380 385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa 1315
 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu
 390 395 400 405

ttc aag gaa cgc ggc 1330
 Phe Lys Glu Arg Gly
 410

<210> 306

<211> 410

<212> PRT

<213> Corynebacterium glutamicum

<400> 306

Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe
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Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp
 20 25 30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
 35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
 50 55 60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
 65 70 75 80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
 85 90 95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
 100 105 110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
 115 120 125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
 130 135 140

Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
 145 150 155 160

His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
 165 170 175

Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
 180 185 190

Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
 195 200 205

Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
 210 215 220
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
 225 230 235 240
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
 245 250 255
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
 260 265 270
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
 275 280 285
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
 290 295 300
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
 305 310 315 320
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
 325 330 335
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
 340 345 350
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
 355 360 365
 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
 370 375 380
 Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala
 385 390 395 400
 Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly
 405 410

<210> 307

<211> 3579

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(3556)

<223> RXN00023

<400> 307

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 gaaacggcac ccacaccgct gatcttgaag gagaaccacc atg acg tcg atg aat 115
 Met Thr Ser Met Asn
 1 5

 ctg cct att gag ttg gct acg ctg tct gac cag gct gtg gac aag gtg 163
 Leu Pro Ile Glu Leu Ala Thr Leu Ser Asp Gln Ala Val Asp Lys Val
 10 15 20

cgc tcc tgg ctg gag tac agc aaa aag gaa agc gtg ccc aat gcc gat	211
Arg Ser Trp Leu Glu Tyr Ser Lys Lys Glu Ser Val Pro Asn Ala Asp	
25 30 35	
gcg aag cgt cta gct gca gtg ttg cag gat cct aat ggt ttg gaa ttc	259
Ala Lys Arg Leu Ala Ala Val Leu Gln Asp Pro Asn Gly Leu Glu Phe	
40 45 50	
acg gtt ggt ttc gtg gat cga gtg gtt cga act gag gat cgt gaa gcg	307
Thr Val Gly Phe Val Asp Arg Val Val Arg Thr Glu Asp Arg Glu Ala	
55 60 65	
gca gcg cat gcg ttg tat gag ttg ggc aag att gct ccg tcg acg atg	355
Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile Ala Pro Ser Thr Met	
70 75 80 85	
tcc ttt ttg gat cgg gcg cag att cag gcc ggt tct ttg gtg ggg cgg	403
Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly Ser Leu Val Gly Arg	
90 95 100	
gcg ttg ccg cag gtt gtg gtt cct gcg gcg cgg gct cga atc cgg cag	451
Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg Ala Arg Ile Arg Gln	
105 110 115	
atg gtt ggg cac atg att gtg gat gcc cgc gac aag cag ttc gcc aag	499
Met Val Gly His Met Ile Val Asp Ala Arg Asp Lys Gln Phe Ala Lys	
120 125 130	
gct gtc gct gag att cag tcg gat ggg cac cgc ctg aac atc aat ttg	547
Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg Leu Asn Ile Asn Leu	
135 140 145	
cta ggt gaa gcg gtg ttg ggc cga aag gag gca gcg aag cat ttg gat	595
Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala Ala Lys His Leu Asp	
150 155 160 165	
gac acg gtg cgg ttg ttg cgc cgt ccg gat gtg gaa tat gtg tcc atc	643
Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val Glu Tyr Val Ser Ile	
170 175 180	
aag gtc tct tcg gtg gca tcg cag att tcg atg tgg ggt ttc gaa gac	691
Lys Val Ser Ser Val Ala Ser Gln Ile Ser Met Trp Gly Phe Glu Asp	
185 190 195	
acc gtt aat tat gtt gtg gaa cag ctg aca cct tta tat ata gag gcc	739
Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro Leu Tyr Ile Glu Ala	
200 205 210	
gcg cgg gcg ccg aaa ggc acg aag ttc atc aac ctg gac atg gag gaa	787
Ala Arg Ala Pro Lys Gly Thr Lys Phe Ile Asn Leu Asp Met Glu Glu	
215 220 225	
tac cgc gat ctg cgc ctg act atg gag gtg ttc aag cgg ctg ctc tcc	835
Tyr Arg Asp Leu Arg Leu Thr Met Glu Val Phe Lys Arg Leu Leu Ser	
230 235 240 245	
aat cca gag ctg cat gaa cta gaa gcc gga att gtg ttg cag gcg tac	883
Asn Pro Glu Leu His Glu Leu Glu Ala Gly Ile Val Leu Gln Ala Tyr	
250 255 260	
ctt ccc gat gcc ctc ggt gca atc cag gac ttg gcg cag ttc ggc cgc	931

Leu	Pro	Asp	Ala	Leu	Gly	Ala	Ile	Gln	Asp	Leu	Ala	Gln	Phe	Gly	Arg		
			265					270					275				
gag	cgc	gtc	aac	aca	ggc	ggg	gcg	ggc	gtt	aag	gtt	cgc	ctg	gtc	aag	979	
Glu	Arg	Val	Asn	Thr	Gly	Gly	Ala	Gly	Val	Lys	Val	Arg	Leu	Val	Lys		
		280					285					290					
ggt	gct	aat	ttg	cct	atg	gag	cac	gtc	cac	gcg	cag	atc	acc	ggc	tgg	1027	
Gly	Ala	Asn	Leu	Pro	Met	Glu	His	Val	His	Ala	Gln	Ile	Thr	Gly	Trp		
	295					300					305						
cca	gtt	gcc	aca	gaa	cct	tcc	aaa	caa	gcc	acc	gat	gcc	aat	tac	aag	1075	
Pro	Val	Ala	Thr	Glu	Pro	Ser	Lys	Gln	Ala	Thr	Asp	Ala	Asn	Tyr	Lys		
310					315					320					325		
cgc	gtc	ctc	tat	tgg	acg	atg	cgc	aaa	gaa	aac	atg	gag	ggc	ctg	cgc	1123	
Arg	Val	Leu	Tyr	Trp	Thr	Met	Arg	Lys	Glu	Asn	Met	Glu	Gly	Leu	Arg		
			330					335						340			
ctg	ggc	gtt	gcc	ggc	cac	aac	ctt	ttc	gac	ata	gca	ttc	gca	cat	ttg	1171	
Leu	Gly	Val	Ala	Gly	His	Asn	Leu	Phe	Asp	Ile	Ala	Phe	Ala	His	Leu		
			345					350					355				
ctc	tct	gtg	gag	cgt	ggg	gta	gcg	gac	cgt	gtg	gag	ttc	gaa	atg	ctg	1219	
Leu	Ser	Val	Glu	Arg	Gly	Val	Ala	Asp	Arg	Val	Glu	Phe	Glu	Met	Leu		
		360					365					370					
cag	ggc	atg	gcg	tcc	gat	cag	gcg	cgc	gcc	gtc	agc	gtt	gac	gtc	ggt	1267	
Gln	Gly	Met	Ala	Ser	Asp	Gln	Ala	Arg	Ala	Val	Ser	Val	Asp	Val	Gly		
	375					380					385						
gag	ctg	ctg	ctt	tac	gta	cca	gcc	gtg	cgc	cca	caa	gaa	ttc	gac	gtg	1315	
Glu	Leu	Leu	Leu	Tyr	Val	Pro	Ala	Val	Arg	Pro	Gln	Glu	Phe	Asp	Val		
390					395					400					405		
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Asn	Phe	Met	Ser	Ala	Ile	Phe	Asp	Leu	Asp	Ala	Asp	Asn	Pro	Ser	Phe		
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Lys	Arg	Glu	Glu	Ser	Arg	Phe	Arg	Ala	Ser	Ile	Ser	Asp	Leu	Ala	Thr		
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ctc	atc	gac	gtg	ccc	gcg	ccc	ggc	ccc	aac	cac	aca	caa	gac	cgc	agc	1507	
Leu	Ile	Asp	Val	Pro	Ala	Pro	Gly	Pro	Asn	His	Thr	Gln	Asp	Arg	Ser		
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Lys	Glu	Thr	Leu	Leu	Asp	Ala	Pro	Leu	Val	Pro	Phe	Ile	Asn	Glu	Pro		
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gac	acc	aac	cca	gcg	ctc	atc	caa	aac	caa	cag	tgg	gcc	aca	aaa	gcc	1603	
Asp	Thr	Asn	Pro	Ala	Leu	Ile	Gln	Asn	Gln	Gln	Trp	Ala	Thr	Lys	Ala		
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Glu	Val	Leu	Glu	Glu	Gly	Asp	Val	Asp	Lys	Leu	Ile	Asn	Asp	Val	Arg			
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gac	gct	gct	gaa	gcg	tgg	gca	gcg	cgc	cca	gcc	cgt	gaa	cgc	gct	gag	1747		
Asp	Ala	Ala	Glu	Ala	Trp	Ala	Ala	Arg	Pro	Ala	Arg	Glu	Arg	Ala	Glu			
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att	ttg	tac	aag	acc	gcc	gag	att	ttg	cgc	gtg	cga	cgc	gga	cac	ctg	1795		
Ile	Leu	Tyr	Lys	Thr	Ala	Glu	Ile	Leu	Arg	Val	Arg	Arg	Gly	His	Leu			
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atc	tca	gtg	acg	gcc	gcg	gag	gtg	ggc	aaa	gct	gtg	gaa	caa	acc	gac	1843		
Ile	Ser	Val	Thr	Ala	Ala	Glu	Val	Gly	Lys	Ala	Val	Glu	Gln	Thr	Asp			
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Pro	Glu	Ile	Ser	Glu	Ala	Ile	Asp	Phe	Ala	Arg	Tyr	Tyr	Ala	His	Leu			
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Ala	Leu	Glu	Leu	Asp	Asp	Val	Asp	Asn	Ala	Glu	Phe	Thr	Pro	Asp	Arg			
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gtc	gtt	gtg	gtg	acc	ccg	ccc	tgg	aat	ttc	ccc	atc	gcg	atc	ccc	gct	1987		
Val	Val	Val	Val	Thr	Pro	Pro	Trp	Asn	Phe	Pro	Ile	Ala	Ile	Pro	Ala			
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Gly	Ser	Thr	Phe	Ala	Ala	Leu	Ala	Ala	Gly	Ala	Gly	Val	Ile	His	Lys			
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Pro	Ser	Lys	Pro	Ser	Gln	His	Cys	Ser	Ala	Ala	Val	Val	Glu	Ala	Leu			
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Trp	Glu	Ala	Gly	Val	Pro	Arg	Glu	Val	Leu	His	Cys	Ile	Tyr	Pro	Ala			
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aat	cgc	gat	gtt	gga	tgt	gcg	ttg	atc	agc	cat	gaa	cac	gtc	gac	cgc	2179		
Asn	Arg	Asp	Val	Gly	Cys	Ala	Leu	Ile	Ser	His	Glu	His	Val	Asp	Arg			
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gtc	att	ttg	acc	ggc	tcc	tcc	gag	acc	gcc	gcg	atg	ttc	tcc	tcc	tgg	2227		
Val	Ile	Leu	Thr	Gly	Ser	Ser	Glu	Thr	Ala	Ala	Met	Phe	Ser	Ser	Trp			
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cga	cca	gaa	ctc	acc	atc	aac	ggc	gaa	acc	tcc	ggc	aaa	aac	gcc	atc	2275		
Arg	Pro	Glu	Leu	Thr	Ile	Asn	Gly	Glu	Thr	Ser	Gly	Lys	Asn	Ala	Ile			
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gtg	gtc	acc	cca	tct	gcc	gac	cgc	gac	ctc	gcc	gtc	gcc	gac	ctg	gtg	2323		
Val	Val	Thr	Pro	Ser	Ala	Asp	Arg	Asp	Leu	Ala	Val	Ala	Asp	Leu	Val			
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aaa	tcc	gcc	ttc	ggc	cat	gca	gga	caa	aaa	tgt	tcc	gca	gcc	tcc	ctc	2371		
Lys	Ser	Ala	Phe	Gly	His	Ala	Gly	Gln	Lys	Cys	Ser	Ala	Ala	Ser	Leu			
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760 765 770	
ctg gta gac gcc gca tcc tca ctc atc gtc gac tgg cct acc aac ccc	2467
Leu Val Asp Ala Ala Ser Ser Leu Ile Val Asp Trp Pro Thr Asn Pro	
775 780 785	
tcc gca acc gtc gga cca ctc acc gaa ctc ccc agc gat aaa ctc cac	2515
Ser Ala Thr Val Gly Pro Leu Thr Glu Leu Pro Ser Asp Lys Leu His	
790 795 800 805	
cac gcc cta acc acc ctc gaa gaa gga gaa agc tgg ctg ctg aaa ccc	2563
His Ala Leu Thr Thr Leu Glu Glu Gly Glu Ser Trp Leu Leu Lys Pro	
810 815 820	
cga caa ctc gac gac acc ggc cga ctc tgg tca ccc ggc atc aaa gaa	2611
Arg Gln Leu Asp Asp Thr Gly Arg Leu Trp Ser Pro Gly Ile Lys Glu	
825 830 835	
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Gly Val Lys Pro Gly Thr Phe Phe His Leu Thr Glu Val Phe Gly Pro	
840 845 850	
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Val Leu Gly Leu Met Lys Ala Thr Asp Leu Asn Glu Ala Ile Glu Phe	
855 860 865	
caa aac ggc aac gac ttc gga ctc acc ggc gga ctc caa tcc ctc gac	2755
Gln Asn Gly Asn Asp Phe Gly Leu Thr Gly Gly Leu Gln Ser Leu Asp	
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Ala Asp Glu Val Arg Thr Trp Leu Asp His Val Asp Val Gly Asn Ala	
890 895 900	
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Tyr Val Asn Arg Gly Ile Thr Gly Ala Ile Val Gln Arg Gln Ser Phe	
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ccc aac tat gtc atg ctc atg gga acc tgg gcc gac gcg cca agc cac	2947
Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala Asp Ala Pro Ser His	
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cac gcc cca cgc gaa aca aac ccg ctg atc agc aaa ctg gat ctc ccc	2995
His Ala Pro Arg Glu Thr Asn Pro Leu Ile Ser Lys Leu Asp Leu Pro	
950 955 960 965	
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Gly Glu Glu Leu Glu Trp Leu Glu Lys Ala Asn Ala Ser Asp Glu Thr	
970 975 980	
gca tgg aac acg gaa ttc ggc agc cca cgc gac ccc tcc ggc ctc gat	3091
Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp Pro Ser Gly Leu Asp	
985 990 995	

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 Val Glu Ala Asn Ile Phe Arg Tyr Arg Pro Ala Glu Val Val Leu Arg
 1000 1005 1010
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 Leu Asp Asp Ser Ala Thr Pro Arg Glu Thr Ala Arg Ala Leu Leu Ala
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 Ala Arg Arg Ala Gly Val Thr Pro Arg Val Leu Gln Thr Pro Gly Val
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 Ser Glu Gln Val Arg Glu Val Leu Ser Ala Ala Gly Val Ser Ala Glu
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 Thr Val Asp Asp Ser Val Phe Ile Ser Asn Val Leu Arg Gly Glu Tyr
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 Asp Glu Asn Ser Ser Val Arg Val Arg Tyr Leu Gly Lys Val Ser Asp
 1080 1085 1090
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 Thr Val Arg Glu Arg Leu Ser Val Arg Pro Glu Val Val Leu Leu Asp
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 Glu Gln Ala Ile Ser Met Thr Leu His Arg Phe Gly Asn Pro Val Ala
 1130 1135 1140
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 Val Pro Asn Ala Asp Ala Lys Arg Leu Ala Ala Val Leu Gln Asp Pro
 35 40 45
 Asn Gly Leu Glu Phe Thr Val Gly Phe Val Asp Arg Val Val Arg Thr
 50 55 60

Glu Asp Arg Glu Ala Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile
 65 70 75 80
 Ala Pro Ser Thr Met Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly
 85 90 95
 Ser Leu Val Gly Arg Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg
 100 105 110
 Ala Arg Ile Arg Gln Met Val Gly His Met Ile Val Asp Ala Arg Asp
 115 120 125
 Lys Gln Phe Ala Lys Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg
 130 135 140
 Leu Asn Ile Asn Leu Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala
 145 150 155 160
 Ala Lys His Leu Asp Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val
 165 170 175
 Glu Tyr Val Ser Ile Lys Val Ser Ser Val Ala Ser Gln Ile Ser Met
 180 185 190
 Trp Gly Phe Glu Asp Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro
 195 200 205
 Leu Tyr Ile Glu Ala Ala Arg Ala Pro Lys Gly Thr Lys Phe Ile Asn
 210 215 220
 Leu Asp Met Glu Glu Tyr Arg Asp Leu Arg Leu Thr Met Glu Val Phe
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 Lys Arg Leu Leu Ser Asn Pro Glu Leu His Glu Leu Glu Ala Gly Ile
 245 250 255
 Val Leu Gln Ala Tyr Leu Pro Asp Ala Leu Gly Ala Ile Gln Asp Leu
 260 265 270
 Ala Gln Phe Gly Arg Glu Arg Val Asn Thr Gly Gly Ala Gly Val Lys
 275 280 285
 Val Arg Leu Val Lys Gly Ala Asn Leu Pro Met Glu His Val His Ala
 290 295 300
 Gln Ile Thr Gly Trp Pro Val Ala Thr Glu Pro Ser Lys Gln Ala Thr
 305 310 315 320
 Asp Ala Asn Tyr Lys Arg Val Leu Tyr Trp Thr Met Arg Lys Glu Asn
 325 330 335
 Met Glu Gly Leu Arg Leu Gly Val Ala Gly His Asn Leu Phe Asp Ile
 340 345 350
 Ala Phe Ala His Leu Leu Ser Val Glu Arg Gly Val Ala Asp Arg Val
 355 360 365
 Glu Phe Glu Met Leu Gln Gly Met Ala Ser Asp Gln Ala Arg Ala Val
 370 375 380
 Ser Val Asp Val Gly Glu Leu Leu Leu Tyr Val Pro Ala Val Arg Pro

385		390		395		400
Gln Glu Phe Asp Val Ala Ile Ser Tyr Leu Val Arg Arg Leu Glu Glu						
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Asn Ala Ala Ser Glu Asn Phe Met Ser Ala Ile Phe Asp Leu Asp Ala						
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Asp Asn Pro Ser Phe Lys Arg Glu Glu Ser Arg Phe Arg Ala Ser Ile						
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Ser Asp Leu Ala Thr Leu Ile Asp Val Pro Ala Pro Gly Pro Asn His						
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Thr Gln Asp Arg Ser Lys Glu Thr Leu Leu Asp Ala Pro Leu Val Pro						
		465		470		475
				480		
Phe Ile Asn Glu Pro Asp Thr Asn Pro Ala Leu Ile Gln Asn Gln Gln						
		485		490		495
Trp Ala Thr Lys Ala Val Ala Thr Ala Ala Glu Pro Gly Trp Leu Glu						
		500		505		510
Lys Gln Thr Lys Pro Glu Val Leu Glu Glu Gly Asp Val Asp Lys Leu						
		515		520		525
Ile Asn Asp Val Arg Asp Ala Ala Glu Ala Trp Ala Ala Arg Pro Ala						
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Arg Glu Arg Ala Glu Ile Leu Tyr Lys Thr Ala Glu Ile Leu Arg Val						
		545		550		555
				560		
Arg Arg Gly His Leu Ile Ser Val Thr Ala Ala Glu Val Gly Lys Ala						
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Val Glu Gln Thr Asp Pro Glu Ile Ser Glu Ala Ile Asp Phe Ala Arg						
		580		585		590
Tyr Tyr Ala His Leu Ala Leu Glu Leu Asp Asp Val Asp Asn Ala Glu						
		595		600		605
Phe Thr Pro Asp Arg Val Val Val Val Thr Pro Pro Trp Asn Phe Pro						
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Ile Ala Ile Pro Ala Gly Ser Thr Phe Ala Ala Leu Ala Ala Gly Ala						
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				640		
Gly Val Ile His Lys Pro Ser Lys Pro Ser Gln His Cys Ser Ala Ala						
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Val Val Glu Ala Leu Trp Glu Ala Gly Val Pro Arg Glu Val Leu His						
		660		665		670
Cys Ile Tyr Pro Ala Asn Arg Asp Val Gly Cys Ala Leu Ile Ser His						
		675		680		685
Glu His Val Asp Arg Val Ile Leu Thr Gly Ser Ser Glu Thr Ala Ala						
		690		695		700
Met Phe Ser Ser Trp Arg Pro Glu Leu Thr Ile Asn Gly Glu Thr Ser						
		705		710		715
				720		

Gly Lys Asn Ala Ile Val Val Thr Pro Ser Ala Asp Arg Asp Leu Ala
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 Val Ala Asp Leu Val Lys Ser Ala Phe Gly His Ala Gly Gln Lys Cys
 740 745 750
 Ser Ala Ala Ser Leu Gly Ile Leu Val Gly Ser Val Tyr Glu Ser Glu
 755 760 765
 Arg Phe Arg Lys Gln Leu Val Asp Ala Ala Ser Ser Leu Ile Val Asp
 770 775 780
 Trp Pro Thr Asn Pro Ser Ala Thr Val Gly Pro Leu Thr Glu Leu Pro
 785 790 795 800
 Ser Asp Lys Leu His His Ala Leu Thr Thr Leu Glu Glu Gly Glu Ser
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 Trp Leu Leu Lys Pro Arg Gln Leu Asp Asp Thr Gly Arg Leu Trp Ser
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 Pro Gly Ile Lys Glu Gly Val Lys Pro Gly Thr Phe Phe His Leu Thr
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 Glu Val Phe Gly Pro Val Leu Gly Leu Met Lys Ala Thr Asp Leu Asn
 850 855 860
 Glu Ala Ile Glu Phe Gln Asn Gly Asn Asp Phe Gly Leu Thr Gly Gly
 865 870 875 880
 Leu Gln Ser Leu Asp Ala Asp Glu Val Arg Thr Trp Leu Asp His Val
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 Asp Val Gly Asn Ala Tyr Val Asn Arg Gly Ile Thr Gly Ala Ile Val
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 Gln Arg Gln Ser Phe Gly Gly Trp Lys Lys Ser Ser Val Gly Leu Gly
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 Ser Lys Ala Gly Gly Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala
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 Asp Ala Pro Ser His His Ala Pro Arg Glu Thr Asn Pro Leu Ile Ser
 945 950 955 960
 Lys Leu Asp Leu Pro Gly Glu Glu Leu Glu Trp Leu Glu Lys Ala Asn
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 Ala Ser Asp Glu Thr Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp
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 Pro Ser Gly Leu Asp Val Glu Ala Asn Ile Phe Arg Tyr Arg Pro Ala
 995 1000 1005
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 Arg Ala Leu Leu Ala Ala Arg Arg Ala Gly Val Thr Pro Arg Val Leu
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Gln Thr Pro Gly Val Ser Glu Gln Val Arg Glu Val Leu Ser Ala Ala
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Gly Val Ser Ala Glu Thr Val Asp Asp Ser Val Phe Ile Ser Asn Val
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Leu Arg Gly Glu Tyr Asp Glu Asn Ser Ser Val Arg Val Arg Tyr Leu
 1075 1080 1085

Gly Lys Val Ser Asp Thr Val Arg Glu Arg Leu Ser Val Arg Pro Glu
 1090 1095 1100

Val Val Leu Leu Asp Asp Ala Val Thr Ala Ser Gly Arg Val Glu Leu
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Arg Tyr Trp Leu Lys Glu Gln Ala Ile Ser Met Thr Leu His Arg Phe
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Gly Asn Pro Val Ala Ala Phe His Glu Leu Ala Glu Glu Leu Lys Arg
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 <223> FRXA00023

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gcc aca ccc cga gaa act gcc cgc gca ttg ttg gca gcc cgt cgc gcc 96
 Ala Thr Pro Arg Glu Thr Ala Arg Ala Leu Leu Ala Ala Arg Arg Ala
 20 25 30

ggg gtt act ccg cga gtt ctt caa aca cca ggt gtt tca gag caa gtc 144
 Gly Val Thr Pro Arg Val Leu Gln Thr Pro Gly Val Ser Glu Gln Val
 35 40 45

cgc gaa gta ttg tcc gct gct gga gtg agt gca gaa aca gtc gat gat 192
 Arg Glu Val Leu Ser Ala Ala Gly Val Ser Ala Glu Thr Val Asp Asp
 50 55 60

tcg gta ttt att tcc aac gtg ttg cgc ggc gaa tac gac gag aac tcc 240
 Ser Val Phe Ile Ser Asn Val Leu Arg Gly Glu Tyr Asp Glu Asn Ser
 65 70 75 80

agc gtc cga gtc cgc tac ctg ggc aaa gtt agc gac act gtc cgt gaa 288
 Ser Val Arg Val Arg Tyr Leu Gly Lys Val Ser Asp Thr Val Arg Glu
 85 90 95

cgc cta tct gta cgg ccc gaa gtt gtt ctg ctt gac gat gca gta act 336

Arg Leu Ser Val Arg Pro Glu Val Val Leu Leu Asp Asp Ala Val Thr
 100 105 110

gcc tcc ggt cga gtt gaa tta cgt tac tgg ctc aaa gaa caa gca att 384
 Ala Ser Gly Arg Val Glu Leu Arg Tyr Trp Leu Lys Glu Gln Ala Ile
 115 120 125

tcc atg acg ttg cac cgt ttt gga aac cca gtt gcg gcc ttc cac gag 432
 Ser Met Thr Leu His Arg Phe Gly Asn Pro Val Ala Ala Phe His Glu
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<213> Corynebacterium glutamicum

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His Phe Pro Leu Arg Pro Ala Glu Val Val Leu Arg Leu Asp Asp Ser
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 20 25 30

Gly Val Thr Pro Arg Val Leu Gln Thr Pro Gly Val Ser Glu Gln Val
 35 40 45

Arg Glu Val Leu Ser Ala Ala Gly Val Ser Ala Glu Thr Val Asp Asp
 50 55 60

Ser Val Phe Ile Ser Asn Val Leu Arg Gly Glu Tyr Asp Glu Asn Ser
 65 70 75 80

Ser Val Arg Val Arg Tyr Leu Gly Lys Val Ser Asp Thr Val Arg Glu
 85 90 95

Arg Leu Ser Val Arg Pro Glu Val Val Leu Leu Asp Asp Ala Val Thr
 100 105 110

Ala Ser Gly Arg Val Glu Leu Arg Tyr Trp Leu Lys Glu Gln Ala Ile
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Leu Ala Glu Glu Leu Lys Arg
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                                   Met Thr Ser Met Asn
                                   1           5

ctg cct att gag ttg gct acg ctg tct gac cag gct gtg gac aag gtg 163
Leu Pro Ile Glu Leu Ala Thr Leu Ser Asp Gln Ala Val Asp Lys Val
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Arg Ser Trp Leu Glu Tyr Ser Lys Lys Glu Ser Val Pro Asn Ala Asp
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gcg aag cgt cta gct gca gtg ttg cag gat cct aat ggt ttg gaa ttc 259
Ala Lys Arg Leu Ala Ala Val Leu Gln Asp Pro Asn Gly Leu Glu Phe
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acg gtt ggt ttc gtg gat cga gtg gtt cga act gag gat cgt gaa gcg 307
Thr Val Gly Phe Val Asp Arg Val Val Arg Thr Glu Asp Arg Glu Ala
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gca gcg cat gcg ttg tat gag ttg ggc aag att gct ccg tcg acg atg 355
Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile Ala Pro Ser Thr Met
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gcg ttg ccg cag gtt gtg gtt cct gcg gcg cgg gct cga atc cgg cag 451
Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg Ala Arg Ile Arg Gln
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Met Val Gly His Met Ile Val Asp Ala Arg Asp Lys Gln Phe Ala Lys
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gct gtc gct gag att cag tcg gat ggg cac cgc ctg aac atc aat ttg 547
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cta ggt gaa gcg gtg ttg ggc cga aag gaa gca gcg aag cat ttg gat 595
Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala Ala Lys His Leu Asp
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gac acg gtg cgg ttg ttg cgc cgt ccg gat gtg gaa tat gtg tcn nnn 643
Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val Glu Tyr Val Ser Xaa
              170              175              180

nnn ntc tct tcg gtg gca tcg cag att tcg atg tgg ggt ttc gaa gac 691
Xaa Xaa Ser Ser Val Ala Ser Gln Ile Ser Met Trp Gly Phe Glu Asp
              185              190              195

acc gtt aat tat gtt gtg gaa cag ctg aca cct tta tat ata gag ccc 739
Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro Leu Tyr Ile Glu Pro
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tac	cgc	gat	ctg	cgc	ctg	act	atg	gag	gtg	ttc	aag	cgg	ctg	ctc	tcc	835
Tyr	Arg	Asp	Leu	Arg	Leu	Thr	Met	Glu	Val	Phe	Lys	Arg	Leu	Leu	Ser	
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aat	cca	gag	ctg	cat	gaa	cta	gaa	gcc	gga	att	gtg	ttg	cag	gcg	tac	883
Asn	Pro	Glu	Leu	His	Glu	Leu	Glu	Ala	Gly	Ile	Val	Leu	Gln	Ala	Tyr	
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ctt	ccc	gat	gcc	ctc	ggc	gca	atc	cag	gac	ttg	gcg	cag	ttc	ggc	cgc	931
Leu	Pro	Asp	Ala	Leu	Gly	Ala	Ile	Gln	Asp	Leu	Ala	Gln	Phe	Gly	Arg	
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gag	cgc	gtc	aac	aca	ggc	ggg	gcg	ggc	gtt	aag	gtt	cgc	ctg	gtc	aag	979
Glu	Arg	Val	Asn	Thr	Gly	Gly	Ala	Gly	Val	Lys	Val	Arg	Leu	Val	Lys	
		280					285					290				
ggc	gct	aat	ttg	cct	atg	gag	cac	gtc	cac	gcg	cag	atc	acc	ggc	tgg	1027
Gly	Ala	Asn	Leu	Pro	Met	Glu	His	Val	His	Ala	Gln	Ile	Thr	Gly	Trp	
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cca	gtt	gcc	aca	gaa	cct	tcc	aaa	caa	gcc	acc	gat	gcc	aat	tac	aag	1075
Pro	Val	Ala	Thr	Glu	Pro	Ser	Lys	Gln	Ala	Thr	Asp	Ala	Asn	Tyr	Lys	
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cgc	gtc	ctc	tat	tgg	acg	atg	cgc	aaa	gaa	aac	atg	gag	ggc	ctg	cgc	1123
Arg	Val	Leu	Tyr	Trp	Thr	Met	Arg	Lys	Glu	Asn	Met	Glu	Gly	Leu	Arg	
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ctg	ggc	gtt	gcc	ggc	cac	aac	ctt	ttc	gac	ata	gca	ttc	gca	cat	ttg	1171
Leu	Gly	Val	Ala	Gly	His	Asn	Leu	Phe	Asp	Ile	Ala	Phe	Ala	His	Leu	
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ctc	tct	gtg	gag	cgt	ggg	gta	gcg	gac	cgt	gtg	gag	ttc	gaa	atg	ctg	1219
Leu	Ser	Val	Glu	Arg	Gly	Val	Ala	Asp	Arg	Val	Glu	Phe	Glu	Met	Leu	
		360					365					370				
cag	ggc	atg	gcg	tcc	gat	cag	gcg	cgc	gcc	gtc	agc	gtt	gac	gtc	ggc	1267
Gln	Gly	Met	Ala	Ser	Asp	Gln	Ala	Arg	Ala	Val	Ser	Val	Asp	Val	Gly	
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gag	ctg	ctg	ctt	tac	gta	cca	gcc	gtg	cgc	cca	caa	gaa	ttc	gac	gtg	1315
Glu	Leu	Leu	Leu	Tyr	Val	Pro	Ala	Val	Arg	Pro	Gln	Glu	Phe	Asp	Val	
390					395					400					405	
gcc	att	tct	tac	ctc	gtg	cgc	cgc	ctc	gag	gaa	aac	gcc	gcg	agc	gaa	1363
Ala	Ile	Ser	Tyr	Leu	Val	Arg	Arg	Leu	Glu	Glu	Asn	Ala	Ala	Ser	Glu	
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aac	ttc	atg	tcc	gcc	atc	ttc	gac	ctc	gac	gcc	gac	aac	ccg	tcc	ttc	1411
Asn	Phe	Met	Ser	Ala	Ile	Phe	Asp	Leu	Asp	Ala	Asp	Asn	Pro	Ser	Phe	
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Lys	Arg	Glu	Glu	Ser	Arg	Phe	Arg	Ala	Ser	Ile	Ser	Asp	Leu	Ala	Thr	
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ctc	atc	gac	gtg	ccc	gcg	ccc	ggc	ccc	aac	cac	aca	caa	gac	cgc	agc	1507

Leu	Ile	Asp	Val	Pro	Ala	Pro	Gly	Pro	Asn	His	Thr	Gln	Asp	Arg	Ser	
455						460					465					
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Lys	Glu	Thr	Leu	Leu	Asp	Ala	Pro	Leu	Val	Pro	Phe	Ile	Asn	Glu	Pro	
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Asp	Thr	Asn	Pro	Ala	Leu	Ile	Gln	Asn	Gln	Gln	Trp	Ala	Thr	Lys	Ala	
				490					495					500		
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Val	Ala	Thr	Ala	Ala	Glu	Pro	Gly	Trp	Leu	Glu	Lys	Gln	Thr	Lys	Pro	
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Glu	Val	Leu	Glu	Glu	Gly	Asp	Val	Asp	Lys	Leu	Ile	Asn	Asp	Val	Arg	
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gac	gct	gct	gaa	gcg	tgg	gca	gcg	cgc	cca	gcc	cgt	gaa	cgc	gct	gag	1747
Asp	Ala	Ala	Glu	Ala	Trp	Ala	Ala	Arg	Pro	Ala	Arg	Glu	Arg	Ala	Glu	
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Ile	Leu	Tyr	Lys	Thr	Ala	Glu	Ile	Leu	Arg	Val	Arg	Arg	Gly	His	Leu	
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atc	tca	gtg	acg	gcc	gcg	gag	gtg	ggc	aaa	gct	gtg	gaa	caa	acc	gac	1843
Ile	Ser	Val	Thr	Ala	Ala	Glu	Val	Gly	Lys	Ala	Val	Glu	Gln	Thr	Asp	
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Pro	Glu	Ile	Ser	Glu	Ala	Ile	Asp	Phe	Ala	Arg	Tyr	Tyr	Ala	His	Leu	
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gcc	ctg	gaa	ttg	gac	gac	gta	gac	aat	gcg	gaa	ttc	acc	cca	gat	cgc	1939
Ala	Leu	Glu	Leu	Asp	Asp	Val	Asp	Asn	Ala	Glu	Phe	Thr	Pro	Asp	Arg	
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gtc	gtt	gtg	gtg	acc	ccg	ccc	tgg	aat	ttc	ccc	atc	gcg	atc	ccc	gct	1987
Val	Val	Val	Val	Thr	Pro	Pro	Trp	Asn	Phe	Pro	Ile	Ala	Ile	Pro	Ala	
	615					620					625					
gga	tcg	act	ttc	gca	gca	ctc	gcg	gcg	ggc	gct	ggc	gtg	atc	cac	aaa	2035
Gly	Ser	Thr	Phe	Ala	Ala	Leu	Ala	Ala	Gly	Ala	Gly	Val	Ile	His	Lys	
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ccc	tca	aag	cct	agc	caa	cat	tgc	tcc	gct	gca	gtg	gtc	gaa	gcc	ctc	2083
Pro	Ser	Lys	Pro	Ser	Gln	His	Cys	Ser	Ala	Ala	Val	Val	Glu	Ala	Leu	
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tgg	gaa	gcc	ggc	gtt	ccc	cgc	gag	gtt	ctg	cat	tgc	att	tac	cca	gct	2131
Trp	Glu	Ala	Gly	Val	Pro	Arg	Glu	Val	Leu	His	Cys	Ile	Tyr	Pro	Ala	
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aat	cgc	gat	gtt	gga	tgt	gcg	ttg	atc	agc	cat	gaa	cac	gtc	gac	cgc	2179
Asn	Arg	Asp	Val	Gly	Cys	Ala	Leu	Ile	Ser	His	Glu	His	Val	Asp	Arg	
		680					685					690				
gtc	att	ttg	acc	ggc	tcc	tcc	gag	acc	gcc	gcg	atg	ttc	tcc	tcc	tgg	2227
Val	Ile	Leu	Thr	Gly	Ser	Ser	Glu	Thr	Ala	Ala	Met	Phe	Ser	Ser	Trp	

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tcc gca acc gtc gga cca ctc acc gaa ctc ccc agc gat aaa ctc cac Ser Ala Thr Val Gly Pro Leu Thr Glu Leu Pro Ser Asp Lys Leu His 790 795 800 805			2515
cac gcc cta acc acc ctc gaa gaa gga gaa agc tgg ctg ctg aaa ccc His Ala Leu Thr Thr Leu Glu Glu Gly Glu Ser Trp Leu Leu Lys Pro 810 815 820			2563
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caa aac ggc aac gac ttc gga ctc acc ggc gga ctc caa tcc ctc gac Gln Asn Gly Asn Asp Phe Gly Leu Thr Gly Gly Leu Gln Ser Leu Asp 870 875 880 885			2755
gcc gac gaa gtc cgc acc tgg ctt gac cac gtc gat gtc gga aac gcc Ala Asp Glu Val Arg Thr Trp Leu Asp His Val Asp Val Gly Asn Ala 890 895 900			2803
tac gtc aac cgc ggc atc acc ggc gcc att gtc caa cgc caa tcc ttc Tyr Val Asn Arg Gly Ile Thr Gly Ala Ile Val Gln Arg Gln Ser Phe 905 910 915			2851
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ccc aac tat gtc atg ctc atg gga acc tgg gcc gac gcg cca agc cac Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala Asp Ala Pro Ser His 935 940 945			2947

cac gcc cca cgc gaa aca aac ccg ctg atc agc aaa ctg gat ctc ccc 2995
 His Ala Pro Arg Glu Thr Asn Pro Leu Ile Ser Lys Leu Asp Leu Pro
 950 955 960 965

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 Gly Glu Glu Leu Glu Trp Leu Glu Lys Ala Asn Ala Ser Asp Glu Thr
 970 975 980

gca tgg aac acg gaa ttc ggc agc cca cgc gac ccc tcc ggc ctc gat 3091
 Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp Pro Ser Gly Leu Asp
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Asn Gly Leu Glu Phe Thr Val Gly Phe Val Asp Arg Val Val Arg Thr
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Glu Asp Arg Glu Ala Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile
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Ala Pro Ser Thr Met Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly
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Ser Leu Val Gly Arg Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg
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Ala Arg Ile Arg Gln Met Val Gly His Met Ile Val Asp Ala Arg Asp
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Lys Gln Phe Ala Lys Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg
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Leu Asn Ile Asn Leu Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala
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Ala Lys His Leu Asp Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val
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Glu Tyr Val Ser Xaa Xaa Xaa Ser Ser Val Ala Ser Gln Ile Ser Met
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Trp Gly Phe Glu Asp Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro

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Lys	Arg	Leu	Leu	Ser	Asn	Pro	Glu	Leu	His	Glu	Leu	Glu	Ala	Gly	Ile
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Ala	Gln	Phe	Gly	Arg	Glu	Arg	Val	Asn	Thr	Gly	Gly	Ala	Gly	Val	Lys
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Val	Arg	Leu	Val	Lys	Gly	Ala	Asn	Leu	Pro	Met	Glu	His	Val	His	Ala
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Gln	Ile	Thr	Gly	Trp	Pro	Val	Ala	Thr	Glu	Pro	Ser	Lys	Gln	Ala	Thr
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Asp	Ala	Asn	Tyr	Lys	Arg	Val	Leu	Tyr	Trp	Thr	Met	Arg	Lys	Glu	Asn
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Ala	Phe	Ala	His	Leu	Leu	Ser	Val	Glu	Arg	Gly	Val	Ala	Asp	Arg	Val
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Glu	Phe	Glu	Met	Leu	Gln	Gly	Met	Ala	Ser	Asp	Gln	Ala	Arg	Ala	Val
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Ser	Val	Asp	Val	Gly	Glu	Leu	Leu	Leu	Tyr	Val	Pro	Ala	Val	Arg	Pro
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Gln	Glu	Phe	Asp	Val	Ala	Ile	Ser	Tyr	Leu	Val	Arg	Arg	Leu	Glu	Glu
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Asn	Ala	Ala	Ser	Glu	Asn	Phe	Met	Ser	Ala	Ile	Phe	Asp	Leu	Asp	Ala
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Ser	Asp	Leu	Ala	Thr	Leu	Ile	Asp	Val	Pro	Ala	Pro	Gly	Pro	Asn	His
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Thr	Gln	Asp	Arg	Ser	Lys	Glu	Thr	Leu	Leu	Asp	Ala	Pro	Leu	Val	Pro
465					470					475					480
Phe	Ile	Asn	Glu	Pro	Asp	Thr	Asn	Pro	Ala	Leu	Ile	Gln	Asn	Gln	Gln
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				500				505						510	
Lys	Gln	Thr	Lys	Pro	Glu	Val	Leu	Glu	Glu	Gly	Asp	Val	Asp	Lys	Leu
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Ile	Asn	Asp	Val	Arg	Asp	Ala	Ala	Glu	Ala	Trp	Ala	Ala	Arg	Pro	Ala		
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Val	Glu	Gln	Thr	Asp	Pro	Glu	Ile	Ser	Glu	Ala	Ile	Asp	Phe	Ala	Arg		
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Tyr	Tyr	Ala	His	Leu	Ala	Leu	Glu	Leu	Asp	Asp	Val	Asp	Asn	Ala	Glu		
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Phe	Thr	Pro	Asp	Arg	Val	Val	Val	Val	Thr	Pro	Pro	Trp	Asn	Phe	Pro		
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Val	Val	Glu	Ala	Leu	Trp	Glu	Ala	Gly	Val	Pro	Arg	Glu	Val	Leu	His		
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Cys	Ile	Tyr	Pro	Ala	Asn	Arg	Asp	Val	Gly	Cys	Ala	Leu	Ile	Ser	His		
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Glu	His	Val	Asp	Arg	Val	Ile	Leu	Thr	Gly	Ser	Ser	Glu	Thr	Ala	Ala		
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Met	Phe	Ser	Ser	Trp	Arg	Pro	Glu	Leu	Thr	Ile	Asn	Gly	Glu	Thr	Ser		
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Gly	Lys	Asn	Ala	Ile	Val	Val	Thr	Pro	Ser	Ala	Asp	Arg	Asp	Leu	Ala		
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Val	Ala	Asp	Leu	Val	Lys	Ser	Ala	Phe	Gly	His	Ala	Gly	Gln	Lys	Cys		
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Arg	Phe	Arg	Lys	Gln	Leu	Val	Asp	Ala	Ala	Ser	Ser	Leu	Ile	Val	Asp		
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Trp	Pro	Thr	Asn	Pro	Ser	Ala	Thr	Val	Gly	Pro	Leu	Thr	Glu	Leu	Pro		
785					790					795					800		
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 Glu Ala Ile Glu Phe Gln Asn Gly Asn Asp Phe Gly Leu Thr Gly Gly
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 Leu Gln Ser Leu Asp Ala Asp Glu Val Arg Thr Trp Leu Asp His Val
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 Asp Val Gly Asn Ala Tyr Val Asn Arg Gly Ile Thr Gly Ala Ile Val
 900 905 910
 Gln Arg Gln Ser Phe Gly Gly Trp Lys Lys Ser Ser Val Gly Leu Gly
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 Ser Lys Ala Gly Gly Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala
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 Asp Ala Pro Ser His His Ala Pro Arg Glu Thr Asn Pro Leu Ile Ser
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 Lys Leu Asp Leu Pro Gly Glu Glu Leu Glu Trp Leu Glu Lys Ala Asn
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 Met Ser Glu Glu Lys
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 Leu Thr Val Ala Glu Leu Met Ala Arg Ala Ala Lys Glu Gly Arg Ser
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 Val Ser Val Ala Glu Leu Thr Gly Ser Ile Pro Ala Val Lys Glu Lys

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acc ttg gga atg gtg ggc atc atc cac gct ttg cgc acc tca cgt gat Thr Leu Gly Met Val Gly Ile Ile His Ala Leu Arg Thr Ser Arg Asp 230 235 240 245			835
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<213> *Corynebacterium glutamicum*

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Lys Glu Gly Arg Ser Thr Asp Ala Pro Arg Arg Arg Arg Arg Arg Ser
          20           25           30

Ile Glu Asp Gly Gly Val Ser Val Ala Glu Leu Thr Gly Ser Ile Pro
          35           40           45

Ala Val Lys Glu Lys Pro Ala Glu Ser Lys His Ser Ser Val Pro Ile
          50           55           60

Asp Ala Pro Ala Glu Pro Glu Val Val Glu Ala Pro Lys Pro Glu Pro
          65           70           75           80

Ala Glu Glu Val Glu Val Ala Ser Val Glu Gly Asp Val Asp Lys Gln
          85           90           95

Glu Thr Pro Glu Arg Pro Ala Pro Ser Asn Glu Glu Thr Met Val Leu
          100          105          110

Arg Ile Val Asp Glu Lys Asp Pro Ile Ser Leu Thr Thr Gly Ala Phe
          115          120          125

Pro Val Val Pro Ala Val Ala Ala Lys Pro Ala Pro Val Val Arg Ala
          130          135          140

Glu Lys Asp Ala Asp Val Glu Thr Ala Val Lys Ala Asp Phe Ala Glu
          145          150          155          160

Val Glu Val Asp Asn Thr Asp Thr Thr Gln Met Ala Val Val Glu Glu
          165          170          175

Val Asp Glu Glu Pro Glu Gln Glu Asn Lys Met Ser Val Phe Ala Ile
          180          185          190

Ile Met Met Ala Ile Val Gly Val Val Leu Gly Val Val Val Phe Leu
          195          200          205

Gly Phe Glu Met Leu Trp Glu Arg Leu Asn Lys Trp Ile Val Ala Val
          210          215          220

Leu Ala Val Gly Val Thr Leu Gly Met Val Gly Ile Ile His Ala Leu
          225          230          235          240

Arg Thr Ser Arg Asp Gly Phe Ser Met Val Leu Ala Gly Ile Val Gly
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Leu Val Met Thr Phe Gly Pro Leu Ala Ile Val Met
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<210> 315

<211> 774

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(751)

<223> RXA01491

<400> 315

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gggcagcatg tgtggccata tccagtgatg gaggtggaca atg ctg gat gag tct 115
                                         Met Leu Asp Glu Ser
                                         1 5

ttg ttt cca aat tcg gca aag ttt tct ttc att aaa act ggc gat gct 163
Leu Phe Pro Asn Ser Ala Lys Phe Ser Phe Ile Lys Thr Gly Asp Ala
                        10 15 20

gtt aat tta gac cat ttc cat cag ttg cat ccg ttg gaa aag gca ctg 211
Val Asn Leu Asp His Phe His Gln Leu His Pro Leu Glu Lys Ala Leu
                        25 30 35

gta gcg cac tcg gtt gat att aga aaa gca gag ttt gga gat gcc agg 259
Val Ala His Ser Val Asp Ile Arg Lys Ala Glu Phe Gly Asp Ala Arg
                        40 45 50

tgg tgt gca cat cag gca ctc caa gct ttg gga cga gat agc ggt gat 307
Trp Cys Ala His Gln Ala Leu Gln Ala Leu Gly Arg Asp Ser Gly Asp
                        55 60 65

ccc att ttg cgt ggg gaa cga gga atg cca ttg tgg cct tct tcg gtg 355
Pro Ile Leu Arg Gly Glu Arg Gly Met Pro Leu Trp Pro Ser Ser Val
                        70 75 80 85

tct ggt tca ttg acc cac act gac gga ttc cga gct gct gtt gtg gcg 403
Ser Gly Ser Leu Thr His Thr Asp Gly Phe Arg Ala Ala Val Val Ala
                        90 95 100

cca cga ttg ttg gtg cgt tct atg gga ttg gat gcc gaa cct gcg gag 451
Pro Arg Leu Leu Val Arg Ser Met Gly Leu Asp Ala Glu Pro Ala Glu
                        105 110 115

ccg ttg ccc aag gat gtt ttg ggt tca atc gct cgg gtg ggg gag att 499
Pro Leu Pro Lys Asp Val Leu Gly Ser Ile Ala Arg Val Gly Glu Ile
                        120 125 130

cct caa ctt aag cgc ttg gag gaa caa ggt gtg cac tgc gcg gat cgc 547
Pro Gln Leu Lys Arg Leu Glu Glu Gln Gly Val His Cys Ala Asp Arg
                        135 140 145

ctg ctg ttt tgt gcc aag gaa gca aca tac aaa gcg tgg ttc ccg ctg 595
Leu Leu Phe Cys Ala Lys Glu Ala Thr Tyr Lys Ala Trp Phe Pro Leu
                        150 155 160 165

acg cat agg tgg ctt ggt ttt gaa caa gct gag atc gac ttg cgt gat 643
Thr His Arg Trp Leu Gly Phe Glu Gln Ala Glu Ile Asp Leu Arg Asp
                        170 175 180

gat ggc act ttt gtg tcc tat ttg ctg gtt cga cca act cca gtg ccg 691
Asp Gly Thr Phe Val Ser Tyr Leu Leu Val Arg Pro Thr Pro Val Pro
                        185 190 195

ttt att tca ggt aaa tgg gta ctg cgt gat ggt tat gtc ata gct gcg 739

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Phe Ile Ser Gly Lys Trp Val Leu Arg Asp Gly Tyr Val Ile Ala Ala
 200 205 210

act gca gtg act tgaactggat ggagaggata cct
 Thr Ala Val Thr
 215

774

<210> 316
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 316
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 Lys Thr Gly Asp Ala Val Asn Leu Asp His Phe His Gln Leu His Pro
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 Leu Glu Lys Ala Leu Val Ala His Ser Val Asp Ile Arg Lys Ala Glu
 35 40 45
 Phe Gly Asp Ala Arg Trp Cys Ala His Gln Ala Leu Gln Ala Leu Gly
 50 55 60
 Arg Asp Ser Gly Asp Pro Ile Leu Arg Gly Glu Arg Gly Met Pro Leu
 65 70 75 80
 Trp Pro Ser Ser Val Ser Gly Ser Leu Thr His Thr Asp Gly Phe Arg
 85 90 95
 Ala Ala Val Val Ala Pro Arg Leu Leu Val Arg Ser Met Gly Leu Asp
 100 105 110
 Ala Glu Pro Ala Glu Pro Leu Pro Lys Asp Val Leu Gly Ser Ile Ala
 115 120 125
 Arg Val Gly Glu Ile Pro Gln Leu Lys Arg Leu Glu Glu Gln Gly Val
 130 135 140
 His Cys Ala Asp Arg Leu Leu Phe Cys Ala Lys Glu Ala Thr Tyr Lys
 145 150 155 160
 Ala Trp Phe Pro Leu Thr His Arg Trp Leu Gly Phe Glu Gln Ala Glu
 165 170 175
 Ile Asp Leu Arg Asp Asp Gly Thr Phe Val Ser Tyr Leu Leu Val Arg
 180 185 190
 Pro Thr Pro Val Pro Phe Ile Ser Gly Lys Trp Val Leu Arg Asp Gly
 195 200 205
 Tyr Val Ile Ala Ala Thr Ala Val Thr
 210 215

<210> 317
 <211> 1287
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1264)

<223> RXA02155

<400> 317

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gcaaacacaaa caaacacatc taattcagta ggagttccac atg gca gaa aaa ggc 115
Met Ala Glu Lys Gly
1 5

att acc gcg ccg aaa ggc ttc gtt gct tct gca acg acc gcg ggt att 163
Ile Thr Ala Pro Lys Gly Phe Val Ala Ser Ala Thr Thr Ala Gly Ile
10 15 20

aaa gct tct ggc aat cct gac atg gcg ttg gtg gtt aac cag ggt cca 211
Lys Ala Ser Gly Asn Pro Asp Met Ala Leu Val Val Asn Gln Gly Pro
25 30 35

gag ttt tcc gca gcg gcc gtg ttt aca cgt aac cga gtt ttc gca gcg 259
Glu Phe Ser Ala Ala Ala Val Phe Thr Arg Asn Arg Val Phe Ala Ala
40 45 50

cct gtg aag gtg agc cga gag aac gtt gct gat ggc cag atc agg gct 307
Pro Val Lys Val Ser Arg Glu Asn Val Ala Asp Gly Gln Ile Arg Ala
55 60 65

gtt ttg tac aac gct ggt aat gct aat gcg tgt aat ggt ctg cag ggt 355
Val Leu Tyr Asn Ala Gly Asn Ala Asn Ala Cys Asn Gly Leu Gln Gly
70 75 80 85

gag aag gat gct cgt gag tct gtt tct cat cta gct caa aat ttg ggc 403
Glu Lys Asp Ala Arg Glu Ser Val Ser His Leu Ala Gln Asn Leu Gly
90 95 100

ttg gag gat tcc gat att ggt gtg tgt tcc act ggt ctt att ggt gag 451
Leu Glu Asp Ser Asp Ile Gly Val Cys Ser Thr Gly Leu Ile Gly Glu
105 110 115

ttg ctt ccg atg gat aag ctc aat gca ggt att gat cag ctg acc gct 499
Leu Leu Pro Met Asp Lys Leu Asn Ala Gly Ile Asp Gln Leu Thr Ala
120 125 130

gag ggc gct ttg ggt gac aat ggt gca gct gct gcc aag gcg atc atg 547
Glu Gly Ala Leu Gly Asp Asn Gly Ala Ala Ala Ala Lys Ala Ile Met
135 140 145

acc act gac acg gtg gat aag gaa acc gtc gtg ttt gct gat ggt tgg 595
Thr Thr Asp Thr Val Asp Lys Glu Thr Val Val Phe Ala Asp Gly Trp
150 155 160 165

act gtc ggc gga atg ggc aag ggc gtg ggc atg atg gcg ccg tct ctt 643
Thr Val Gly Gly Met Gly Lys Gly Val Gly Met Met Ala Pro Ser Leu
170 175 180

gcc acc atg ctg gtc tgc ttg acc act gat gca tcc gtt act cag gaa 691
Ala Thr Met Leu Val Cys Leu Thr Thr Asp Ala Ser Val Thr Gln Glu
185 190 195

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atg gct cag atc gcg ctg gct aat gct acg gcc gtt acg ttt gac acc 739
Met Ala Gln Ile Ala Leu Ala Asn Ala Thr Ala Val Thr Phe Asp Thr
      200                      205                      210

ctg gat att gat gga tca acc tcc acc aat gac acc gtg ttc ctg ctg 787
Leu Asp Ile Asp Gly Ser Thr Ser Thr Asn Asp Thr Val Phe Leu Leu
      215                      220                      225

gca tct ggc gct agc gga atc acc cca act cag gat gaa ctc aac gat 835
Ala Ser Gly Ala Ser Gly Ile Thr Pro Thr Gln Asp Glu Leu Asn Asp
      230                      235                      240                      245

gcg gtg tac gca gct tgt tct gat atc gca gcg aag ctt cag gct gat 883
Ala Val Tyr Ala Ala Cys Ser Asp Ile Ala Ala Lys Leu Gln Ala Asp
      250                      255                      260

gca gag ggt gtg acc aag cgc gtt gct gtg aca gtg gtg gga acc acc 931
Ala Glu Gly Val Thr Lys Arg Val Ala Val Thr Val Val Gly Thr Thr
      265                      270                      275

aac aac gag cag gcg att aat gcg gct cgc act gtt gct cgt gac aat 979
Asn Asn Glu Gln Ala Ile Asn Ala Ala Arg Thr Val Ala Arg Asp Asn
      280                      285                      290

ttg ttc aag tgc gca atg ttt gga tct gat cca aac tgg ggt cgc gtg 1027
Leu Phe Lys Cys Ala Met Phe Gly Ser Asp Pro Asn Trp Gly Arg Val
      295                      300                      305

ttg gct gca gtc ggc atg gct gat gct gat atg gaa cca gag aag att 1075
Leu Ala Ala Val Gly Met Ala Asp Ala Asp Met Glu Pro Glu Lys Ile
      310                      315                      320                      325

tct gtg ttc ttc aat ggt caa gca gta tgc ctt gat tcc act ggc gct 1123
Ser Val Phe Phe Asn Gly Gln Ala Val Cys Leu Asp Ser Thr Gly Ala
      330                      335                      340

cct ggt gct cgt gag gtg gat ctt tcc ggc gct gac att gat gtc cga 1171
Pro Gly Ala Arg Glu Val Asp Leu Ser Gly Ala Asp Ile Asp Val Arg
      345                      350                      355

att gat ttg ggc acc agt ggg gaa ggc cag gca aca gtt cga acc act 1219
Ile Asp Leu Gly Thr Ser Gly Glu Gly Gln Ala Thr Val Arg Thr Thr
      360                      365                      370

gac ctg agc ttc tcc tac gtg gag atc aac tcc gcg tac agc tct 1264
Asp Leu Ser Phe Ser Tyr Val Glu Ile Asn Ser Ala Tyr Ser Ser
      375                      380                      385

taaaaagaaa cagcactcca act 1287

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<210> 318

<211> 388

<212> PRT

<213> Corynebacterium glutamicum

<400> 318

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Met Ala Glu Lys Gly Ile Thr Ala Pro Lys Gly Phe Val Ala Ser Ala
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Thr Thr Ala Gly Ile Lys Ala Ser Gly Asn Pro Asp Met Ala Leu Val

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20				25				30							
Val	Asn	Gln	Gly	Pro	Glu	Phe	Ser	Ala	Ala	Ala	Val	Phe	Thr	Arg	Asn
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Arg	Val	Phe	Ala	Ala	Pro	Val	Lys	Val	Ser	Arg	Glu	Asn	Val	Ala	Asp
	50					55					60				
Gly	Gln	Ile	Arg	Ala	Val	Leu	Tyr	Asn	Ala	Gly	Asn	Ala	Asn	Ala	Cys
65					70					75					80
Asn	Gly	Leu	Gln	Gly	Glu	Lys	Asp	Ala	Arg	Glu	Ser	Val	Ser	His	Leu
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Ala	Gln	Asn	Leu	Gly	Leu	Glu	Asp	Ser	Asp	Ile	Gly	Val	Cys	Ser	Thr
			100					105					110		
Gly	Leu	Ile	Gly	Glu	Leu	Leu	Pro	Met	Asp	Lys	Leu	Asn	Ala	Gly	Ile
		115					120					125			
Asp	Gln	Leu	Thr	Ala	Glu	Gly	Ala	Leu	Gly	Asp	Asn	Gly	Ala	Ala	Ala
	130					135					140				
Ala	Lys	Ala	Ile	Met	Thr	Thr	Asp	Thr	Val	Asp	Lys	Glu	Thr	Val	Val
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Phe	Ala	Asp	Gly	Trp	Thr	Val	Gly	Gly	Met	Gly	Lys	Gly	Val	Gly	Met
				165				170						175	
Met	Ala	Pro	Ser	Leu	Ala	Thr	Met	Leu	Val	Cys	Leu	Thr	Thr	Asp	Ala
			180					185					190		
Ser	Val	Thr	Gln	Glu	Met	Ala	Gln	Ile	Ala	Leu	Ala	Asn	Ala	Thr	Ala
		195					200					205			
Val	Thr	Phe	Asp	Thr	Leu	Asp	Ile	Asp	Gly	Ser	Thr	Ser	Thr	Asn	Asp
	210					215					220				
Thr	Val	Phe	Leu	Leu	Ala	Ser	Gly	Ala	Ser	Gly	Ile	Thr	Pro	Thr	Gln
225					230					235					240
Asp	Glu	Leu	Asn	Asp	Ala	Val	Tyr	Ala	Ala	Cys	Ser	Asp	Ile	Ala	Ala
				245				250						255	
Lys	Leu	Gln	Ala	Asp	Ala	Glu	Gly	Val	Thr	Lys	Arg	Val	Ala	Val	Thr
			260					265					270		
Val	Val	Gly	Thr	Thr	Asn	Asn	Glu	Gln	Ala	Ile	Asn	Ala	Ala	Arg	Thr
		275					280					285			
Val	Ala	Arg	Asp	Asn	Leu	Phe	Lys	Cys	Ala	Met	Phe	Gly	Ser	Asp	Pro
	290					295					300				
Asn	Trp	Gly	Arg	Val	Leu	Ala	Ala	Val	Gly	Met	Ala	Asp	Ala	Asp	Met
305					310					315					320
Glu	Pro	Glu	Lys	Ile	Ser	Val	Phe	Phe	Asn	Gly	Gln	Ala	Val	Cys	Leu
				325					330					335	
Asp	Ser	Thr	Gly	Ala	Pro	Gly	Ala	Arg	Glu	Val	Asp	Leu	Ser	Gly	Ala
			340					345					350		

Asp Ile Asp Val Arg Ile Asp Leu Gly Thr Ser Gly Glu Gly Gln Ala
355 360 365

Thr Val Arg Thr Thr Asp Leu Ser Phe Ser Tyr Val Glu Ile Asn Ser
370 375 380

Ala Tyr Ser Ser
385

<210> 319

<211> 1074

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1051)

<223> RXA02156

<400> 319

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aacagcactc caactaaca gcagggaaaa gggcacaggc atg aat gac ttg atc 115
Met Asn Asp Leu Ile
1 5

aaa gat tta ggc tct gag gtg cgc gca aat gtc ctc gct gag gcg ttg 163
Lys Asp Leu Gly Ser Glu Val Arg Ala Asn Val Leu Ala Glu Ala Leu
10 15 20

cca tgg ttg cag cac ttc cgc gac aag att gtt gtc gtg aaa tat ggc 211
Pro Trp Leu Gln His Phe Arg Asp Lys Ile Val Val Val Lys Tyr Gly
25 30 35

gga aac gcc atg gtg gat gat gat ctc aag gct gct ttt gct gcc gac 259
Gly Asn Ala Met Val Asp Asp Asp Leu Lys Ala Ala Phe Ala Ala Asp
40 45 50

atg gtc ttc ttg cgc acc gtg ggc gca aaa cca gtg gtg gtg cac ggt 307
Met Val Phe Leu Arg Thr Val Gly Ala Lys Pro Val Val Val His Gly
55 60 65

ggg gga cct cag att tct gag atg cta aac cgt gtg ggt ctc cag ggc 355
Gly Gly Pro Gln Ile Ser Glu Met Leu Asn Arg Val Gly Leu Gln Gly
70 75 80 85

gag ttc aag ggt ggt ttc cgt gtg acc act cct gag gtc atg gac att 403
Glu Phe Lys Gly Gly Phe Arg Val Thr Thr Pro Glu Val Met Asp Ile
90 95 100

gtg cgc atg gtg ctc ttt ggt cag gtc ggt cgc gat tta gtt ggt ttg 451
Val Arg Met Val Leu Phe Gly Gln Val Gly Arg Asp Leu Val Gly Leu
105 110 115

atc aac tct cat ggc cct tac gct gtg gga acc tcc ggt gag gat gcc 499
Ile Asn Ser His Gly Pro Tyr Ala Val Gly Thr Ser Gly Glu Asp Ala
120 125 130

ggc ctg ttt acc gcg cag aag cgc atg gtc aac atc gat ggc gta ccc 547

Gly Leu Phe Thr Ala Gln Lys Arg Met Val Asn Ile Asp Gly Val Pro
 135 140 145
 act gat att ggt ttg gtc gga gac atc att aat gtc gat gcc tct tcc 595
 Thr Asp Ile Gly Leu Val Gly Asp Ile Ile Asn Val Asp Ala Ser Ser
 150 155 160 165
 ttg atg gat atc atc gag gcc ggt cgc att cct gtg gtc tct acg att 643
 Leu Met Asp Ile Ile Glu Ala Gly Arg Ile Pro Val Val Ser Thr Ile
 170 175 180
 gct cca ggc gaa gac ggc cag att tac aac att aac gcc gat acc gca 691
 Ala Pro Gly Glu Asp Gly Gln Ile Tyr Asn Ile Asn Ala Asp Thr Ala
 185 190 195
 gca ggt gct ttg gct gca gcg att ggt gca gaa cgc ctg ctg gtt ctc 739
 Ala Gly Ala Leu Ala Ala Ala Ile Gly Ala Glu Arg Leu Leu Val Leu
 200 205 210
 acc aat gtg gaa ggt ctg tac acc gat tgg cct gat aag agc tca ctg 787
 Thr Asn Val Glu Gly Leu Tyr Thr Asp Trp Pro Asp Lys Ser Ser Leu
 215 220 225
 gtg tcc aag atc aag gcc acc gag ctg gag gcc att ctt ccg gga ctt 835
 Val Ser Lys Ile Lys Ala Thr Glu Leu Glu Ala Ile Leu Pro Gly Leu
 230 235 240 245
 gat tcc ggc atg att cca aag atg gag tct tgc ttg aac gcg gtg cgt 883
 Asp Ser Gly Met Ile Pro Lys Met Glu Ser Cys Leu Asn Ala Val Arg
 250 255 260
 ggg gga gta agc gct gct cat gtc att gac ggc cgc atc gcg cac tcg 931
 Gly Gly Val Ser Ala Ala His Val Ile Asp Gly Arg Ile Ala His Ser
 265 270 275
 gtg ttg ctg gag ctt ttg acc atg ggt gga att ggc acg atg gtg ctg 979
 Val Leu Leu Glu Leu Leu Thr Met Gly Gly Ile Gly Thr Met Val Leu
 280 285 290
 ccg gat gtt ttt gat cgg gag aat tat cct gaa ggc acc gtt ttt aga 1027
 Pro Asp Val Phe Asp Arg Glu Asn Tyr Pro Glu Gly Thr Val Phe Arg
 295 300 305
 aaa gac gac aag gat ggg gaa ctg taaatgagca cgctggaaac ttg 1074
 Lys Asp Asp Lys Asp Gly Glu Leu
 310 315

<210> 320

<211> 317

<212> PRT

<213> Corynebacterium glutamicum

<400> 320

Met Asn Asp Leu Ile Lys Asp Leu Gly Ser Glu Val Arg Ala Asn Val
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Leu Ala Glu Ala Leu Pro Trp Leu Gln His Phe Arg Asp Lys Ile Val
 20 25 30

Val Val Lys Tyr Gly Gly Asn Ala Met Val Asp Asp Asp Leu Lys Ala

35					40					45					
Ala	Phe	Ala	Ala	Asp	Met	Val	Phe	Leu	Arg	Thr	Val	Gly	Ala	Lys	Pro
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Val	Val	Val	His	Gly	Gly	Gly	Pro	Gln	Ile	Ser	Glu	Met	Leu	Asn	Arg
65				70				75				80			
Val	Gly	Leu	Gln	Gly	Glu	Phe	Lys	Gly	Gly	Phe	Arg	Val	Thr	Thr	Pro
85					90					95					
Glu	Val	Met	Asp	Ile	Val	Arg	Met	Val	Leu	Phe	Gly	Gln	Val	Gly	Arg
100				105				110							
Asp	Leu	Val	Gly	Leu	Ile	Asn	Ser	His	Gly	Pro	Tyr	Ala	Val	Gly	Thr
115				120				125							
Ser	Gly	Glu	Asp	Ala	Gly	Leu	Phe	Thr	Ala	Gln	Lys	Arg	Met	Val	Asn
130				135				140							
Ile	Asp	Gly	Val	Pro	Thr	Asp	Ile	Gly	Leu	Val	Gly	Asp	Ile	Ile	Asn
145				150				155				160			
Val	Asp	Ala	Ser	Ser	Leu	Met	Asp	Ile	Ile	Glu	Ala	Gly	Arg	Ile	Pro
165				170				175							
Val	Val	Ser	Thr	Ile	Ala	Pro	Gly	Glu	Asp	Gly	Gln	Ile	Tyr	Asn	Ile
180				185				190							
Asn	Ala	Asp	Thr	Ala	Ala	Gly	Ala	Leu	Ala	Ala	Ala	Ile	Gly	Ala	Glu
195				200				205							
Arg	Leu	Leu	Val	Leu	Thr	Asn	Val	Glu	Gly	Leu	Tyr	Thr	Asp	Trp	Pro
210				215				220							
Asp	Lys	Ser	Ser	Leu	Val	Ser	Lys	Ile	Lys	Ala	Thr	Glu	Leu	Glu	Ala
225				230				235				240			
Ile	Leu	Pro	Gly	Leu	Asp	Ser	Gly	Met	Ile	Pro	Lys	Met	Glu	Ser	Cys
245				250				255							
Leu	Asn	Ala	Val	Arg	Gly	Gly	Val	Ser	Ala	Ala	His	Val	Ile	Asp	Gly
260				265				270							
Arg	Ile	Ala	His	Ser	Val	Leu	Leu	Glu	Leu	Leu	Thr	Met	Gly	Gly	Ile
275				280				285							
Gly	Thr	Met	Val	Leu	Pro	Asp	Val	Phe	Asp	Arg	Glu	Asn	Tyr	Pro	Glu
290				295				300							
Gly	Thr	Val	Phe	Arg	Lys	Asp	Asp	Lys	Asp	Gly	Glu	Leu			
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<210> 321

<211> 903

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(880)

<223> RXN02153

<400> 321

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                                         Met Ile Met His Asn
                                         1           5

gtg tat ggt gta act atg aca atc aag gtt gca atc gca gga gcc agt 163
Val Tyr Gly Val Thr Met Thr Ile Lys Val Ala Ile Ala Gly Ala Ser
                        10                15                20

gga tat gcc ggc gga gaa atc ctt cgt ctc ctt tta ggc cat cca gct 211
Gly Tyr Ala Gly Gly Glu Ile Leu Arg Leu Leu Leu Gly His Pro Ala
                        25                30                35

tat gca tct ggt gaa cta gaa atc gga gca ctc acc gcg gca tca acc 259
Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu Thr Ala Ala Ser Thr
                        40                45                50

gca ggc agc acg ctc ggt gaa ttg atg cca cac att ccg cag ttg gcg 307
Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His Ile Pro Gln Leu Ala
                        55                60                65

gat cgt gtt att caa gac acc aca gct gaa act cta gcc ggt cat gat 355
Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr Leu Ala Gly His Asp
                        70                75                80                85

gtc gta ttt cta gga ctt cca cac gga ttc tct gca gaa att gca ctt 403
Val Val Phe Leu Gly Leu Pro His Gly Phe Ser Ala Glu Ile Ala Leu
                        90                95                100

cag ctc gga cca gat gtc aca gtg att gac tgt gca gct gac ttt cgt 451
Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys Ala Ala Asp Phe Arg
                        105                110                115

ctg caa aat gct gca gat tgg gag aag ttc tac ggc tca gag cac cag 499
Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr Gly Ser Glu His Gln
                        120                125                130

gga aca tgg cct tat ggc att cca gaa atg cca gga cac cgc gag gct 547
Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro Gly His Arg Glu Ala
                        135                140                145

ctt cgt ggt gct aag cgt gta gca gtg cca gga tgt ttc cca acc ggt 595
Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly Cys Phe Pro Thr Gly
                        150                155                160                165

gca acc ttg gct ctt ctt cct gcg gtt caa gcg gga ctt atc gag cca 643
Ala Thr Leu Ala Leu Leu Pro Ala Val Gln Ala Gly Leu Ile Glu Pro
                        170                175                180

gat gtt tcc gta gtg tcc atc acc ggc gta tca ggt gca ggt aag aaa 691
Asp Val Ser Val Val Ser Ile Thr Gly Val Ser Gly Ala Gly Lys Lys
                        185                190                195

gca tct gtt gca cta ctt ggc tcg gaa acc atg ggt tca ctc aag gcg 739
Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met Gly Ser Leu Lys Ala
                        200                205                210

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tac aac acc tcc gga aag cac cgc cac acc ccg gaa att gcc cag aac 787
 Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro Glu Ile Ala Gln Asn
 215 220 225

ctc ggc gaa gtc agc gac aag cca gtc aag gtg agc ttc acc cca gtg 835
 Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val Ser Phe Thr Pro Val
 230 235 240 245

ctt gca ccg tta cct cgc gaa ttc tca cca ctg caa ccg cac ctt 880
 Leu Ala Pro Leu Pro Arg Glu Phe Ser Pro Leu Gln Pro His Leu
 250 255 260

tgaaagaagg cgttaccgca gaa 903

<210> 322

<211> 260

<212> PRT

<213> Corynebacterium glutamicum

<400> 322

Met Ile Met His Asn Val Tyr Gly Val Thr Met Thr Ile Lys Val Ala
 1 5 10 15

Ile Ala Gly Ala Ser Gly Tyr Ala Gly Gly Glu Ile Leu Arg Leu Leu
 20 25 30

Leu Gly His Pro Ala Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu
 35 40 45

Thr Ala Ala Ser Thr Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His
 50 55 60

Ile Pro Gln Leu Ala Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr
 65 70 75 80

Leu Ala Gly His Asp Val Val Phe Leu Gly Leu Pro His Gly Phe Ser
 85 90 95

Ala Glu Ile Ala Leu Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys
 100 105 110

Ala Ala Asp Phe Arg Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr
 115 120 125

Gly Ser Glu His Gln Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro
 130 135 140

Gly His Arg Glu Ala Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly
 145 150 155 160

Cys Phe Pro Thr Gly Ala Thr Leu Ala Leu Leu Pro Ala Val Gln Ala
 165 170 175

Gly Leu Ile Glu Pro Asp Val Ser Val Val Ser Ile Thr Gly Val Ser
 180 185 190

Gly Ala Gly Lys Lys Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met
 195 200 205

Gly Ser Leu Lys Ala Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro
 210 215 220

Glu Ile Ala Gln Asn Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val
 225 230 235 240

Ser Phe Thr Pro Val Leu Ala Pro Leu Pro Arg Glu Phe Ser Pro Leu
 245 250 255

Gln Pro His Leu
 260

<210> 323
 <211> 903
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(880)
 <223> FRXA02153

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 cccccgcaat gaatcaaaaa tttatgcatg aataatttgc atg atc atg cat aac 115
 Met Ile Met His Asn
 1 5

gtg tat ggt gta act atg aca atc aag gtt gca atc gca gga gcc agt 163
 Val Tyr Gly Val Thr Met Thr Ile Lys Val Ala Ile Ala Gly Ala Ser
 10 15 20

gga tat gcc ggc gga gaa atc ctt cgt ctc ctt tta ggc cat cca gct 211
 Gly Tyr Ala Gly Gly Glu Ile Leu Arg Leu Leu Leu Gly His Pro Ala
 25 30 35

tat gca tct ggt gaa cta gaa atc gga gca ctc acc gcg gca tca acc 259
 Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu Thr Ala Ala Ser Thr
 40 45 50

gca ggc agc acg ctc ggt gaa ttg atg cca cac att ccg cag ttg gcg 307
 Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His Ile Pro Gln Leu Ala
 55 60 65

gat cgt gtt att caa gac acc aca gct gaa act cta gcc ggt cat gat 355
 Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr Leu Ala Gly His Asp
 70 75 80 85

gtc gta ttt cta gga ctt cca cac gga ttc tct gca gaa att gca ctt 403
 Val Val Phe Leu Gly Leu Pro His Gly Phe Ser Ala Glu Ile Ala Leu
 90 95 100

cag ctc gga cca gat gtc aca gtg att gac tgt gca gct gac ttt cgt 451
 Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys Ala Ala Asp Phe Arg
 105 110 115

ctg caa aat gct gca gat tgg gag aag ttc tac ggc tca gag cac cag 499
 Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr Gly Ser Glu His Gln
 120 125 130

gga aca tgg cct tat ggc att cca gaa atg cca gga cac cgc gag gct 547
 Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro Gly His Arg Glu Ala
 135 140 145

 ctt cgt ggt gct aag cgt gta gca gtg cca gga tgt ttc cca acc ggt 595
 Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly Cys Phe Pro Thr Gly
 150 155 160 165

 gca acc ttg gct ctt ctt cct gcg gtt caa gcg gga ctt atc gag cca 643
 Ala Thr Leu Ala Leu Leu Pro Ala Val Gln Ala Gly Leu Ile Glu Pro
 170 175 180

 gat gtt tcc gta gtg tcc atc acc ggc gta tca ggt gca ggt aag aaa 691
 Asp Val Ser Val Val Ser Ile Thr Gly Val Ser Gly Ala Gly Lys Lys
 185 190 195

 gca tct gtt gca cta ctt ggc tcg gaa acc atg ggt tca ctc aag gcg 739
 Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met Gly Ser Leu Lys Ala
 200 205 210

 tac aac acc tcc gga aag cac cgc cac acc ccg gaa att gcc cag aac 787
 Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro Glu Ile Ala Gln Asn
 215 220 225

 ctc ggc gaa gtc agc gac aag cca gtc aag gtg agc ttc acc cca gtg 835
 Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val Ser Phe Thr Pro Val
 230 235 240 245

 ctt gca ccg tta cct cgc gaa ttc tca cca ctg caa ccg cac ctt 880
 Leu Ala Pro Leu Pro Arg Glu Phe Ser Pro Leu Gln Pro His Leu
 250 255 260

 tgaaagaagg cgttaccgca gaa 903

<210> 324

<211> 260

<212> PRT

<213> Corynebacterium glutamicum

<400> 324

Met Ile Met His Asn Val Tyr Gly Val Thr Met Thr Ile Lys Val Ala
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 Ile Ala Gly Ala Ser Gly Tyr Ala Gly Gly Glu Ile Leu Arg Leu Leu
 20 25 30

 Leu Gly His Pro Ala Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu
 35 40 45

 Thr Ala Ala Ser Thr Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His
 50 55 60

 Ile Pro Gln Leu Ala Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr
 65 70 75 80

 Leu Ala Gly His Asp Val Val Phe Leu Gly Leu Pro His Gly Phe Ser
 85 90 95

 Ala Glu Ile Ala Leu Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys

100					105					110					
Ala	Ala	Asp	Phe	Arg	Leu	Gln	Asn	Ala	Ala	Asp	Trp	Glu	Lys	Phe	Tyr
		115					120					125			
Gly	Ser	Glu	His	Gln	Gly	Thr	Trp	Pro	Tyr	Gly	Ile	Pro	Glu	Met	Pro
		130					135					140			
Gly	His	Arg	Glu	Ala	Leu	Arg	Gly	Ala	Lys	Arg	Val	Ala	Val	Pro	Gly
							150					155			160
Cys	Phe	Pro	Thr	Gly	Ala	Thr	Leu	Ala	Leu	Leu	Pro	Ala	Val	Gln	Ala
				165					170					175	
Gly	Leu	Ile	Glu	Pro	Asp	Val	Ser	Val	Val	Ser	Ile	Thr	Gly	Val	Ser
			180					185					190		
Gly	Ala	Gly	Lys	Lys	Ala	Ser	Val	Ala	Leu	Leu	Gly	Ser	Glu	Thr	Met
			195				200					205			
Gly	Ser	Leu	Lys	Ala	Tyr	Asn	Thr	Ser	Gly	Lys	His	Arg	His	Thr	Pro
							215					220			
Glu	Ile	Ala	Gln	Asn	Leu	Gly	Glu	Val	Ser	Asp	Lys	Pro	Val	Lys	Val
							230					235			240
Ser	Phe	Thr	Pro	Val	Leu	Ala	Pro	Leu	Pro	Arg	Glu	Phe	Ser	Pro	Leu
				245					250					255	
Gln	Pro	His	Leu												
			260												

<210> 325

<211> 414

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(391)

<223> RXA02154

<400> 325

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caccggttacc	tcgcgaattc	tcaccactgc	aaccgcacct	ttg	aaa	gaa	ggc	gtt	115
				Leu	Lys	Glu	Gly	Val	
				1				5	

acc	gca	gaa	cag	gct	cgc	gca	gta	tat	gaa	gag	ttc	tat	gca	cag	gaa	163
Thr	Ala	Glu	Gln	Ala	Arg	Ala	Val	Tyr	Glu	Glu	Phe	Tyr	Ala	Gln	Glu	
			10					15						20		

acc	ttc	gtg	cat	gtt	ctt	cca	gaa	ggc	gca	cag	cca	caa	acc	caa	gca	211
Thr	Phe	Val	His	Val	Leu	Pro	Glu	Gly	Ala	Gln	Pro	Gln	Thr	Gln	Ala	
			25					30					35			

gtt	ctt	ggc	tcc	aac	atg	tgc	cac	gtg	cag	gta	gaa	att	gat	gag	gaa	259
Val	Leu	Gly	Ser	Asn	Met	Cys	His	Val	Gln	Val	Glu	Ile	Asp	Glu	Glu	
			40				45					50				

act tgg cca cag gtc att att aat acg tac ggc acc cca cca gtt gag	163
Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly Thr Pro Pro Val Glu	
10 15 20	
ctg gtg tcc ggc aag ggc gca acc gtc act gat gac cag ggc aat gtc	211
Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp Asp Gln Gly Asn Val	
25 30 35	
tac atc gac ttg ctc gcg ggc atc gca gtc aac gcg ttg ggc cac gcc	259
Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn Ala Leu Gly His Ala	
40 45 50	
cac ccg gcg atc atc gag gcg gtc acc aac cag atc ggc caa ctt ggt	307
His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln Ile Gly Gln Leu Gly	
55 60 65	
cac gtc tca aac ttg ttc gca tcc agg ccc gtc gtc gag gtc gcc gag	355
His Val Ser Asn Leu Phe Ala Ser Arg Pro Val Val Glu Val Ala Glu	
70 75 80 85	
gag ctc atc aag cgt ttt tcg ctt gac gac gcc acc ctc gcc gcg caa	403
Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala Thr Leu Ala Ala Gln	
90 95 100	
acc cgg gtt ttc ttc tgc aac tcg ggc gcc gaa gca aac gag gct gct	451
Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu Ala Asn Glu Ala Ala	
105 110 115	
ttc aag att gca cgc ttg act ggt cgt tcc cgg att ctg gct gca gtt	499
Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg Ile Leu Ala Ala Val	
120 125 130	
cat ggt ttc cac ggc cgc acc atg ggt tcc ctc gcg ctg act ggc cag	547
His Gly Phe His Gly Arg Thr Met Gly Ser Leu Ala Leu Thr Gly Gln	
135 140 145	
cca gac aag cgt gaa gcg ttc ctg cca atg cca agc ggt gtg gag ttc	595
Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro Ser Gly Val Glu Phe	
150 155 160 165	
tac cct tac ggc gac acc gat tac ttg cgc aaa atg gta gaa acc aac	643
Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys Met Val Glu Thr Asn	
170 175 180	
cca acg gat gtg gct gct atc ttc ctc gag cca atc cag ggt gaa acg	691
Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro Ile Gln Gly Glu Thr	
185 190 195	
ggc gtt gtt cca gca cct gaa gga ttc ctc aag gca gtg cgc gag ctg	739
Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys Ala Val Arg Glu Leu	
200 205 210	
tgc gat gag tac ggc atc ttg atg atc acc gat gaa gtc cag act ggc	787
Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp Glu Val Gln Thr Gly	
215 220 225	
gtt ggc cgt acc ggc gat ttc ttt gca cat cag cac gat ggc gtt gtt	835
Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln His Asp Gly Val Val	
230 235 240 245	
ccc gat gtg gtg acc atg gcc aag gga ctt ggc ggc ggt ctt ccc atc	883

Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly Gly Gly Leu Pro Ile
 250 255 260

ggt gct tgt ttg gcc act ggc cgt gca gct gaa ttg atg acc cca ggc 931
 Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu Leu Met Thr Pro Gly
 265 270 275

aag cac ggc acc act ttc ggt ggc aac cca gtt gct tgt gca gct gcc 979
 Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val Ala Cys Ala Ala Ala
 280 285 290

aag gca gtg ctg tct gtt gtc gat gac gct ttc tgc gca gaa gtt gcc 1027
 Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe Cys Ala Glu Val Ala
 295 300 305

cgc aag ggc gag ctg ttc aag gaa ctt ctt gcc aag gtt gac ggc gtt 1075
 Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala Lys Val Asp Gly Val
 310 315 320 325

gta gac gtc cgt ggc agg ggc ttg atg ttg ggc gtg gtg ctg gag cgc 1123
 Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly Val Val Leu Glu Arg
 330 335 340

gac gtc gca aag caa gct gtt ctt gat ggt ttt aag cac ggc gtt att 1171
 Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe Lys His Gly Val Ile
 345 350 355

ttg aat gca ccg gcg gac aac att atc cgt ttg acc ccg ccg ctg gtg 1219
 Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu Thr Pro Pro Leu Val
 360 365 370

atc acc gac gaa gaa atc gca gac gca gtc aag gct att gcc gag aca 1267
 Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys Ala Ile Ala Glu Thr
 375 380 385

atc gca taaaggactc aaacttatga ctt 1296
 Ile Ala
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<210> 328
 <211> 391
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 328
 Met Ser Thr Leu Glu Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly
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Thr Pro Pro Val Glu Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp
 20 25 30

Asp Gln Gly Asn Val Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn
 35 40 45

Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln
 50 55 60

Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val
 65 70 75 80

Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala
 85 90 95
 Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu
 100 105 110
 Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg
 115 120 125
 Ile Leu Ala Ala Val His Gly Phe His Gly Arg Thr Met Gly Ser Leu
 130 135 140
 Ala Leu Thr Gly Gln Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro
 145 150 155 160
 Ser Gly Val Glu Phe Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys
 165 170 175
 Met Val Glu Thr Asn Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro
 180 185 190
 Ile Gln Gly Glu Thr Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys
 195 200 205
 Ala Val Arg Glu Leu Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp
 210 215 220
 Glu Val Gln Thr Gly Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln
 225 230 235 240
 His Asp Gly Val Val Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly
 245 250 255
 Gly Gly Leu Pro Ile Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu
 260 265 270
 Leu Met Thr Pro Gly Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val
 275 280 285
 Ala Cys Ala Ala Ala Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe
 290 295 300
 Cys Ala Glu Val Ala Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala
 305 310 315 320
 Lys Val Asp Gly Val Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly
 325 330 335
 Val Val Leu Glu Arg Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe
 340 345 350
 Lys His Gly Val Ile Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu
 355 360 365
 Thr Pro Pro Leu Val Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys
 370 375 380
 Ala Ile Ala Glu Thr Ile Ala
 385 390

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<222> (101) .. (1468)
<223> RXS02970
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ttattttaag	acttcataat	attttgggga	gtgaactggt	ttg	gca	ttg	aag	ggg	115							
				Leu	Ala	Leu	Lys	Gly								
									1						5	
tac	acc	aac	ttt	gac	ggg	gaa	ttc	atc	gaa	ttc	gga	tct	gtg	caa	gca	163
Tyr	Thr	Asn	Phe	Asp	Gly	Glu	Phe	Ile	Glu	Phe	Gly	Ser	Val	Gln	Ala	
				10					15					20		
aaa	gaa	gag	gaa	aaa	cgg	gca	ttc	gac	aac	gat	cgc	gcg	cac	gtt	ttc	211
Lys	Glu	Glu	Glu	Lys	Arg	Ala	Phe	Asp	Asn	Asp	Arg	Ala	His	Val	Phe	
			25					30					35			
cac	tcc	tgg	tcc	gcg	cag	gac	aaa	atc	agc	ccc	aaa	gta	tgg	gca	gct	259
His	Ser	Trp	Ser	Ala	Gln	Asp	Lys	Ile	Ser	Pro	Lys	Val	Trp	Ala	Ala	
		40					45					50				
gcc	gaa	ggg	tcc	acg	ctg	tac	gac	ttc	gac	ggc	aac	gcc	ttc	atc	gac	307
Ala	Glu	Gly	Ser	Thr	Leu	Tyr	Asp	Phe	Asp	Gly	Asn	Ala	Phe	Ile	Asp	
	55					60					65					
atg	ggg	tcc	caa	ctt	gtc	tcg	gca	aac	tta	ggc	cac	aac	aac	cct	cga	355
Met	Gly	Ser	Gln	Leu	Val	Ser	Ala	Asn	Leu	Gly	His	Asn	Asn	Pro	Arg	
70					75					80					85	
tta	gtt	gag	gcg	atc	cag	cgc	caa	gca	gcc	cgg	ttg	acc	aac	atc	aac	403
Leu	Val	Glu	Ala	Ile	Gln	Arg	Gln	Ala	Ala	Arg	Leu	Thr	Asn	Ile	Asn	
				90					95					100		
ccg	gcc	ttc	ggc	aat	gat	gtg	cgc	tct	gat	gtt	gct	gca	aag	atc	gtg	451
Pro	Ala	Phe	Gly	Asn	Asp	Val	Arg	Ser	Asp	Val	Ala	Ala	Lys	Ile	Val	
			105					110					115			
tcg	atg	gcc	cgt	ggc	gaa	ttc	tcc	cac	gtg	ttt	ttc	acc	aac	ggc	ggc	499
Ser	Met	Ala	Arg	Gly	Glu	Phe	Ser	His	Val	Phe	Phe	Thr	Asn	Gly	Gly	
		120					125					130				
gcc	gac	gcc	atc	gag	cac	tcc	atc	cgc	atg	gct	cgc	ctg	cac	acc	gga	547
Ala	Asp	Ala	Ile	Glu	His	Ser	Ile	Arg	Met	Ala	Arg	Leu	His	Thr	Gly	
	135					140					145					
cgc	aac	aaa	att	ctg	tcc	gca	tac	cgc	agc	tac	cac	ggc	gca	acc	gga	595
Arg	Asn	Lys	Ile	Leu	Ser	Ala	Tyr	Arg	Ser	Tyr	His	Gly	Ala	Thr	Gly	
150					155					160					165	
tcc	gcg	atg	atg	ctc	acc	ggc	gaa	cac	cgc	cgc	ctg	ggc	aac	ccc	acc	643
Ser	Ala	Met	Met	Leu	Thr	Gly	Glu	His	Arg	Arg	Leu	Gly	Asn	Pro	Thr	
				170					175					180		

acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc	691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
185 190 195	
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys	
200 205 210	
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
215 220 225	
atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca	835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
230 235 240 245	
gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc	883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile	
250 255 260	
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa	931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys	
265 270 275	
ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc	979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile	
280 285 290	
acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc	1027
Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile	
295 300 305	
gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc	1075
Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser	
310 315 320 325	
ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag	1123
Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys	
330 335 340	
gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct	1171
Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala	
345 350 355	
cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa	1219
Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu	
360 365 370	
gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca	1267
Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala	
375 380 385	
gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa	1315
Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu	
390 395 400 405	
ttc aag gaa cgc ggc gtg tgg ccg atg atc tcc ggc aac cga ttc cac	1363
Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His	
410 415 420	
atc gcg ccg ccg ctg acc acc act gat gac gaa ttg gta gca ctg ctg	1411

Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu
 425 430 435

gac gcg gtg gaa gct gca gcc caa gct gtc gag ctg acc ttc gct ggg 1459
 Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu Leu Thr Phe Ala Gly
 440 445 450

gcg ttg ttc taagttttct agataacaag gcc 1491
 Ala Leu Phe
 455

<210> 330

<211> 456

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 330

Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe
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Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp
 20 25 30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
 35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
 50 55 60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
 65 70 75 80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
 85 90 95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
 100 105 110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
 115 120 125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
 130 135 140

Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
 145 150 155 160

His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
 165 170 175

Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
 180 185 190

Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
 195 200 205

Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
 210 215 220

Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly

225					230					235					240	
Ile	Ile	Leu	Pro	Pro 245	Ala	Gly	Tyr	Leu	Asn 250	Gly	Val	Arg	Glu	Leu 255	Cys	
Asn	Lys	His	Gly 260	Ile	Leu	Phe	Ile	Ala 265	Asp	Glu	Val	Met	Val 270	Gly	Phe	
Gly	Arg	Thr 275	Gly	Lys	Leu	Phe	Ala 280	Tyr	Glu	His	Ala	Gly 285	Asp	Asp	Phe	
Gln	Pro 290	Asp	Met	Ile	Thr	Phe 295	Ala	Lys	Gly	Val	Asn 300	Ala	Gly	Tyr	Ala	
Pro 305	Leu	Gly	Gly	Ile 310	Val	Met	Thr	Gln	Ser	Ile 315	Arg	Asp	Thr	Phe	Gly 320	
Ser	Glu	Ala	Tyr	Ser 325	Gly	Gly	Leu	Thr	Tyr 330	Ser	Gly	His	Pro	Leu 335	Ala	
Val	Ala	Pro	Ala 340	Lys	Ala	Ala	Leu	Glu 345	Ile	Tyr	Ala	Glu	Gly 350	Glu	Ile	
Ile	Pro 355	Arg	Val	Ala	Arg	Leu	Gly 360	Ala	Glu	Leu	Ile 365	Glu	Pro	Arg	Leu	
Arg	Glu 370	Leu	Ala	Glu	Glu	Asn 375	Val	Ala	Ile	Ala	Asp 380	Val	Arg	Gly	Ile	
Gly 385	Phe	Phe	Trp	Ala	Val 390	Glu	Phe	Asn	Ala	Asp 395	Ala	Thr	Ala	Met	Ala 400	
Ala	Gly	Ala	Ala	Glu 405	Phe	Lys	Glu	Arg	Gly 410	Val	Trp	Pro	Met	Ile 415	Ser	
Gly	Asn	Arg	Phe 420	His	Ile	Ala	Pro	Pro 425	Leu	Thr	Thr	Thr	Asp 430	Asp	Glu	
Leu	Val	Ala 435	Leu	Leu	Asp	Ala	Val 440	Glu	Ala	Ala	Ala	Gln 445	Ala	Val	Glu	
Leu	Thr 450	Phe	Ala	Gly	Ala	Leu	Phe 455									

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<210> 331
<211> 1330
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1330)
<223> FRXA01009
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<400> 331
aaccgacaaa acagccgttc acgtgctaaa gcagctcggc ttgatctagg gtgaggtgag 60

ttatttaaag acttcataat attttgggga gtgaactggg ttg gca ttg aag ggt 115
                                Leu Ala Leu Lys Gly
                                1           5

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tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca	163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala	
10 15 20	
aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc	211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe	
25 30 35	
cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct	259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala	
40 45 50	
gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac	307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp	
55 60 65	
atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga	355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg	
70 75 80 85	
tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac	403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn	
90 95 100	
ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg	451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val	
105 110 115	
tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc	499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly	
120 125 130	
gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga	547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly	
135 140 145	
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga	595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly	
150 155 160 165	
tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc	643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr	
170 175 180	
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc	691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
185 190 195	
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys	
200 205 210	
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
215 220 225	
atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca	835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
230 235 240 245	

gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc 883
 Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile
 250 255 260

ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa 931
 Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys
 265 270 275

ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc 979
 Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile
 280 285 290

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc 1027
 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile
 295 300 305

gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc 1075
 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser
 310 315 320 325

ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag 1123
 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys
 330 335 340

gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct 1171
 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala
 345 350 355

cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa 1219
 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu
 360 365 370

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca 1267
 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala
 375 380 385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa 1315
 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu
 390 395 400 405

ttc aag gaa cgc ggc 1330
 Phe Lys Glu Arg Gly
 410

<210> 332

<211> 410

<212> PRT

<213> Corynebacterium glutamicum

<400> 332

Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe
 1 5 10 15

Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp
 20 25 30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
 35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly

50	55	60
Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly 65 70 75 80		
His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg 85 90 95		
Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val 100 105 110		
Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe 115 120 125		
Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala 130 135 140		
Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr 145 150 155 160		
His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg 165 170 175		
Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro 180 185 190		
Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys 195 200 205		
Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala 210 215 220		
Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly 225 230 235 240		
Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys 245 250 255		
Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe 260 265 270		
Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe 275 280 285		
Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala 290 295 300		
Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly 305 310 315 320		
Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala 325 330 335		
Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile 340 345 350		
Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu 355 360 365		
Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile 370 375 380		

Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala
385 390 395 400

Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly
405 410

<210> 333

<211> 1080

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1057)

<223> RXA02158

<400> 333

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aaggctattg ccgagacaat cgcataaagg actcaaactt atg act tca caa cca 115
Met Thr Ser Gln Pro
1 5

cag gtt cgc cat ttt ctg gct gat gat gat ctc acc cct gca gag cag 163
Gln Val Arg His Phe Leu Ala Asp Asp Asp Leu Thr Pro Ala Glu Gln
10 15 20

gca gag gtt ttg acc cta gcc gca aag ctc aag gca gcg ccg ttt tcg 211
Ala Glu Val Leu Thr Leu Ala Ala Lys Leu Lys Ala Ala Pro Phe Ser
25 30 35

gag cgt cca ctc gag gga cca aag tcc gtt gca gtt ctt ttt gat aag 259
Glu Arg Pro Leu Glu Gly Pro Lys Ser Val Ala Val Leu Phe Asp Lys
40 45 50

act tca act cgt act cgc ttc tcc ttc gac gcg ggc atc gct cat ttg 307
Thr Ser Thr Arg Thr Arg Phe Ser Phe Asp Ala Gly Ile Ala His Leu
55 60 65

ggt gga cac gcc atc gtc gtg gat tcc ggt agc tca cag atg ggt aag 355
Gly Gly His Ala Ile Val Val Asp Ser Gly Ser Ser Gln Met Gly Lys
70 75 80 85

ggc gag tcc ctg cag gac acc gca gct gta ttg tcc cgc tac gtg gaa 403
Gly Glu Ser Leu Gln Asp Thr Ala Ala Val Leu Ser Arg Tyr Val Glu
90 95 100

gca att gtg tgg cgc acc tac gca cac agc aat ttc cac gcc atg gcg 451
Ala Ile Val Trp Arg Thr Tyr Ala His Ser Asn Phe His Ala Met Ala
105 110 115

gag acg tcc act gtg ccg ctg gtg aac tcc ttg tcc gat gat ctg cac 499
Glu Thr Ser Thr Val Pro Leu Val Asn Ser Leu Ser Asp Asp Leu His
120 125 130

cca tgc cag att ctg gct gat ctg cag act atc gtg gaa aac ctc agc 547
Pro Cys Gln Ile Leu Ala Asp Leu Gln Thr Ile Val Glu Asn Leu Ser
135 140 145

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cct gaa gaa ggc cca gca ggc ctt aag ggt aag aag gct gtg tac ctg 595
Pro Glu Glu Gly Pro Ala Gly Leu Lys Gly Lys Lys Ala Val Tyr Leu
150                      155                      160                      165

ggc gat ggc gac aac aac atg gcc aac tcc tac atg att ggc ttt gcc 643
Gly Asp Gly Asp Asn Asn Met Ala Asn Ser Tyr Met Ile Gly Phe Ala
170                      175                      180

acc gcg ggc atg gat att tcc atc atc gct cct gaa ggg ttc cag cct 691
Thr Ala Gly Met Asp Ile Ser Ile Ile Ala Pro Glu Gly Phe Gln Pro
185                      190                      195

cgt gcg gaa ttc gtg gag cgc gcg gaa aag cgt ggc cag gaa acc ggc 739
Arg Ala Glu Phe Val Glu Arg Ala Glu Lys Arg Gly Gln Glu Thr Gly
200                      205                      210

gcg aag gtt gtt gtc acc gac agc ctc gac gag gtt gcc ggc gcc gat 787
Ala Lys Val Val Val Thr Asp Ser Leu Asp Glu Val Ala Gly Ala Asp
215                      220                      225

gtt gtc atc acc gat acc tgg gta tcc atg ggt atg gaa aac gac ggc 835
Val Val Ile Thr Asp Thr Trp Val Ser Met Gly Met Glu Asn Asp Gly
230                      235                      240                      245

atc gat cgc acc aca cct ttc gtt cct tac cag gtc aac gat gag gtc 883
Ile Asp Arg Thr Thr Pro Phe Val Pro Tyr Gln Val Asn Asp Glu Val
250                      255                      260

atg gcg aaa gct aac gac ggc gcc atc ttc ctg cac tgc ctt cct gcc 931
Met Ala Lys Ala Asn Asp Gly Ala Ile Phe Leu His Cys Leu Pro Ala
265                      270                      275

tac cgt ggc aaa gaa gtg gca gcc tcc gtg att gat gga cca gcg tcc 979
Tyr Arg Gly Lys Glu Val Ala Ala Ser Val Ile Asp Gly Pro Ala Ser
280                      285                      290

aaa gtt ttc gat gaa gca gaa aac cgc ctc cac gct cag aaa gca ctg 1027
Lys Val Phe Asp Glu Ala Glu Asn Arg Leu His Ala Gln Lys Ala Leu
295                      300                      305

ctg gtg tgg ctg ctg gcc aac cag ccg agg taagacatgt cccttggtc 1077
Leu Val Trp Leu Leu Ala Asn Gln Pro Arg
310                      315

aac 1080

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<210> 334

<211> 319

<212> PRT

<213> Corynebacterium glutamicum

<400> 334

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Met Thr Ser Gln Pro Gln Val Arg His Phe Leu Ala Asp Asp Asp Leu
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Thr Pro Ala Glu Gln Ala Glu Val Leu Thr Leu Ala Ala Lys Leu Lys
20                      25                      30

Ala Ala Pro Phe Ser Glu Arg Pro Leu Glu Gly Pro Lys Ser Val Ala
35                      40                      45

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Val Leu Phe Asp Lys Thr Ser Thr Arg Thr Arg Phe Ser Phe Asp Ala
 50 55 60
 Gly Ile Ala His Leu Gly Gly His Ala Ile Val Val Asp Ser Gly Ser
 65 70 75 80
 Ser Gln Met Gly Lys Gly Glu Ser Leu Gln Asp Thr Ala Ala Val Leu
 85 90 95
 Ser Arg Tyr Val Glu Ala Ile Val Trp Arg Thr Tyr Ala His Ser Asn
 100 105 110
 Phe His Ala Met Ala Glu Thr Ser Thr Val Pro Leu Val Asn Ser Leu
 115 120 125
 Ser Asp Asp Leu His Pro Cys Gln Ile Leu Ala Asp Leu Gln Thr Ile
 130 135 140
 Val Glu Asn Leu Ser Pro Glu Glu Gly Pro Ala Gly Leu Lys Gly Lys
 145 150 155 160
 Lys Ala Val Tyr Leu Gly Asp Gly Asp Asn Asn Met Ala Asn Ser Tyr
 165 170 175
 Met Ile Gly Phe Ala Thr Ala Gly Met Asp Ile Ser Ile Ile Ala Pro
 180 185 190
 Glu Gly Phe Gln Pro Arg Ala Glu Phe Val Glu Arg Ala Glu Lys Arg
 195 200 205
 Gly Gln Glu Thr Gly Ala Lys Val Val Val Thr Asp Ser Leu Asp Glu
 210 215 220
 Val Ala Gly Ala Asp Val Val Ile Thr Asp Thr Trp Val Ser Met Gly
 225 230 235 240
 Met Glu Asn Asp Gly Ile Asp Arg Thr Thr Pro Phe Val Pro Tyr Gln
 245 250 255
 Val Asn Asp Glu Val Met Ala Lys Ala Asn Asp Gly Ala Ile Phe Leu
 260 265 270
 His Cys Leu Pro Ala Tyr Arg Gly Lys Glu Val Ala Ala Ser Val Ile
 275 280 285
 Asp Gly Pro Ala Ser Lys Val Phe Asp Glu Ala Glu Asn Arg Leu His
 290 295 300
 Ala Gln Lys Ala Leu Leu Val Trp Leu Leu Ala Asn Gln Pro Arg
 305 310 315

<210> 335

<211> 1326

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1303)

<223> RXA02160

<400> 335

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ttttcgagga ataccaaccc tttcaacaca ataattttct ttaaacaatcc ttgctgtcca 60

ccacggctgg caaggaactt aaaatgaagg agcacacctc atg act aac cgc atc 115
                                   Met Thr Asn Arg Ile
                                   1           5

gtt ctt gca tac tcc ggc ggt ctg gac acc act gtg gca att cca tac 163
Val Leu Ala Tyr Ser Gly Gly Leu Asp Thr Thr Val Ala Ile Pro Tyr
                        10                15                20

ctg aag aag atg att gat ggt gaa gtc atc gca gtt tcc ctc gac ctg 211
Leu Lys Lys Met Ile Asp Gly Glu Val Ile Ala Val Ser Leu Asp Leu
                        25                30                35

ggc cag ggt gga gag aac atg gac aac gtt cgc cag cgt gca ttg gat 259
Gly Gln Gly Gly Glu Asn Met Asp Asn Val Arg Gln Arg Ala Leu Asp
                        40                45                50

gcc ggt gca gct gag tcc atc gtt gtt gat gca aag gat gag ttc gct 307
Ala Gly Ala Ala Glu Ser Ile Val Val Asp Ala Lys Asp Glu Phe Ala
                        55                60                65

gag gag tac tgc ctg cca acc atc aag gca aac ggc atg tac atg aag 355
Glu Glu Tyr Cys Leu Pro Thr Ile Lys Ala Asn Gly Met Tyr Met Lys
                        70                75                80                85

cag tac cca ctg gtt tct gca atc tcc cgc cca ctg atc gtc aag cac 403
Gln Tyr Pro Leu Val Ser Ala Ile Ser Arg Pro Leu Ile Val Lys His
                        90                95                100

ctc gtt gag gct ggc aag cag ttc aac ggt acc cac gtt gca cac ggc 451
Leu Val Glu Ala Gly Lys Gln Phe Asn Gly Thr His Val Ala His Gly
                        105                110                115

tgc act ggt aag ggc aac gac cag gtt cgt ttc gag gtc ggc ttc atg 499
Cys Thr Gly Lys Gly Asn Asp Gln Val Arg Phe Glu Val Gly Phe Met
                        120                125                130

gac acc gat cca aac ctg gag atc att gca cct gct cgt gac ttc gca 547
Asp Thr Asp Pro Asn Leu Glu Ile Ile Ala Pro Ala Arg Asp Phe Ala
                        135                140                145

tgg acc cgc gac aag gct atc gcc ttc gcc gag gag aac aac gtt cca 595
Trp Thr Arg Asp Lys Ala Ile Ala Phe Ala Glu Glu Asn Asn Val Pro
                        150                155                160                165

atc gag cag tcc gtg aag tcc cca ttc tcc atc gac cag aac gtc tgg 643
Ile Glu Gln Ser Val Lys Ser Pro Phe Ser Ile Asp Gln Asn Val Trp
                        170                175                180

ggc cgc gct att gag acc ggt tac ctg gaa gat ctg tgg aat gct cca 691
Gly Arg Ala Ile Glu Thr Gly Tyr Leu Glu Asp Leu Trp Asn Ala Pro
                        185                190                195

acc aag gac atc tac gca tac acc gag gat cca gct ctg ggt aac gct 739
Thr Lys Asp Ile Tyr Ala Tyr Thr Glu Asp Pro Ala Leu Gly Asn Ala
                        200                205                210

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cca gat gag gtc atc atc tcc ttc gag ggt ggc aag cca gtc tcc atc 787
Pro Asp Glu Val Ile Ile Ser Phe Glu Gly Gly Lys Pro Val Ser Ile
215 220 225

gat ggc cgt cca gtc tcc gta ctg cag gct att gaa gag ctg aac cgt 835
Asp Gly Arg Pro Val Ser Val Leu Gln Ala Ile Glu Glu Leu Asn Arg
230 235 240 245

cgt gca ggc gca cag ggc gtt ggc cgc ctt gac atg gtt gag gac cgt 883
Arg Ala Gly Ala Gln Gly Val Gly Arg Leu Asp Met Val Glu Asp Arg
250 255 260

ctc gtg ggc atc aag tcc cgc gaa atc tac gaa gca cca ggc gca atc 931
Leu Val Gly Ile Lys Ser Arg Glu Ile Tyr Glu Ala Pro Gly Ala Ile
265 270 275

gca ctg att aag gct cac gag gct ttg gaa gat gtc acc atc gag cgc 979
Ala Leu Ile Lys Ala His Glu Ala Leu Glu Asp Val Thr Ile Glu Arg
280 285 290

gaa ctg gct cgc tac aag cgc ggc gtt gac gca cgt tgg gct gag gaa 1027
Glu Leu Ala Arg Tyr Lys Arg Gly Val Asp Ala Arg Trp Ala Glu Glu
295 300 305

gta tac gac ggc ctg tgg ttc gga cct ctg aag cgc tcc ctg gac gcg 1075
Val Tyr Asp Gly Leu Trp Phe Gly Pro Leu Lys Arg Ser Leu Asp Ala
310 315 320 325

ttc att gat tcc acc cag gag cac gtc acc ggc gat atc cgc atg gtt 1123
Phe Ile Asp Ser Thr Gln Glu His Val Thr Gly Asp Ile Arg Met Val
330 335 340

ctg cac gca ggt tcc atc acc atc aat ggt cgt cgt tcc agc cac tcc 1171
Leu His Ala Gly Ser Ile Thr Ile Asn Gly Arg Arg Ser Ser His Ser
345 350 355

ctg tac gac ttc aac ctg gct acc tac gac acc ggc gac acc ttc gac 1219
Leu Tyr Asp Phe Asn Leu Ala Thr Tyr Asp Thr Gly Asp Thr Phe Asp
360 365 370

cag acc ctg gct aag ggc ttt gtc cag ctg cac ggt ctg tcc tcc aag 1267
Gln Thr Leu Ala Lys Gly Phe Val Gln Leu His Gly Leu Ser Ser Lys
375 380 385

atc gct aac aag cgc gat cgc gaa gct ggc aac aac taagccacct 1313
Ile Ala Asn Lys Arg Asp Arg Glu Ala Gly Asn Asn
390 395 400

tttcaagcat cca 1326

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<210> 336

<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 336

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Met Thr Asn Arg Ile Val Leu Ala Tyr Ser Gly Gly Leu Asp Thr Thr
1 5 10 15

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Val Ala Ile Pro Tyr Leu Lys Lys Met Ile Asp Gly Glu Val Ile Ala

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20					25					30						
Val	Ser	Leu	Asp	Leu	Gly	Gln	Gly	Gly	Glu	Asn	Met	Asp	Asn	Val	Arg	
35					40					45						
Gln	Arg	Ala	Leu	Asp	Ala	Gly	Ala	Ala	Glu	Ser	Ile	Val	Val	Asp	Ala	
50					55					60						
Lys	Asp	Glu	Phe	Ala	Glu	Glu	Tyr	Cys	Leu	Pro	Thr	Ile	Lys	Ala	Asn	
65					70					75					80	
Gly	Met	Tyr	Met	Lys	Gln	Tyr	Pro	Leu	Val	Ser	Ala	Ile	Ser	Arg	Pro	
85					90					95						
Leu	Ile	Val	Lys	His	Leu	Val	Glu	Ala	Gly	Lys	Gln	Phe	Asn	Gly	Thr	
100					105					110						
His	Val	Ala	His	Gly	Cys	Thr	Gly	Lys	Gly	Asn	Asp	Gln	Val	Arg	Phe	
115					120					125						
Glu	Val	Gly	Phe	Met	Asp	Thr	Asp	Pro	Asn	Leu	Glu	Ile	Ile	Ala	Pro	
130					135					140						
Ala	Arg	Asp	Phe	Ala	Trp	Thr	Arg	Asp	Lys	Ala	Ile	Ala	Phe	Ala	Glu	
145					150					155					160	
Glu	Asn	Asn	Val	Pro	Ile	Glu	Gln	Ser	Val	Lys	Ser	Pro	Phe	Ser	Ile	
165					170					175						
Asp	Gln	Asn	Val	Trp	Gly	Arg	Ala	Ile	Glu	Thr	Gly	Tyr	Leu	Glu	Asp	
180					185					190						
Leu	Trp	Asn	Ala	Pro	Thr	Lys	Asp	Ile	Tyr	Ala	Tyr	Thr	Glu	Asp	Pro	
195					200					205						
Ala	Leu	Gly	Asn	Ala	Pro	Asp	Glu	Val	Ile	Ile	Ser	Phe	Glu	Gly	Gly	
210					215					220						
Lys	Pro	Val	Ser	Ile	Asp	Gly	Arg	Pro	Val	Ser	Val	Leu	Gln	Ala	Ile	
225					230					235					240	
Glu	Glu	Leu	Asn	Arg	Arg	Ala	Gly	Ala	Gln	Gly	Val	Gly	Arg	Leu	Asp	
245					250					255						
Met	Val	Glu	Asp	Arg	Leu	Val	Gly	Ile	Lys	Ser	Arg	Glu	Ile	Tyr	Glu	
260					265					270						
Ala	Pro	Gly	Ala	Ile	Ala	Leu	Ile	Lys	Ala	His	Glu	Ala	Leu	Glu	Asp	
275					280					285						
Val	Thr	Ile	Glu	Arg	Glu	Leu	Ala	Arg	Tyr	Lys	Arg	Gly	Val	Asp	Ala	
290					295					300						
Arg	Trp	Ala	Glu	Glu	Val	Tyr	Asp	Gly	Leu	Trp	Phe	Gly	Pro	Leu	Lys	
305					310					315					320	
Arg	Ser	Leu	Asp	Ala	Phe	Ile	Asp	Ser	Thr	Gln	Glu	His	Val	Thr	Gly	
325					330					335						
Asp	Ile	Arg	Met	Val	Leu	His	Ala	Gly	Ser	Ile	Thr	Ile	Asn	Gly	Arg	
340					345					350						

Arg Ser Ser His Ser Leu Tyr Asp Phe Asn Leu Ala Thr Tyr Asp Thr
 355 360 365

Gly Asp Thr Phe Asp Gln Thr Leu Ala Lys Gly Phe Val Gln Leu His
 370 375 380

Gly Leu Ser Ser Lys Ile Ala Asn Lys Arg Asp Arg Glu Ala Gly Asn
 385 390 395 400

Asn

<210> 337

<211> 1554

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1531)

<223> RXN02162

<400> 337

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gactagaact tcaagtattt agaaagtaga agaacaccac atg gaa cag cac gga 115
 Met Glu Gln His Gly
 1 5

acc aat gaa ggt gcg ctg tgg ggc ggc cgc ttc tcc ggt gga ccc tcc 163
 Thr Asn Glu Gly Ala Leu Trp Gly Gly Arg Phe Ser Gly Gly Pro Ser
 10 15 20

gag gcc atg ttc gcc ttg agt gtc tcc act cat ttc gac tgg gtt ttg 211
 Glu Ala Met Phe Ala Leu Ser Val Ser Thr His Phe Asp Trp Val Leu
 25 30 35

gcc cct tat gat gtg ttg gcc tcc aag gca cac gcc aag gtt ttg cac 259
 Ala Pro Tyr Asp Val Leu Ala Ser Lys Ala His Ala Lys Val Leu His
 40 45 50

caa gca gat cta ctt tct gat gaa gat cta gcc acc atg ctg gct ggg 307
 Gln Ala Asp Leu Leu Ser Asp Glu Asp Leu Ala Thr Met Leu Ala Gly
 55 60 65

ctt gat cag ctg ggc aag gat gtc gcc gac gga acc ttc ggt ccg ctg 355
 Leu Asp Gln Leu Gly Lys Asp Val Ala Asp Gly Thr Phe Gly Pro Leu
 70 75 80 85

cct tct gat gag gat gtg cac ggc gcg atg gaa cgc ggt gtg att gac 403
 Pro Ser Asp Glu Asp Val His Gly Ala Met Glu Arg Gly Val Ile Asp
 90 95 100

cgc gtt ggt cct gag gtg ggc ggc cgt ctg cgc gct ggt cgt tcc cgc 451
 Arg Val Gly Pro Glu Val Gly Gly Arg Leu Arg Ala Gly Arg Ser Arg
 105 110 115

aac gac cag gtg gca acc ctg ttc cgc atg tgg gtc cgc gac gca gtg 499
 Asn Asp Gln Val Ala Thr Leu Phe Arg Met Trp Val Arg Asp Ala Val

120					125					130						
cgc	gac	atc	gcg	ctg	gga	aca	acc	gag	ctt	gtc	gac	gcc	ctc	agc	gcc	547
Arg	Asp	Ile	Ala	Leu	Gly	Thr	Thr	Glu	Leu	Val	Asp	Ala	Leu	Ser	Ala	
135					140					145						
caa	gct	aag	gca	cat	gca	ggc	gcg	atc	atg	cca	ggc	aag	acc	cac	ttc	595
Gln	Ala	Lys	Ala	His	Ala	Gly	Ala	Ile	Met	Pro	Gly	Lys	Thr	His	Phe	
150					155					160					165	
cag	gca	gct	cag	ccg	gtc	ctt	ctg	gca	cac	cag	ctg	ctg	gca	cac	gca	643
Gln	Ala	Ala	Gln	Pro	Val	Leu	Leu	Ala	His	Gln	Leu	Leu	Ala	His	Ala	
170					175					180						
cag	cct	ttg	ctg	cg	gat	att	gat	cgt	atc	cgt	gac	ctg	gac	aag	cgt	691
Gln	Pro	Leu	Leu	Arg	Asp	Ile	Asp	Arg	Ile	Arg	Asp	Leu	Asp	Lys	Arg	
185					190					195						
ctt	gcg	gtg	tct	cct	tac	gg	tcc	ggc	gca	ctt	gct	gg	tcc	tct	ttg	739
Leu	Ala	Val	Ser	Pro	Tyr	Gly	Ser	Gly	Ala	Leu	Ala	Gly	Ser	Ser	Leu	
200					205					210						
aag	ctc	aac	cct	gaa	gca	atc	gct	gaa	gaa	ctc	ggc	ttt	gat	tcc	gca	787
Lys	Leu	Asn	Pro	Glu	Ala	Ile	Ala	Glu	Glu	Leu	Gly	Phe	Asp	Ser	Ala	
215					220					225						
gca	gat	aac	tcc	att	gat	gcc	acc	agc	tcc	cg	gat	ttc	gca	tct	gaa	835
Ala	Asp	Asn	Ser	Ile	Asp	Ala	Thr	Ser	Ser	Arg	Asp	Phe	Ala	Ser	Glu	
230					235					240					245	
acc	gcc	ttc	gtg	ctg	gcg	cag	ctt	gca	gtg	gat	atg	tcc	cg	ttg	gct	883
Thr	Ala	Phe	Val	Leu	Ala	Gln	Leu	Ala	Val	Asp	Met	Ser	Arg	Leu	Ala	
250					255					260						
gaa	gaa	atc	atc	gca	tgg	tgc	acc	cca	gaa	ttt	gg	tac	atc	acc	ttg	931
Glu	Glu	Ile	Ile	Ala	Trp	Cys	Thr	Pro	Glu	Phe	Gly	Tyr	Ile	Thr	Leu	
265					270					275						
tct	gat	tcc	tgg	tcc	aca	ggc	agc	tca	atc	atg	ccg	cag	aag	aag	aac	979
Ser	Asp	Ser	Trp	Ser	Thr	Gly	Ser	Ser	Ile	Met	Pro	Gln	Lys	Lys	Asn	
280					285					290						
cct	gac	gtg	gca	gag	ctg	acc	cgt	ggc	aag	tct	gg	cg	ttg	atc	gg	1027
Pro	Asp	Val	Ala	Glu	Leu	Thr	Arg	Gly	Lys	Ser	Gly	Arg	Leu	Ile	Gly	
295					300					305						
aac	ctc	acc	gg	ctg	ctg	gct	acc	ctg	aag	gca	cag	cct	tta	gcg	tac	1075
Asn	Leu	Thr	Gly	Leu	Leu	Ala	Thr	Leu	Lys	Ala	Gln	Pro	Leu	Ala	Tyr	
310					315					320					325	
aac	cg	gac	ctg	cag	gaa	gat	aag	gaa	cca	atc	gta	gat	tcc	gtg	gcg	1123
Asn	Arg	Asp	Leu	Gln	Glu	Asp	Lys	Glu	Pro	Ile	Val	Asp	Ser	Val	Ala	
330					335					340						
cag	ctc	aac	ctg	ctg	ctc	cct	gca	atg	act	gg	ttg	gtt	tcc	acc	ttg	1171
Gln	Leu	Asn	Leu	Leu	Leu	Pro	Ala	Met	Thr	Gly	Leu	Val	Ser	Thr	Leu	
345					350					355						
acc	ttc	aac	acc	gag	cg	atg	cgt	gaa	ctt	gca	cca	gca	gg	ttc	acc	1219
Thr	Phe	Asn	Thr	Glu	Arg	Met	Arg	Glu	Leu	Ala	Pro	Ala	Gly	Phe	Thr	
360					365					370						

ctt gcc acc gac ttg gct gag tgg atg gtg cgc cag ggc gtt cca ttc 1267
 Leu Ala Thr Asp Leu Ala Glu Trp Met Val Arg Gln Gly Val Pro Phe
 375 380 385

cgt gag gca cac gaa gca tcc ggc gct tgc gtg cgg atc gcg gag tcc 1315
 Arg Glu Ala His Glu Ala Ser Gly Ala Cys Val Arg Ile Ala Glu Ser
 390 395 400 405

agg gga gtg gac ctt atc gat ctc act gat gaa gaa ctc agt ggc gtt 1363
 Arg Gly Val Asp Leu Ile Asp Leu Thr Asp Glu Glu Leu Ser Gly Val
 410 415 420

gat gca cgt ctg acc cca gag gta cgg gaa gtg ctc acc att gat ggt 1411
 Asp Ala Arg Leu Thr Pro Glu Val Arg Glu Val Leu Thr Ile Asp Gly
 425 430 435

gca gtg gct tcc cgt gca acg cgc ggt gga acc gcg ggc gtg cgg gtt 1459
 Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr Ala Gly Val Arg Val
 440 445 450

gcg gag caa cgc gca cgt gtc gat gcc gca agt acc gct cac gcg gag 1507
 Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser Thr Ala His Ala Glu
 455 460 465

tgg gca cgt gcg ggg gta cgt cga taagcattag tttatggcct gtg 1554
 Trp Ala Arg Ala Gly Val Arg Arg
 470 475

<210> 338

<211> 477

<212> PRT

<213> Corynebacterium glutamicum

<400> 338

Met Glu Gln His Gly Thr Asn Glu Gly Ala Leu Trp Gly Gly Arg Phe
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Ser Gly Gly Pro Ser Glu Ala Met Phe Ala Leu Ser Val Ser Thr His
 20 25 30

Phe Asp Trp Val Leu Ala Pro Tyr Asp Val Leu Ala Ser Lys Ala His
 35 40 45

Ala Lys Val Leu His Gln Ala Asp Leu Leu Ser Asp Glu Asp Leu Ala
 50 55 60

Thr Met Leu Ala Gly Leu Asp Gln Leu Gly Lys Asp Val Ala Asp Gly
 65 70 75 80

Thr Phe Gly Pro Leu Pro Ser Asp Glu Asp Val His Gly Ala Met Glu
 85 90 95

Arg Gly Val Ile Asp Arg Val Gly Pro Glu Val Gly Gly Arg Leu Arg
 100 105 110

Ala Gly Arg Ser Arg Asn Asp Gln Val Ala Thr Leu Phe Arg Met Trp
 115 120 125

Val Arg Asp Ala Val Arg Asp Ile Ala Leu Gly Thr Thr Glu Leu Val

130	135	140
Asp Ala Leu Ser Ala Gln Ala Lys Ala His Ala Gly Ala Ile Met Pro		
145	150	155 160
Gly Lys Thr His Phe Gln Ala Ala Gln Pro Val Leu Leu Ala His Gln		
	165	170 175
Leu Leu Ala His Ala Gln Pro Leu Leu Arg Asp Ile Asp Arg Ile Arg		
	180	185 190
Asp Leu Asp Lys Arg Leu Ala Val Ser Pro Tyr Gly Ser Gly Ala Leu		
	195	200 205
Ala Gly Ser Ser Leu Lys Leu Asn Pro Glu Ala Ile Ala Glu Glu Leu		
	210	215 220
Gly Phe Asp Ser Ala Ala Asp Asn Ser Ile Asp Ala Thr Ser Ser Arg		
	225	230 235 240
Asp Phe Ala Ser Glu Thr Ala Phe Val Leu Ala Gln Leu Ala Val Asp		
	245	250 255
Met Ser Arg Leu Ala Glu Glu Ile Ile Ala Trp Cys Thr Pro Glu Phe		
	260	265 270
Gly Tyr Ile Thr Leu Ser Asp Ser Trp Ser Thr Gly Ser Ser Ile Met		
	275	280 285
Pro Gln Lys Lys Asn Pro Asp Val Ala Glu Leu Thr Arg Gly Lys Ser		
	290	295 300
Gly Arg Leu Ile Gly Asn Leu Thr Gly Leu Leu Ala Thr Leu Lys Ala		
	305	310 315 320
Gln Pro Leu Ala Tyr Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile		
	325	330 335
Val Asp Ser Val Ala Gln Leu Asn Leu Leu Leu Pro Ala Met Thr Gly		
	340	345 350
Leu Val Ser Thr Leu Thr Phe Asn Thr Glu Arg Met Arg Glu Leu Ala		
	355	360 365
Pro Ala Gly Phe Thr Leu Ala Thr Asp Leu Ala Glu Trp Met Val Arg		
	370	375 380
Gln Gly Val Pro Phe Arg Glu Ala His Glu Ala Ser Gly Ala Cys Val		
	385	390 395 400
Arg Ile Ala Glu Ser Arg Gly Val Asp Leu Ile Asp Leu Thr Asp Glu		
	405	410 415
Glu Leu Ser Gly Val Asp Ala Arg Leu Thr Pro Glu Val Arg Glu Val		
	420	425 430
Leu Thr Ile Asp Gly Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr		
	435	440 445
Ala Gly Val Arg Val Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser		
	450	455 460

Thr Ala His Ala Glu Trp Ala Arg Ala Gly Val Arg Arg
465 470 475

<210> 339

<211> 906

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(883)

<223> FRXA02161

<400> 339

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gactagaact tcaagtattt agaaagtaga agaacaccac atg gaa cag cac gga 115
Met Glu Gln His Gly
1 5

acc aat gaa ggt gcg ctg tgg ggc ggc cgc ttc tcc ggt gga ccc tcc 163
Thr Asn Glu Gly Ala Leu Trp Gly Gly Arg Phe Ser Gly Gly Pro Ser
10 15 20

gag gcc atg ttc gcc ttg agt gtc tcc act cat ttc gac tgg gtt ttg 211
Glu Ala Met Phe Ala Leu Ser Val Ser Thr His Phe Asp Trp Val Leu
25 30 35

gcc cct tat gat gtg ttg gcc tcc aag gca cac gcc aag gtt ttg cac 259
Ala Pro Tyr Asp Val Leu Ala Ser Lys Ala His Ala Lys Val Leu His
40 45 50

caa gca gat cta ctt tct gat gaa gat cta gcc acc atg ctg gct ggg 307
Gln Ala Asp Leu Leu Ser Asp Glu Asp Leu Ala Thr Met Leu Ala Gly
55 60 65

ctt gat cag ctg ggc aag gat gtc gcc gac gga acc ttc ggt ccg ctg 355
Leu Asp Gln Leu Gly Lys Asp Val Ala Asp Gly Thr Phe Gly Pro Leu
70 75 80 85

cct tct gat gag gat gtg cac ggc gcg atg gaa cgc ggt gtg att gac 403
Pro Ser Asp Glu Asp Val His Gly Ala Met Glu Arg Gly Val Ile Asp
90 95 100

cgc gtt ggt cct gag gtg ggc ggc cgt ctg cgc gct ggt cgt tcc cgc 451
Arg Val Gly Pro Glu Val Gly Gly Arg Leu Arg Ala Gly Arg Ser Arg
105 110 115

aac gac cag gtg gca acc ctg ttc cgc atg tgg gtc cgc gac gca gtg 499
Asn Asp Gln Val Ala Thr Leu Phe Arg Met Trp Val Arg Asp Ala Val
120 125 130

cgc gac atc gcg ctg gga aca acc gag ctt gtc gac gcc ctc agc gcc 547
Arg Asp Ile Ala Leu Gly Thr Thr Glu Leu Val Asp Ala Leu Ser Ala
135 140 145

caa gct aag gca cat gca ggc gcg atc atg cca ggc aag acc cac ttc 595
Gln Ala Lys Ala His Ala Gly Ala Ile Met Pro Gly Lys Thr His Phe
150 155 160 165

cag gca gct cag ccg gtc ctt ctg gca cac cag ctg ctg gca cac gca 643
 Gln Ala Ala Gln Pro Val Leu Leu Ala His Gln Leu Leu Ala His Ala
 170 175 180

cag cct ttg ctg cgc gat att gat cgt atc cgt gac ctg gac aag cgt 691
 Gln Pro Leu Leu Arg Asp Ile Asp Arg Ile Arg Asp Leu Asp Lys Arg
 185 190 195

ctt gcg gtg tct cct tac ggt tcc ggc gca ctt gct ggt tcc tct ttg 739
 Leu Ala Val Ser Pro Tyr Gly Ser Gly Ala Leu Ala Gly Ser Ser Leu
 200 205 210

aag ctc aac cct gaa gca atc gct gaa gaa ctc ggc ttt gat tcc gca 787
 Lys Leu Asn Pro Glu Ala Ile Ala Glu Glu Leu Gly Phe Asp Ser Ala
 215 220 225

gca gat aac tcc att gat gcc acc agc tcc cgc gat ttc gca tct gaa 835
 Ala Asp Asn Ser Ile Asp Ala Thr Ser Ser Arg Asp Phe Ala Ser Glu
 230 235 240 245

acc gcc ttc gtg ctg gcg cag ctt gca ngc gga tat gtc ccg ctt ggc 883
 Thr Ala Phe Val Leu Ala Gln Leu Ala Xaa Gly Tyr Val Pro Leu Gly
 250 255 260

tgaagaaatc atcgcatggt gca 906

<210> 340

<211> 261

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 340

Met Glu Gln His Gly Thr Asn Glu Gly Ala Leu Trp Gly Gly Arg Phe
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Ser Gly Gly Pro Ser Glu Ala Met Phe Ala Leu Ser Val Ser Thr His
 20 25 30

Phe Asp Trp Val Leu Ala Pro Tyr Asp Val Leu Ala Ser Lys Ala His
 35 40 45

Ala Lys Val Leu His Gln Ala Asp Leu Leu Ser Asp Glu Asp Leu Ala
 50 55 60

Thr Met Leu Ala Gly Leu Asp Gln Leu Gly Lys Asp Val Ala Asp Gly
 65 70 75 80

Thr Phe Gly Pro Leu Pro Ser Asp Glu Asp Val His Gly Ala Met Glu
 85 90 95

Arg Gly Val Ile Asp Arg Val Gly Pro Glu Val Gly Gly Arg Leu Arg
 100 105 110

Ala Gly Arg Ser Arg Asn Asp Gln Val Ala Thr Leu Phe Arg Met Trp
 115 120 125

Val Arg Asp Ala Val Arg Asp Ile Ala Leu Gly Thr Thr Glu Leu Val
 130 135 140

Asp Ala Leu Ser Ala Gln Ala Lys Ala His Ala Gly Ala Ile Met Pro
 145 150 155 160
 Gly Lys Thr His Phe Gln Ala Ala Gln Pro Val Leu Leu Ala His Gln
 165 170 175
 Leu Leu Ala His Ala Gln Pro Leu Leu Arg Asp Ile Asp Arg Ile Arg
 180 185 190
 Asp Leu Asp Lys Arg Leu Ala Val Ser Pro Tyr Gly Ser Gly Ala Leu
 195 200 205
 Ala Gly Ser Ser Leu Lys Leu Asn Pro Glu Ala Ile Ala Glu Glu Leu
 210 215 220
 Gly Phe Asp Ser Ala Ala Asp Asn Ser Ile Asp Ala Thr Ser Ser Arg
 225 230 235 240
 Asp Phe Ala Ser Glu Thr Ala Phe Val Leu Ala Gln Leu Ala Xaa Gly
 245 250 255
 Tyr Val Pro Leu Gly
 260

<210> 341
 <211> 786
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(763)
 <223> FRXA02162

<400> 341
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 tctgaaaccg ccttcgtgct ggcgcagctt gcangtggat atg tcc cgc ttg gct 115
 Met Ser Arg Leu Ala
 1 5
 gaa gaa atc atc gca tgg tgc acc cca gaa ttt ggt tac atc acc ttg 163
 Glu Glu Ile Ile Ala Trp Cys Thr Pro Glu Phe Gly Tyr Ile Thr Leu
 10 15 20
 tct gat tcc tgg tcc aca ggc agc tca atc atg ccg cag aag aag aac 211
 Ser Asp Ser Trp Ser Thr Gly Ser Ser Ile Met Pro Gln Lys Lys Asn
 25 30 35
 cct gac gtg gca gag ctg acc cgt ggc aag tct ggt cgc ttg atc ggt 259
 Pro Asp Val Ala Glu Leu Thr Arg Gly Lys Ser Gly Arg Leu Ile Gly
 40 45 50
 aac ctc acc ggt ctg ctg gct acc ctg aag gca cag cct tta gcg tac 307
 Asn Leu Thr Gly Leu Leu Ala Thr Leu Lys Ala Gln Pro Leu Ala Tyr
 55 60 65
 aac cgc gac ctg cag gaa gat aag gaa cca atc gta gat tcc gtg gcg 355
 Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile Val Asp Ser Val Ala
 70 75 80 85

cag ctc aac ctg ctg ctc cct gca atg act ggt ttg gtt tcc acc ttg 403
 Gln Leu Asn Leu Leu Leu Pro Ala Met Thr Gly Leu Val Ser Thr Leu
 90 95 100
 acc ttc aac acc gag cgc atg cgt gaa ctt gca cca gca ggt ttc acc 451
 Thr Phe Asn Thr Glu Arg Met Arg Glu Leu Ala Pro Ala Gly Phe Thr
 105 110 115
 ctt gcc acc gac ttg gct gag tgg atg gtg cgc cag ggc gtt cca ttc 499
 Leu Ala Thr Asp Leu Ala Glu Trp Met Val Arg Gln Gly Val Pro Phe
 120 125 130
 cgt gag gca cac gaa gca tcc ggc gct tgc gtg cgg atc gcg gag tcc 547
 Arg Glu Ala His Glu Ala Ser Gly Ala Cys Val Arg Ile Ala Glu Ser
 135 140 145
 agg gga gtg gac ctt atc gat ctc act gat gaa gaa ctc agt ggc gtt 595
 Arg Gly Val Asp Leu Ile Asp Leu Thr Asp Glu Glu Leu Ser Gly Val
 150 155 160 165
 gat gca cgt ctg acc cca gag gta cgg gaa gtg ctc acc att gat ggt 643
 Asp Ala Arg Leu Thr Pro Glu Val Arg Glu Val Leu Thr Ile Asp Gly
 170 175 180
 gca gtg gct tcc cgt gca acg cgc ggt gga acc gcg ggc gtg cgg gtt 691
 Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr Ala Gly Val Arg Val
 185 190 195
 gcg gag caa cgc gca cgt gtc gat gcc gca agt acc gct cac gcg gag 739
 Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser Thr Ala His Ala Glu
 200 205 210
 tgg gca cgt gcg ggg gta cgt cga taagcattag tttatggcct gtg 786
 Trp Ala Arg Ala Gly Val Arg
 215 220

<210> 342

<211> 221

<212> PRT

<213> Corynebacterium glutamicum

<400> 342

Met Ser Arg Leu Ala Glu Glu Ile Ile Ala Trp Cys Thr Pro Glu Phe
 1 5 10 15
 Gly Tyr Ile Thr Leu Ser Asp Ser Trp Ser Thr Gly Ser Ser Ile Met
 20 25 30
 Pro Gln Lys Lys Asn Pro Asp Val Ala Glu Leu Thr Arg Gly Lys Ser
 35 40 45
 Gly Arg Leu Ile Gly Asn Leu Thr Gly Leu Leu Ala Thr Leu Lys Ala
 50 55 60
 Gln Pro Leu Ala Tyr Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile
 65 70 75 80
 Val Asp Ser Val Ala Gln Leu Asn Leu Leu Leu Pro Ala Met Thr Gly
 85 90 95

Leu Val Ser Thr Leu Thr Phe Asn Thr Glu Arg Met Arg Glu Leu Ala
 100 105 110
 Pro Ala Gly Phe Thr Leu Ala Thr Asp Leu Ala Glu Trp Met Val Arg
 115 120 125
 Gln Gly Val Pro Phe Arg Glu Ala His Glu Ala Ser Gly Ala Cys Val
 130 135 140
 Arg Ile Ala Glu Ser Arg Gly Val Asp Leu Ile Asp Leu Thr Asp Glu
 145 150 155 160
 Glu Leu Ser Gly Val Asp Ala Arg Leu Thr Pro Glu Val Arg Glu Val
 165 170 175
 Leu Thr Ile Asp Gly Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr
 180 185 190
 Ala Gly Val Arg Val Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser
 195 200 205
 Thr Ala His Ala Glu Trp Ala Arg Ala Gly Val Arg Arg
 210 215 220

<210> 343
 <211> 1269
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1246)
 <223> RXA02262

<400> 343
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 tcgataagca aaaaatcgct gatactcgaa aggcctcaaa atg acc gca acc tac 115
 Met Thr Ala Thr Tyr
 1 5
 acc act gaa acc gcc atc aat ttc ttg ttc ttg agc gaa ccg gac atg 163
 Thr Thr Glu Thr Ala Ile Asn Phe Leu Phe Leu Ser Glu Pro Asp Met
 10 15 20
 atc gcg gcc gga gtc aaa gac gtc gcg caa tgc gtc gat gtc atg gag 211
 Ile Ala Ala Gly Val Lys Asp Val Ala Gln Cys Val Asp Val Met Glu
 25 30 35
 gaa acg ctc gtg ctc ttg gcg cag ggc gac tac aaa atg gcc ggt ttg 259
 Glu Thr Leu Val Leu Leu Ala Gln Gly Asp Tyr Lys Met Ala Gly Leu
 40 45 50
 aac tcc aac tcg cat ggc gcg atg atc acc ttc ccg gaa aac cca gaa 307
 Asn Ser Asn Ser His Gly Ala Met Ile Thr Phe Pro Glu Asn Pro Glu
 55 60 65
 ttt gaa ggc atg ccc aag gac ggc ccc gac cgc cga ttc atg gcg atg 355
 Phe Glu Gly Met Pro Lys Asp Gly Pro Asp Arg Arg Phe Met Ala Met

70	75	80	85	
ccc gca tac ctc ggc ggg cga ttc aaa aac acc ggc gtg aag tgg tac				403
Pro Ala Tyr Leu Gly Gly Arg Phe Lys Asn Thr Gly Val Lys Trp Tyr	90	95	100	
gga tcc aac gcg gaa aac aag gcc tca ggc ttg cct cgc tcg atc cac				451
Gly Ser Asn Ala Glu Asn Lys Ala Ser Gly Leu Pro Arg Ser Ile His	105	110	115	
acc ttc gtc ctc aac gac acg gtc acc ggt gca ccg aag gcc atc atg				499
Thr Phe Val Leu Asn Asp Thr Val Thr Gly Ala Pro Lys Ala Ile Met	120	125	130	
tcc gcg aac ctg ctg tcc gcc tac cgc acc ggc gcg gtt ccc ggc gtg				547
Ser Ala Asn Leu Leu Ser Ala Tyr Arg Thr Gly Ala Val Pro Gly Val	135	140	145	
ggc gtg aag cac tta gcg gtc gcc gac gcg aca acc ttg gct gtc gtc				595
Gly Val Lys His Leu Ala Val Ala Asp Ala Thr Thr Leu Ala Val Val	150	155	160	165
gga cct ggt gtc atg gcg aaa acc atc acc gaa gcg tgc atc gca gag				643
Gly Pro Gly Val Met Ala Lys Thr Ile Thr Glu Ala Cys Ile Ala Glu	170	175	180	
cgc cca gga atc acc acc atc aag atc aag gga cgc agc gaa cgc ggc				691
Arg Pro Gly Ile Thr Thr Ile Lys Ile Lys Gly Arg Ser Glu Arg Gly	185	190	195	
atc aac gcc ttt gca aca tgg gcg ttg gaa aaa ttc ccc gag atc gaa				739
Ile Asn Ala Phe Ala Thr Trp Ala Leu Glu Lys Phe Pro Glu Ile Glu	200	205	210	
gtg gtc gcc gtc gga tct gaa gaa gac gtg gtc aaa gac gcc gac atc				787
Val Val Ala Val Gly Ser Glu Glu Asp Val Val Lys Asp Ala Asp Ile	215	220	225	
gtc atc gcc gcc acc acc acg gac gcc gcc ggc tcc tcc gcc ttc cca				835
Val Ile Ala Ala Thr Thr Thr Asp Ala Ala Gly Ser Ser Ala Phe Pro	230	235	240	245
tac ttc aaa aaa gaa tgg ctc aag ccg ggc gca ttg ctg ctg ctt cca				883
Tyr Phe Lys Lys Glu Trp Leu Lys Pro Gly Ala Leu Leu Leu Leu Pro	250	255	260	
gcc gcc ggt cgc ttc gac gac gct tat ttg ctt gac gac gcc cgc ctc				931
Ala Ala Gly Arg Phe Asp Asp Ala Tyr Leu Leu Asp Asp Ala Arg Leu	265	270	275	
gtt gtt gac tac atg ggg ctc tac gaa gcc tgg gca gaa gaa tac ggc				979
Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp Ala Glu Glu Tyr Gly	280	285	290	
cca cag gcc tac caa cta ctc ggc att cca gga acc cac tgg tac gac				1027
Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly Thr His Trp Tyr Asp	295	300	305	
ctg gcg ctg caa gga aaa ctc gac ctt gca aag att tcc cag att ggc				1075
Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys Ile Ser Gln Ile Gly	310	315	320	325

gat atc tgc tcc ggc aag cta ccc gga cgc acc aac gat gag gaa atc 1123
 Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr Asn Asp Glu Glu Ile
 330 335 340

atc ctc tat tcc gtc ggc ggc atg cca gta gaa gac gtc gcc tgg gca 1171
 Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu Asp Val Ala Trp Ala
 345 350 355

acc caa gtg tat gaa aac gcc ctg gaa aaa ggc gtc ggc acc aca ttg 1219
 Thr Gln Val Tyr Glu Asn Ala Leu Glu Lys Gly Val Gly Thr Thr Leu
 360 365 370

aac ctg tgg gaa tca ccc gca ctg gct tgagagaaga aacaacaatg 1266
 Asn Leu Trp Glu Ser Pro Ala Leu Ala
 375 380

aaa 1269

<210> 344

<211> 382

<212> PRT

<213> Corynebacterium glutamicum

<400> 344

Met Thr Ala Thr Tyr Thr Thr Glu Thr Ala Ile Asn Phe Leu Phe Leu
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Ser Glu Pro Asp Met Ile Ala Ala Gly Val Lys Asp Val Ala Gln Cys
 20 25 30

Val Asp Val Met Glu Glu Thr Leu Val Leu Leu Ala Gln Gly Asp Tyr
 35 40 45

Lys Met Ala Gly Leu Asn Ser Asn Ser His Gly Ala Met Ile Thr Phe
 50 55 60

Pro Glu Asn Pro Glu Phe Glu Gly Met Pro Lys Asp Gly Pro Asp Arg
 65 70 75 80

Arg Phe Met Ala Met Pro Ala Tyr Leu Gly Gly Arg Phe Lys Asn Thr
 85 90 95

Gly Val Lys Trp Tyr Gly Ser Asn Ala Glu Asn Lys Ala Ser Gly Leu
 100 105 110

Pro Arg Ser Ile His Thr Phe Val Leu Asn Asp Thr Val Thr Gly Ala
 115 120 125

Pro Lys Ala Ile Met Ser Ala Asn Leu Leu Ser Ala Tyr Arg Thr Gly
 130 135 140

Ala Val Pro Gly Val Gly Val Lys His Leu Ala Val Ala Asp Ala Thr
 145 150 155 160

Thr Leu Ala Val Val Gly Pro Gly Val Met Ala Lys Thr Ile Thr Glu
 165 170 175

Ala Cys Ile Ala Glu Arg Pro Gly Ile Thr Thr Ile Lys Ile Lys Gly
 180 185 190

Arg Ser Glu Arg Gly Ile Asn Ala Phe Ala Thr Trp Ala Leu Glu Lys
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 Phe Pro Glu Ile Glu Val Val Ala Val Gly Ser Glu Glu Asp Val Val
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 Lys Asp Ala Asp Ile Val Ile Ala Ala Thr Thr Thr Asp Ala Ala Gly
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 Ser Ser Ala Phe Pro Tyr Phe Lys Lys Glu Trp Leu Lys Pro Gly Ala
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 Leu Leu Leu Leu Pro Ala Ala Gly Arg Phe Asp Asp Ala Tyr Leu Leu
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 Asp Asp Ala Arg Leu Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp
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 Ala Glu Glu Tyr Gly Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly
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 Thr His Trp Tyr Asp Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys
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 Ile Thr Arg Glu Leu Leu Gly Gly Gly Val Pro Ala Gln Tyr Lys Asp
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 Glu Ser Trp Val Arg Lys Phe Ala Ser Gly Ala Gln Ala Arg His Asp
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